

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM BP DIRECT	GO:0006351--transcription, DNA-templated	205	15.29851	1.77E-08	BBX, ROB	1214	1955	16792	1.45041	7.34E-05	7.34E-05	3.30E-05
GOTERM BP DIRECT	GO:0006977--DNA damage response, signal transduction by p53 class mediator	20	1.492537	3.87E-08	E2F1, RBL	1214	62	16792	4.461923	1.60E-04	8.02E-05	7.21E-05
GOTERM BP DIRECT	GO:0007179--transforming growth factor beta receptor signaling pathway	23	1.716418	4.47E-07	PARD3, PI	1214	92	16792	3.45799	0.001851	6.17E-04	8.34E-04
GOTERM BP DIRECT	GO:0045893--positive regulation of transcription, DNA-templated	68	5.074627	1.80E-06	E2F1, CHU	1214	515	16792	1.826356	0.007423	0.001861	0.003353
GOTERM BP DIRECT	GO:0000086--G2M transition of mitotic cell cycle	27	2.014925	4.74E-06	CEP72, PP	1214	137	16792	2.726007	0.019473	0.003925	0.008848
GOTERM BP DIRECT	GO:0006468--protein phosphorylation	60	4.477612	8.78E-06	CDK19, N	1214	456	16792	1.819995	0.035762	0.006051	0.016385
GOTERM BP DIRECT	GO:1900740--positive regulation of protein insertion into mitochondrial membra	11	0.820896	2.94E-05	E2F1, YW	1214	30	16792	5.071719	0.114742	0.01276	0.054824
GOTERM BP DIRECT	GO:0035194--posttranscriptional gene silencing by RNA	6	0.447761	3.62E-05	AGO1, AG	1214	7	16792	11.85597	0.13946	0.018599	0.067559
GOTERM BP DIRECT	GO:0035280--miRNA loading onto RISC involved in gene silencing by miRNA	6	0.447761	3.62E-05	DICER1, I	1214	7	16792	11.85597	0.13946	0.018599	0.067559
GOTERM BP DIRECT	GO:0000122--negative regulation of transcription from RNA polymerase II prom	82	6.119403	4.16E-05	BACH1, E	1214	720	16792	1.575307	0.158416	0.018981	0.077574
GOTERM BP DIRECT	GO:0035278--miRNA mediated inhibition of translation	7	0.522388	8.87E-05	AGO1, AG	1214	12	16792	9.068644	0.30779	0.036118	0.165388
GOTERM BP DIRECT	GO:0071456--cellular response to hypoxia	19	1.41791	1.56E-04	E2F1, PPA	1214	96	16792	2.737576	0.476229	0.057096	0.290566
GOTERM BP DIRECT	GO:0051726--regulation of cell cycle	22	1.641791	2.07E-04	CDK19, E	1214	124	16792	2.454058	0.57677	0.069146	0.386145
GOTERM BP DIRECT	GO:0075733--intracellular transport of virus	13	0.970149	2.17E-04	NUP98, TS	1214	51	16792	3.525794	0.592633	0.066748	0.403266
GOTERM BP DIRECT	GO:0045892--negative regulation of transcription, RNA-templated	4	0.420985	2.17E-04	E2F1, PPA	1214	499	16792	1.635442	0.592599	0.062185	0.403625
GOTERM BP DIRECT	GO:0045944--positive regulation of transcription from RNA polymerase II prom	101	7.537313	2.54E-04	MORF4L2	1214	981	16792	1.424086	0.651896	0.067933	0.473696
GOTERM BP DIRECT	GO:0001701--in utero embryonic development	28	2.089552	4.30E-04	STIL, GJA	1214	187	16792	2.071096	0.831884	0.105458	0.799111
GOTERM BP DIRECT	GO:0016032--viral process	39	2.910448	4.80E-04	CCL1, CR	1214	299	16792	1.804169	0.863455	0.110525	0.891911
GOTERM BP DIRECT	GO:0006974--cellular response to DNA damage stimulus	30	2.238866	4.86E-04	ARMT1, X	1214	208	16792	1.994994	0.866494	0.105837	0.901948
GOTERM BP DIRECT	GO:0030512--negative regulation of transforming growth factor beta receptor sig	14	1.044776	5.61E-04	GLG1, W	1214	64	16792	3.025741	0.902268	0.115202	1.040936
GOTERM BP DIRECT	GO:0061418--regulation of transcription from RNA polymerase II promoter in re	9	0.671642	6.10E-04	BACH1, U	1214	28	16792	4.445897	0.920304	0.118805	1.131733
GOTERM BP DIRECT	GO:0003181--atrioventricular valve morphogenesis	6	0.447761	6.23E-04	BMP2, TG	1214	11	16792	7.544706	0.924613	0.115825	1.156458
GOTERM BP DIRECT	GO:0003148--outflow tract septum morphogenesis	8	0.597015	8.84E-04	GATA6, S	1214	23	16792	4.811117	0.97441	0.153476	1.635828
GOTERM BP DIRECT	GO:0016236--macroautophagy	15	1.194103	9.77E-04	LAMTOR1	1214	76	16792	2.739992	0.982599	0.161499	1.806369
GOTERM BP DIRECT	GO:0030308--negative regulation of cell growth	20	1.492537	0.01062	CDLBD2	1214	12	16792	2.286274	0.987776	0.167661	1.962273
GOTERM BP DIRECT	GO:0007050--cell cycle arrest	22	1.641791	0.01198	WNT10B	1214	141	16792	2.158178	0.99307	0.180349	2.123234
GOTERM BP DIRECT	GO:0018107--peptidyl-threonine phosphorylation	10	0.746269	0.01251	ACVR1B	1214	38	16792	3.63999	0.994419	0.180904	2.307534
GOTERM BP DIRECT	GO:0048147--negative regulation of fibroblast proliferation	9	0.671642	0.01275	BAX, TR1	1214	31	16792	4.01573	0.994558	0.177927	2.35218
GOTERM BP DIRECT	GO:0035556--intracellular signal transduction	47	3.507463	0.01362	ZBTB33, I	1214	403	16792	1.613157	0.996492	0.182806	2.511372
GOTERM BP DIRECT	GO:0046777--protein autophosphorylation	25	1.865672	0.01415	MAPKAP1	1214	172	16792	2.010459	0.997173	0.183206	2.60611
GOTERM BP DIRECT	GO:0090625--mRNA cleavage involved in gene silencing by siRNA	4	0.298507	0.01423	AGO1, AG	1214	4	16792	13.83196	0.997271	0.178644	2.621562
GOTERM BP DIRECT	GO:0035196--production of miRNAs involved in gene silencing by miRNA	5	0.373134	0.01498	DICER1, I	1214	8	16792	6.644975	0.998	0.181654	2.757564
GOTERM BP DIRECT	GO:0048015--phosphatidylinositol-mediated signaling	18	1.343284	0.01503	NRG4, FG	1214	106	16792	2.348823	0.998046	0.171708	2.76772
GOTERM BP DIRECT	GO:0046686--response to cadmium ion	8	0.597015	0.01526	CDKN1B	1214	25	16792	4.426227	0.998217	0.174535	2.809725
GOTERM BP DIRECT	GO:0060389--pathway-restricted SMAD protein phosphorylation	6	0.447761	0.01537	BMP2, SM	1214	13	16792	6.383982	0.998298	0.171001	2.828271
GOTERM BP DIRECT	GO:0031054--pre-miRNA processing	6	0.447761	0.01537	DICER1, I	1214	13	16792	6.383982	0.998298	0.171001	2.828271
GOTERM BP DIRECT	GO:0007507--heart development	26	1.940299	0.0154	PPAR, B	1214	183	16792	1.965197	0.998324	0.166905	2.834845
GOTERM BP DIRECT	GO:0006357--regulation of transcription from RNA polymerase II promoter	50	3.731343	0.01716	HPAR, F	1214	441	16792	1.568249	0.999192	0.179456	3.153088
GOTERM BP DIRECT	GO:0098609--cell-cell adhesion	34	2.537313	0.02215	PSP90AB	1214	271	16792	1.735375	0.999898	0.219994	3.051989
GOTERM BP DIRECT	GO:0014911--positive regulation of smooth muscle cell migration	7	0.522388	0.02253	NRP1, P	1214	20	16792	4.841186	0.999913	0.218148	4.120453
GOTERM BP DIRECT	GO:0016567--protein ubiquitination	42	3.134328	0.02389	BACH1, X	1214	359	16792	1.618224	0.999951	0.224507	4.363719
GOTERM BP DIRECT	GO:0002480--antigen processing and presentation of exogenous peptide antigen	5	0.373134	0.02542	LNPEP, H	1214	9	16792	7.684422	0.999974	0.231908	4.637802
GOTERM BP DIRECT	GO:0034629--cellular protein complex localization	5	0.373134	0.02542	NACC2, S	1214	9	16792	7.684422	0.999974	0.231908	4.637802
GOTERM BP DIRECT	GO:0000082--G1/S transition of mitotic cell cycle	17	1.268657	0.02577	PPP6C, PK	1214	102	16792	2.305327	0.999977	0.229683	4.700103
GOTERM BP DIRECT	GO:0009749--response to glucose	13	0.970149	0.03192	TXNIP, P	1214	68	16792	2.644345	0.999998	0.270632	5.187513
GOTERM BP DIRECT	GO:0035279--mRNA cleavage involved in gene silencing by miRNA	4	0.298507	0.03366	AGO1, AG	1214	5	16792	11.06557	0.999999	0.277534	6.096101
GOTERM BP DIRECT	GO:1905007--positive regulation of epithelial to mesenchymal transition involve	4	0.298507	0.03366	TGFBR1, I	1214	5	16792	11.06557	0.999999	0.277534	6.096101
GOTERM BP DIRECT	GO:0008283--cell proliferation	42	3.134328	0.0342	PTGES3, I	1214	366	16792	1.587274	0.999999	0.275914	6.191761
GOTERM BP DIRECT	GO:0000209--protein polyubiquitination	25	1.865672	0.03499	MKRN1, U	1214	184	16792	1.879342	1	0.27597	6.329448
GOTERM BP DIRECT	GO:0042147--retrograde transport, endosome to Golgi	13	0.970149	0.03615	STX6, AR	1214	69	16792	2.660222	1	0.278524	6.533808
GOTERM BP DIRECT	GO:0032880--regulation of protein localization	11	0.820896	0.03619	STX6, SU	1214	52	16792	2.925992	1	0.273718	6.539858
GOTERM BP DIRECT	GO:0034644--cellular response to UV	10	0.746269	0.03681	USP28, N	1214	44	16792	3.143627	1	0.272777	6.648148
GOTERM BP DIRECT	GO:0060412--ventricular septum morphogenesis	8	0.597015	0.03843	SMAD7, T	1214	29	16792	3.815713	1	0.278044	6.931132
GOTERM BP DIRECT	GO:0032092--positive regulation of protein binding	12	0.895522	0.03927	HSP90AB	1214	61	16792	2.721041	1	0.278366	7.076771
GOTERM BP DIRECT	GO:0006355--regulation of transcription, DNA-templated	136	10.14925	0.04261	RALY, MC	1214	1504	16792	1.250762	1	0.293312	7.657639
GOTERM BP DIRECT	GO:0006915--apoptotic process	59	4.420985	0.04496	DLG1, IER	1214	567	16792	1.439305	1	0.30184	8.063319
GOTERM BP DIRECT	GO:0032480--negative regulation of type I interferon production	8	0.597015	0.04705	MAVS, CY	1214	30	16792	3.688523	1	0.308548	8.422718
GOTERM BP DIRECT	GO:0045165--cell fate commitment	10	0.746269	0.05025	SPRY2, W	1214	46	16792	3.006948	1	0.320749	8.969453
GOTERM BP DIRECT	GO:0000186--activation of MAPK activity	10	0.746269	0.05025	MAP3K5	1214	46	16792	3.006948	1	0.320749	8.969453
GOTERM BP DIRECT	GO:0090263--positive regulation of canonical Wnt signaling pathway	18	1.343284	0.05065	FZD9, CA	1214	120	16792	2.074794	1	0.347943	10.042
GOTERM BP DIRECT	GO:0050927--positive regulation of positive chemotaxis	5	0.373134	0.05094	S1PR1, F3	1214	11	16792	6.287255	1	0.355873	10.49129
GOTERM BP DIRECT	GO:0007223--Wnt signaling pathway, calcium modulating pathway	9	0.671642	0.05094	PLSCR1, A	1214	39	16792	3.191991	1	0.352008	10.5311
GOTERM BP DIRECT	GO:0006919--activation of cysteine-type endopeptidase activity involved in apo	14	1.044776	0.06333	DLL1, AC	1214	83	16792	2.333102	1	0.364986	11.17585
GOTERM BP DIRECT	GO:0016477--cell migration	23	1.716418	0.06345	FNML3, A	1214	172	16792	1.849623	1	0.360646	11.19671
GOTERM BP DIRECT	GO:0048681--negative regulation of axon regeneration	4	0.298507	0.06637	EPHA4, C	1214	6	16792	9.221307	1	0.35701	11.23947
GOTERM BP DIRECT	GO:0010862--positive regulation of pathway-restricted SMAD protein phosphor	10	0.746269	0.06721	ACVR1B	1214	48	16792	2.881658	1	0.367667	11.8211
GOTERM BP DIRECT	GO:0007032--endosome organization	8	0.597015	0.06857	STX6, TM	1214	32	16792	3.65739	1	0.368804	12.04694
GOTERM BP DIRECT	GO:0030335--positive regulation of cell migration	24	1.791045	0.07044	BMP2, ST	1214	184	16792	1.804169	1	0.371987	12.35455
GOTERM BP DIRECT	GO:0042787--protein ubiquitination involved in ubiquitin-dependent protein cat	21	1.567146	0.07093	MYLIP, A	1214	153	16792	1.898504	1	0.369423	12.43515
GOTERM BP DIRECT	GO:0034976--response to endoplasmic reticulum stress	13	0.970149	0.07201	PDI3A, T	1214	75	16792	2.397574	1	0.369321	12.61252
GOTERM BP DIRECT	GO:1900034--regulation of cellular response to heat	13	0.970149	0.07201	PTGES3, I	1214	75	16792	2.397574	1	0.369321	12.61252
GOTERM BP DIRECT	GO:0006914--autophagy	19	1.41791	0.07249	HMGBl, F	1214	133	16792	1.975994	1	0.366818	12.69095
GOTERM BP DIRECT	GO:0051301--cell division	39	2.910448	0.07771	CDK19, M	1214	350					

GOTERM BP DIRECT	GO:003032--lamellipodium assembly	7	0.522388	0.021695	ABLIM1, I	1214	31	16792	3.123346	1	0.573992	33.58011
GOTERM BP DIRECT	GO:0001836--release of cytochrome c from mitochondria	6	0.447761	0.021982	FZD9, DN	1214	23	16792	3.608338	1	0.580787	33.94318
GOTERM BP DIRECT	GO:0016239--positive regulation of macroautophagy	6	0.447761	0.021982	HIF1A, UL	1214	23	16792	3.608338	1	0.580787	33.94318
GOTERM BP DIRECT	GO:0006511--ubiquitin-dependent protein catabolic process	22	1.641791	0.02239	NPLC4, I	1214	182	16792	1.671995	1	0.584139	34.45493
GOTERM BP DIRECT	GO:0070102--interleukin-6-mediated signaling pathway	4	0.298507	0.022708	GAB1, SM	1214	9	16792	6.147538	1	0.585959	34.85213
GOTERM BP DIRECT	GO:0008354--germ cell migration	4	0.298507	0.022708	TGFBR1, I	1214	9	16792	6.147538	1	0.585959	34.85213
GOTERM BP DIRECT	GO:2000188--regulation of cholesterol homeostasis	4	0.298507	0.022708	RALY, NR	1214	9	16792	6.147538	1	0.585959	34.85213
GOTERM BP DIRECT	GO:0045184--establishment of protein localization	8	0.597015	0.023013	RCC2, NP	1214	40	16792	2.766392	1	0.587524	35.23054
GOTERM BP DIRECT	GO:0043123--positive regulation of I-kappaB kinase/NF-kappaB signaling	20	1.492537	0.023418	MYB, F2	1214	161	16792	1.718256	1	0.590633	35.72924
GOTERM BP DIRECT	GO:0001666--response to hypoxia	21	1.567164	0.02358	BMP2, CA	1214	172	16792	1.688786	1	0.589881	35.92831
GOTERM BP DIRECT	GO:0000165--MAPK cascade	29	2.164179	0.024202	NRG4, CA	1214	262	16792	1.531019	1	0.596244	36.68566
GOTERM BP DIRECT	GO:0010628--positive regulation of gene expression	29	2.164179	0.024202	ELF1, PPA	1214	262	16792	1.531019	1	0.596244	36.68566
GOTERM BP DIRECT	GO:0051895--negative regulation of focal adhesion assembly	5	0.373134	0.024459	DLC1, RC	1214	16	16792	4.322488	1	0.596895	36.99523
GOTERM BP DIRECT	GO:1904355--positive regulation of telomere capping	5	0.373134	0.024459	MMPK1, M	1214	16	16792	4.322488	1	0.596895	36.99523
GOTERM BP DIRECT	GO:1900745--positive regulation of p38MAPK cascade	5	0.373134	0.024459	MMP3K5, I	1214	16	16792	4.322488	1	0.596895	36.99523
GOTERM BP DIRECT	GO:0032924--activin receptor signaling pathway	5	0.373134	0.024459	ACVR1B, I	1214	16	16792	4.322488	1	0.596895	36.99523
GOTERM BP DIRECT	GO:0032212--positive regulation of telomere maintenance via telomerase	7	0.522388	0.025119	MMPK1, M	1214	32	16792	3.025741	1	0.603544	37.78536
GOTERM BP DIRECT	GO:0010506--regulation of autophagy	9	0.671642	0.025805	HMG1B, I	1214	50	16792	2.489753	1	0.610359	38.59717
GOTERM BP DIRECT	GO:0046907--intracellular transport	6	0.447761	0.026161	BLOC1S4, I	1214	24	16792	3.457999	1	0.612283	39.01479
GOTERM BP DIRECT	GO:0048041--focal adhesion assembly	6	0.447761	0.026161	DLC1, PD	1214	24	16792	3.457999	1	0.612283	39.01479
GOTERM BP DIRECT	GO:0006366--transcription from RNA polymerase II promoter	50	3.731343	0.027181	BACH1, F	1214	513	16792	1.348144	1	0.623377	40.19528
GOTERM BP DIRECT	GO:0048661--positive regulation of smooth muscle cell proliferation	10	0.746269	0.027422	IRAK4, S1	1214	60	16792	2.305327	1	0.62354	40.4712
GOTERM BP DIRECT	GO:0031647--regulation of protein stability	11	0.820896	0.028205	MMPK1, U	1214	70	16792	2.173594	1	0.630943	41.35921
GOTERM BP DIRECT	GO:0007265--Ras protein signal transduction	11	0.820896	0.028205	NRAS, US	1214	70	16792	2.173594	1	0.630943	41.35921
GOTERM BP DIRECT	GO:0003104--positive regulation of glomerular filtration	3	0.223881	0.028358	PDGF, F	1214	4	16792	10.37397	1	0.629876	41.53058
GOTERM BP DIRECT	GO:0008356--asymmetric cell division	4	0.223881	0.028358	ACTR2, P	1214	4	16792	10.37397	1	0.629876	41.53058
GOTERM BP DIRECT	GO:1990086--lens fiber cell apoptotic process	3	0.223881	0.028358	ETF1, E2F	1214	4	16792	10.37397	1	0.629876	41.53058
GOTERM BP DIRECT	GO:0033631--cell-cell adhesion mediated by integrin	3	0.223881	0.028358	ITGA5, NI	1214	4	16792	10.37397	1	0.629876	41.53058
GOTERM BP DIRECT	GO:1901031--regulation of response to reactive oxygen species	3	0.223881	0.028358	SES2, SE	1214	4	16792	10.37397	1	0.629876	41.53058
GOTERM BP DIRECT	GO:0032392--DNA geometric change	3	0.223881	0.028358	HMG1B, I	1214	4	16792	10.37397	1	0.629876	41.53058
GOTERM BP DIRECT	GO:0032909--regulation of transforming growth factor beta2 production	3	0.223881	0.028358	HIF1A, SG	1214	4	16792	10.37397	1	0.629876	41.53058
GOTERM BP DIRECT	GO:0010718--positive regulation of epithelial to mesenchymal transition	7	0.522388	0.028884	BMP2, TG	1214	33	16792	2.934052	1	0.633692	42.11903
GOTERM BP DIRECT	GO:0070059--intrinsic apoptotic signaling pathway in response to endoplasmic r	7	0.522388	0.028884	MMP3K5, I	1214	33	16792	2.934052	1	0.633692	42.11903
GOTERM BP DIRECT	GO:0016055--Wnt signaling pathway	22	1.641791	0.029156	CSNK1A1, I	1214	187	16792	1.627289	1	0.634153	42.41982
GOTERM BP DIRECT	GO:0008285--negative regulation of cell proliferation	40	0.985075	0.029726	DLC1, TSC	1214	396	16792	1.397168	1	0.63839	43.04806
GOTERM BP DIRECT	GO:0048208--COPII vesicle coating	10	0.746269	0.030183	SEC23A, F	1214	61	16792	2.267535	1	0.641102	43.54576
GOTERM BP DIRECT	GO:0031589--cell-substrate adhesion	5	0.373134	0.030201	PPARD, PI	1214	17	16792	4.068224	1	0.638378	43.56595
GOTERM BP DIRECT	GO:2000811--negative regulation of anoikis	5	0.373134	0.030201	CAV1, MC	1214	17	16792	4.068224	1	0.638378	43.56595
GOTERM BP DIRECT	GO:0033160--positive regulation of protein import into nucleus, translocation	4	0.298507	0.030728	HSP90AB, I	1214	10	16792	5.532784	1	0.641899	44.13446
GOTERM BP DIRECT	GO:0046902--regulation of mitochondrial membrane permeability	4	0.298507	0.030728	BCL2, TP	1214	10	16792	5.532784	1	0.641899	44.13446
GOTERM BP DIRECT	GO:0042118--endothelial cell activation	4	0.298507	0.030728	TGFBR1, I	1214	10	16792	5.532784	1	0.641899	44.13446
GOTERM BP DIRECT	GO:0097192--extrinsic apoptotic signaling pathway in absence of ligand	7	0.522388	0.033003	MCL1, BA	1214	34	16792	2.847757	1	0.665656	46.53104
GOTERM BP DIRECT	GO:0001837--epithelial to mesenchymal transition	7	0.522388	0.033003	FAM83D, I	1214	34	16792	2.847757	1	0.665656	46.53104
GOTERM BP DIRECT	GO:0060395--SMAD protein signal transduction	10	0.746269	0.033131	LNPEP, BI	1214	62	16792	2.230961	1	0.66243	46.66347
GOTERM BP DIRECT	GO:0042981--regulation of apoptotic process	24	1.791045	0.034587	TNFRSF21, I	1214	213	16792	1.585831	1	0.67738	48.14136
GOTERM BP DIRECT	GO:0045727--positive regulation of translation	9	0.671642	0.035272	MMPK1, E	1214	53	16792	2.348823	1	0.681846	48.82362
GOTERM BP DIRECT	GO:0040008--regulation of growth	9	0.671642	0.035272	MORF4L1, I	1214	53	16792	2.348823	1	0.681846	48.82362
GOTERM BP DIRECT	GO:0045930--negative regulation of mitotic cell cycle	6	0.447761	0.035955	CDKN1B, I	1214	26	16792	3.191991	1	0.686171	49.49585
GOTERM BP DIRECT	GO:0006457--protein folding	21	1.567164	0.035989	HSP90AB, I	1214	180	16792	1.613729	1	0.68375	49.52865
GOTERM BP DIRECT	GO:0060070--canonical Wnt signaling pathway	12	0.895522	0.036027	FZD9, TBI	1214	83	16792	1.999802	1	0.681388	49.56531
GOTERM BP DIRECT	GO:0010039--response to iron	5	0.373134	0.036672	CND1B, B	1214	18	16792	3.842211	1	0.685245	50.19134
GOTERM BP DIRECT	GO:0045089--positive regulation of innate immune response	5	0.373134	0.036672	POLR3G, I	1214	18	16792	3.842211	1	0.685245	50.19134
GOTERM BP DIRECT	GO:0036120--cellular response to platelet-derived growth factor stimulus	5	0.373134	0.036672	CREB1, H	1214	18	16792	3.842211	1	0.685245	50.19134
GOTERM BP DIRECT	GO:0010501--RNA secondary structure unwinding	8	0.597015	0.036906	DDX19A, A	1214	44	16792	2.514902	1	0.6849	50.41669
GOTERM BP DIRECT	GO:0023014--signal transduction by protein phosphorylation	8	0.597015	0.036906	PAK6, AC	1214	44	16792	2.514902	1	0.6849	50.41669
GOTERM BP DIRECT	GO:0010629--negative regulation of gene expression	17	1.268657	0.038454	DLDR, PD	1214	137	16792	1.716375	1	0.697421	51.88256
GOTERM BP DIRECT	GO:0006413--translational initiation	17	1.268657	0.038454	RPL17, RF	1214	137	16792	1.716375	1	0.697421	51.88256
GOTERM BP DIRECT	GO:0048146--positive regulation of fibroblast proliferation	9	0.671642	0.038888	CNNB1, E	1214	54	16792	2.305327	1	0.69891	52.28606
GOTERM BP DIRECT	GO:0090161--Golgi ribbon formation	4	0.298507	0.040029	STX6, ST	1214	11	16792	5.029804	1	0.706929	53.33192
GOTERM BP DIRECT	GO:0031571--mitotic G1 DNA damage checkpoint	4	0.298507	0.040029	RPA2, CC	1214	11	16792	5.029804	1	0.706929	53.33192
GOTERM BP DIRECT	GO:0060213--positive regulation of nuclear-transcribed mRNA poly(A) tail shor	4	0.298507	0.040029	BTG2, AG	1214	11	16792	5.029804	1	0.706929	53.33192
GOTERM BP DIRECT	GO:0030278--regulation of ossification	4	0.298507	0.040029	MMPK1, E	1214	11	16792	5.029804	1	0.706929	53.33192
GOTERM BP DIRECT	GO:0030514--negative regulation of BMP signaling pathway	8	0.597015	0.041086	NBL1, WN	1214	45	16792	2.459015	1	0.713885	54.28091
GOTERM BP DIRECT	GO:0008542--visual learning	8	0.597015	0.041086	AP1, HIF1	1214	45	16792	2.459015	1	0.713885	54.28091
GOTERM BP DIRECT	GO:0007029--endoplasmic reticulum organization	6	0.447761	0.041593	DNM1L, A	1214	27	16792	3.073769	1	0.715806	54.73021
GOTERM BP DIRECT	GO:0055007--cardiac muscle cell differentiation	6	0.447761	0.041593	BMP2, GA	1214	27	16792	3.073769	1	0.715806	54.73021
GOTERM BP DIRECT	GO:0007611--learning or memory	7	0.522388	0.042335	FZD9, EG	1214	36	16792	2.689548	1	0.719715	55.37957
GOTERM BP DIRECT	GO:0042059--negative regulation of epidermal growth factor receptor signaling p	7	0.522388	0.042335	SPRY2, R1	1214	36	16792	2.689548	1	0.719715	55.37957
GOTERM BP DIRECT	GO:0016925--protein sumoylation	15	1.119403	0.04527	NUP98, EC	1214	117	16792	1.773328	1	0.718842	55.94595
GOTERM BP DIRECT	GO:0006897--endocytosis	17	1.268657	0.043047	DNM1L, L	1214	139	16792	1.691769	1	0.720773	55.99458
GOTERM BP DIRECT	GO:0042276--error-prone recombination	5	0.373134	0.043877	RPA2, RF	1214	19	16792	6.33999	1	0.725233	56.70061
GOTERM BP DIRECT	GO:0045672--positive regulation of osteoclast differentiation	5	0.373134	0.043877	IL23R, CR	1214	19	16792	6.33999	1	0.725233	56.70061
GOTERM BP DIRECT	GO:0070987--error-free translation synthesis	5	0.373134	0.043877	RPA2, NP1	1214	19	16792	6.33999	1	0.725233	56.70061
GOTERM BP DIRECT	GO:0006895--Golgi to endosome transport	5	0.373134	0.043877	TGOLN2, I	1214	19	16792	6.33999	1	0.725233	56.70061
GOTERM BP DIRECT	GO:0006089--lactate metabolic process	3	0.223881	0.045019	LDHB, HI	1214	5	16792	8.299176	1	0.732089	57.65547
GOTERM BP DIRECT	GO:0043550--regulation of lipid kinase activity	3	0.223881	0.045019	RBL2, RB	1214	5	16792	8.299176	1	0.732089	57.65547
GOTERM BP DIRECT	GO:1990314--cellular response to insulin-like growth factor stimulus	3	0.223881	0.045019	SLC25A33, I	1214	5	16792	8.299176	1	0.732089	57.65547
GOTERM BP DIRECT	GO:0006686--sphingomyelin biosynthetic process	3	0.223881	0.045019	SAMD8, S	1214	5	16792	8.299176	1	0.732089	57.65547
GOTERM BP DIRECT	GO:0033289--atrial septum primum morphogenesis	3	0.223881	0.045019	SOX4, AC	1214	5	16792	8.299176	1	0.732089	57.65547
GOTERM BP DIRECT	GO:0016575--histone deacetylation	8	0.597015	0.045561	MORF4L1, I	1214	46	16792	2.405558	1	0.733987	58.10176
GOTERM BP DIRECT	GO:0016197--endosomal transport	10	0.746269	0.046905	AP5B1, TS	1214	66	16792	2.095752	1	0.742036	59.18855
GOTERM BP DIRECT	GO:0006367--transcription initiation from RNA polymerase II promoter	18	1.343284	0.047702	E2F2, PPA	1214	152	16792	1.673995	1	0.745693	59.82047
GOTERM BP DIRECT	GO:0045931--positive regulation of mitotic cell cycle	6	0.447761	0.047734	CNNB1, E	1214	28	16792	2.963992	1	0.743591	59.84631
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GOTERM BP DIRECT	GO:0006207--de novo' pyrimidine nucleobase biosynthetic process	3	0.223881	0.064343	DHODH, C	1214	6	16792	6.91598	1	0.806268	71.0816
GOTERM BP DIRECT	GO:1903672--positive regulation of sprouting angiogenesis	3	0.223881	0.064343	HMG1B, I	1214	6	16792	6.91598	1	0.806268	71.0816
GOTERM BP DIRECT	GO:0007346--regulation of mitotic cell cycle	7	0.522388	0.065546	CYLD, CE	1214	40	16792	2.420593	1	0.810455	71.7674
GOTERM BP DIRECT	GO:0043280--positive regulation of cysteine-type endopeptidase activity involve	7	0.522388	0.065546	HMG1B, M	1214	40	16792	2.420593	1	0.810455	71.7674
GOTERM BP DIRECT	GO:0045669--positive regulation of osteoblast differentiation	9	0.671642	0.065756	BMP2, W	1214	60	16792	2.074794	1	0.809639	71.88568
GOTERM BP DIRECT	GO:0007411--axon guidance	18	1.343284	0.067261	ZNF280B, C	1214	159	16792	1.565882	1	0.815149	72.71838
GOTERM BP DIRECT	GO:0002576--platelet degranulation	13	0.907149	0.06765	PHACTR2	1214	103	16792	1.745781	1	0.815194	72.9299
GOTERM BP DIRECT	GO:0071260--cellular response to mechanical stimulus	10	0.746269	0.068855	SCL38A2, C	1214	71	16792	1.948163	1	0.819079	73.57543
GOTERM BP DIRECT	GO:1990090--cellular response to nerve growth factor stimulus	6	0.447761	0.069202	E2F1, APP	1214	31	16792	2.677154	1	0.818908	73.75859
GOTERM BP DIRECT	GO:0010332--response to gamma radiation	6	0.447761	0.069202	BAX, BCL	1214	31	16792	2.677154	1	0.818908	73.75859
GOTERM BP DIRECT	GO:0043552--positive regulation of phosphatidylinositol 3-kinase activity	6	0.447761	0.069202	PDGF, S	1214	31	16792	2.677154	1	0.818908	73.75859
GOTERM BP DIRECT	GO:1904886--beta-catenin destruction complex disassembly	5	0.373134	0.069865	CSNK1A1	1214	22	16792	3.143627	1	0.820192	74.10496
GOTERM BP DIRECT	GO:0006470--protein dephosphorylation	15	1.119403	0.070697	PPP2R1A, C	1214	126	16792	1.646662	1	0.822219	74.53389
GOTERM BP DIRECT	GO:0006950--response to stress	9	0.671642	0.071126	HSP90AB	1214	61	16792	2.040781	1	0.822404	74.75196
GOTERM BP DIRECT	GO:0007219--Notch signaling pathway	14	1.044776	0.071383	DTX4, AP	1214	115	16792	1.683891	1	0.821825	74.88208
GOTERM BP DIRECT	GO:0001649--osteoblast differentiation	13	0.970149	0.071699	BMP3, BV	1214	104	16792	1.728995	1	0.821511	75.0409
GOTERM BP DIRECT	GO:0031397--negative regulation of protein ubiquitination	7	0.522388	0.072312	CAV1, N4	1214	41	16792	2.361554	1	0.822515	75.34668
GOTERM BP DIRECT	GO:0044255--cellular lipid metabolic process	7	0.522388	0.072312	NR1H2, T1	1214	41	16792	2.361554	1	0.822515	75.34668
GOTERM BP DIRECT	GO:1902043--positive regulation of extrinsic apoptotic signaling pathway via c	4	0.298507	0.075204	PEA15, SK	1214	14	16792	3.951989	1	0.833318	76.74161
GOTERM BP DIRECT	GO:0042176--regulation of protein catabolic process	4	0.298507	0.075204	FAM83D, C	1214	14	16792	3.951989	1	0.833318	76.74161
GOTERM BP DIRECT	GO:0010801--negative regulation of peptidyl-threonine phosphorylation	4	0.298507	0.075204	SPRY2, P	1214	14	16792	3.951989	1	0.833318	76.74161
GOTERM BP DIRECT	GO:0003407--neural retina development	4	0.298507	0.075204	ATP2B1, F	1214	14	16792	3.951989	1	0.833318	76.74161
GOTERM BP DIRECT	GO:2001241--positive regulation of extrinsic apoptotic signaling pathway in abs	4	0.298507	0.075204	PPP2R1A, C	1214	14	16792	3.951989	1	0.833318	76.74161
GOTERM BP DIRECT	GO:0051016--barbed-end actin filament capping	4	0.298507	0.075204	TRIOBP, I	1214	14	16792	3.951989	1	0.833318	76.74161
GOTERM BP DIRECT	GO:0030194--positive regulation of blood coagulation	4	0.298507	0.075204	SERPINE1	1214	14	16792	3.951989	1	0.833318	76.74161
GOTERM BP DIRECT	GO:0032461--positive regulation of protein oligomerization	4	0.298507	0.075204	SH3GLB1, C	1214	14	16792	3.951989	1	0.833318	76.74161
GOTERM BP DIRECT	GO:0071425--hematopoietic stem cell proliferation	4	0.298507	0.075204	WNT1, W	1214	14	16792	3.951989	1	0.833318	76.74161
GOTERM BP DIRECT	GO:0006461--protein complex assembly	14	1.044776	0.075346	PPP2R1A, C	1214	116	16792	1.669375	1	0.83212	76.80834
GOTERM BP DIRECT	GO:0046854--phosphatidylinositol phosphorylation	12	0.895522	0.075976	NRG4, FG	1214	94	16792	1.765782	1	0.833073	77.10143
GOTERM BP DIRECT	GO:1900026--positive regulation of substrate adhesion-dependent cell spreading	6	0.447761	0.077366	TRIOBP, /	1214	32	16792	2.593493	1	0.837061	77.73537
GOTERM BP DIRECT	GO:0061024--membrane organization	6	0.447761	0.077366	HNPEP, Y	1214	32	16792	2.593493	1	0.837061	77.73537
GOTERM BP DIRECT	GO:0042220--response to cocaine	6	0.447761	0.077366	HSP90AB	1214	32	16792	2.593493	1	0.837061	77.73537
GOTERM BP DIRECT	GO:0045595--regulation of cell differentiation	6	0.447761	0.077366	SPRY2, PI	1214	32	16792	2.593493	1	0.837061	77.73537
GOTERM BP DIRECT	GO:0001974--blood vessel remodeling	6	0.447761	0.077366	EPAS1, B	1214	32	16792	2.593493	1	0.837061	77.73537
GOTERM BP DIRECT	GO:0007259--JAK-STAT cascade	6	0.447761	0.077366	IFNAR2, F	1214	32	16792	2.593493	1	0.837061	77.73537
GOTERM BP DIRECT	GO:0043547--positive regulation of GTPase activity	51	3.80597	0.077758	DLR1, NR	1214	565	16792	1.248549	1	0.837014	77.91105
GOTERM BP DIRECT	GO:0009791--post-embryonic development	10	0.746269	0.079171	SGPL1, TC	1214	73	16792	1.894789	1	0.840949	78.53421
GOTERM BP DIRECT	GO:0050729--positive regulation of inflammatory response	10	0.746269	0.079171	CDK19, C	1214	73	16792	1.894789	1	0.840949	78.53421
GOTERM BP DIRECT	GO:0001658--branching involved in ureteric bud morphogenesis	7	0.522388	0.079462	WNT1, BA	1214	42	16792	2.305327	1	0.840499	78.66042
GOTERM BP DIRECT	GO:0032967--positive regulation of collagen biosynthetic process	5	0.373134	0.079946	AMELX, I	1214	23	16792	3.006948	1	0.840789	78.68649
GOTERM BP DIRECT	GO:0006479--protein methylation	5	0.373134	0.079946	ARMT1, B	1214	23	16792	3.006948	1	0.840789	78.68649
GOTERM BP DIRECT	GO:0000083--regulation of transcription involved in G1/S transition of mitotic c	5	0.373134	0.079946	BACH1, R	1214	23	16792	3.006948	1	0.840789	78.68649
GOTERM BP DIRECT	GO:0071398--cellular response to fatty acid	5	0.373134	0.079946	CENB1, E	1214	23	16792	3.006948	1	0.840789	78.68649
GOTERM BP DIRECT	GO:0030307--positive regulation of cell growth	11	0.820896	0.080332	IFG42, C	1214	84	16792	1.811328	1	0.840708	79.03342
GOTERM BP DIRECT	GO:0030336--negative regulation of cell migration	12	0.895522	0.08061	DLR1, AD	1214	95	16792	1.747195	1	0.840217	79.15118
GOTERM BP DIRECT	GO:0009611--response to wounding	9	0.671642	0.082643	FZL3, W	1214	63	16792	1.975994	1	0.846244	79.94665
GOTERM BP DIRECT	GO:0043066--negative regulation of apoptotic process	42	3.134328	0.083642	ARL6IP1, P	1214	455	16792	1.276796	1	0.848349	80.39732
GOTERM BP DIRECT	GO:0001525--angiogenesis	23	1.716418	0.084488	SCL12A6, C	1214	223	16792	1.426615	1	0.849868	80.73218
GOTERM BP DIRECT	GO:0000187--activation of MAPK activity	13	0.970149	0.084767	BMP2, M	1214	107	16792	1.680519	1	0.849378	80.84145
GOTERM BP DIRECT	GO:0009636--response to toxic substance	11	0.820896	0.085463	MAPK1, V	1214	85	16792	1.790018	1	0.85035	81.11561
GOTERM BP DIRECT	GO:0010586--miRNA metabolic process	3	0.223881	0.085859	AGO1, AG	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0008064--regulation of actin polymerization or depolymerization	3	0.223881	0.085859	SH2, AR1	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0072643--interferon-gamma secretion	3	0.223881	0.085859	BTN3A1, I	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0000578--embryonic axis specification	3	0.223881	0.085859	STIL, WN	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0071679--commissural neuron axon guidance	3	0.223881	0.085859	NRP1, VE	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0019885--antigen processing and presentation of endogenous peptide antigen	3	0.223881	0.085859	HLA-A, EI	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0048842--positive regulation of axon extension involved in axon guidance	3	0.223881	0.085859	NRP1, VE	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0001844--protein insertion into mitochondrial membrane involved in apopto	3	0.223881	0.085859	BAX, PM	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0006029--proteoglycan metabolic process	3	0.223881	0.085859	BMP2, PP	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0048102--autophagic cell death	3	0.223881	0.085859	CDKN1B, C	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0032287--peripheral nervous system myelin maintenance	3	0.223881	0.085859	MPP5, ND	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0060982--coronary artery morphogenesis	3	0.223881	0.085859	NRP1, TG	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0034616--response to laminar fluid shear stress	3	0.223881	0.085859	SMAD7, S	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0071455--cellular response to hyperoxia	3	0.223881	0.085859	SM1, PP	1214	7	16792	5.927983	1	0.850269	81.26337
GOTERM BP DIRECT	GO:0051297--centrosome organization	6	0.447761	0.086023	CEP120, B	1214	33	16792	2.514902	1	0.84939	81.32616
GOTERM BP DIRECT	GO:1902042--negative regulation of extrinsic apoptotic signaling pathway via c	6	0.447761	0.086023	PEA15, AF	1214	33	16792	2.514902	1	0.84939	81.32616
GOTERM BP DIRECT	GO:0048538--thymus development	7	0.522388	0.086994	MAPK1, M	1214	43	16792	2.251714	1	0.85129	81.69273
GOTERM BP DIRECT	GO:0000184--nuclear-transcribed mRNA catabolic process, nonsense-mediated c	14	1.044776	0.088073	RPL17, PP	1214	119	16792	1.627289	1	0.853514	82.09234
GOTERM BP DIRECT	GO:0032436--positive regulation of proteasomal ubiquitin-dependent protein cat	9	0.671642	0.08879	CSNK1A1	1214	64	16792	1.945119	1	0.854489	82.35286
GOTERM BP DIRECT	GO:0042632--cholesterol homeostasis	9	0.671642	0.08879	NR1H2, A	1214	64	16792	1.945119	1	0.854489	82.35286
GOTERM BP DIRECT	GO:0008631--intrinsic apoptotic signaling pathway in response to oxidative stre	4	0.298507	0.089147	MAP3K5, C	1214	15	16792	3.688523	1	0.854271	82.48152
GOTERM BP DIRECT	GO:0030330--DNA damage response, signal transduction by p53 class mediator	4	0.298507	0.089147	TP53, NDI	1214	15	16792	3.688523	1	0.854271	82.48152
GOTERM BP DIRECT	GO:0032793--positive regulation of CREB transcription factor activity	4	0.298507	0.089147	RPS6KA5, C	1214	15	16792	3.688523	1	0.854271	82.48152
GOTERM BP DIRECT	GO:0035024--negative regulation of Rho protein signal transduction	4	0.298507	0.089147	DLG1, AR	1214	15	16792	3.688523	1	0.854271	82.48152
GOTERM BP DIRECT	GO:0006122--mitochondrial electron transport, ubiquinol to cytochrome c	4	0.298507	0.089147	UQCRC1, C	1214	15	16792	3.688523	1	0.854271	82.48152
GOTERM BP DIRECT	GO:0007623--circadian rhythm	10	0.746269	0.090376	NONO, CF	1214	75	16792	1.844261	1	0.856897	82.91736
GOTERM BP DIRECT	GO:0045737--positive regulation of cyclin-dependent protein serine/threonine kin	5	0.373134	0.090702	CND1, C	1214	24	16792	2.881658	1	0.856575	83.03131
GOTERM BP DIRECT	GO:0030010--establishment of cell polarity	5	0.373134	0.090702	UST, WW	1214	24	16792	2.881658	1	0.856575	83.03131
GOTERM BP DIRECT	GO:0043524--negative regulation of neuron apoptotic process	15	1.119403	0.095072	HSP90AB	1214	132	16792	1.571814	1	0.868707	84.48974
GOTERM BP DIRECT	GO:0001932--regulation of protein phosphorylation	6	0.447761	0.095165	CDC8C	1214	34	16792	2.440934	1	0.867674	84.51925
GOTERM BP DIRECT	GO:0035019--somatic stem cell population maintenance	9	0.671642	0.095194	EPAS1, KI	1214	65	16792	1.915195	1	0.866456	84.52871
GOTERM BP DIRECT	GO:0006021--palate development	10	0.746269	0.096311	SGPL1, SU	1214	76	16792	1.819995	1	0.868447	84.88118
GOTERM BP DIRECT	GO:0019882--antigen processing and presentation	8	0.597015	0.099638	MICB, RA	1214	55	16792	2.011922	1		

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM CC	DIRECT GO:0005829--cytosol	357	26.64179	9.06E-20	TGOLN2,	1269	3315	18224	1.54656	6.35E-17	6.35E-17	1.37E-16
GOTERM CC	DIRECT GO:0005654--nucleoplasm	306	22.83582	6.43E-18	TGOLN2,	1269	2784	18224	1.578463	4.50E-15	2.25E-15	9.70E-15
GOTERM CC	DIRECT GO:0016020--membrane	228	17.01493	2.35E-10	LDHB, DY	1269	2200	18224	1.488313	1.65E-07	5.49E-08	3.55E-07
GOTERM CC	DIRECT GO:0005634--nucleus	475	35.44776	7.46E-10	DLC1, RP1	1269	5415	18224	1.259729	5.22E-07	1.31E-07	1.13E-06
GOTERM CC	DIRECT GO:0005737--cytoplasm	450	33.58209	3.67E-08	DLC1, LD	1269	5222	18224	1.237536	2.57E-05	5.14E-06	5.54E-05
GOTERM CC	DIRECT GO:0005925--focal adhesion	53	3.955224	4.97E-06	PVR, KIF2	1269	391	18224	1.94662	0.003473	5.80E-04	0.007494
GOTERM CC	DIRECT GO:0048471--perinuclear region of cytoplasm	74	5.522388	6.91E-06	SEPT2, NI	1269	621	18224	1.711284	0.004822	6.90E-04	0.010413
GOTERM CC	DIRECT GO:0043231--intracellular membrane-bounded org	67	5	1.59E-05	ACOX1, A	1269	558	18224	1.724339	0.011053	0.001388	0.023942
GOTERM CC	DIRECT GO:0005794--Golgi apparatus	91	6.791045	6.91E-05	TGOLN2,	1269	863	18224	1.514303	0.0472	0.005358	0.10411
GOTERM CC	DIRECT GO:0016605--PML body	19	1.41791	1.29E-04	MKNK2, T	1269	98	18224	2.784259	0.086107	0.008964	0.193797
GOTERM CC	DIRECT GO:0005913--cell-cell adherens junction	42	3.134328	1.37E-04	PVR, HSP	1269	323	18224	1.867363	0.091701	0.008706	0.206996
GOTERM CC	DIRECT GO:0005768--endosome	32	2.38806	2.05E-04	TGOLN2,	1269	225	18224	2.042441	0.133728	0.011892	0.308797
GOTERM CC	DIRECT GO:0005769--early endosome	32	2.38806	2.81E-04	HMG1B1, T	1269	229	18224	2.006765	0.17886	0.015044	0.423645
GOTERM CC	DIRECT GO:0035068--micro-ribonucleoprotein complex	5	0.373134	3.12E-04	AGO1, AC	1269	6	18224	11.96743	0.196382	0.015495	0.469905
GOTERM CC	DIRECT GO:0034045--pre-autophagosomal structure memb	7	0.522388	4.89E-04	ATG2B, U	1269	16	18224	6.2829	0.289956	0.02257	0.735004
GOTERM CC	DIRECT GO:0016442--RISC complex	6	0.447761	5.24E-04	DICER1, I	1269	11	18224	7.833226	0.307197	0.022677	0.787557
GOTERM CC	DIRECT GO:0015629--actin cytoskeleton	30	2.238806	5.82E-04	ABLIM1, I	1269	218	18224	1.976273	0.334604	0.023678	0.873795
GOTERM CC	DIRECT GO:0005741--mitochondrial outer membrane	23	1.716418	6.39E-04	MAVS, D	1269	149	18224	2.216785	0.360846	0.024561	0.959684
GOTERM CC	DIRECT GO:0070578--RISC-loading complex	5	0.373134	6.88E-04	DICER1, I	1269	7	18224	10.2578	0.382486	0.025052	1.03315
GOTERM CC	DIRECT GO:0000932--cytoplasmic mRNA processing body	15	1.119403	8.87E-04	PAN3, CN	1269	78	18224	2.761714	0.462825	0.03594	1.329873
GOTERM CC	DIRECT GO:0017053--transcriptional repressor complex	12	0.895522	0.001237	TBL1XR1,	1269	55	18224	3.13329	0.579459	0.040409	1.848844
GOTERM CC	DIRECT GO:0000139--Golgi membrane	62	4.626866	0.001269	CDIPT, PI	1269	591	18224	1.50656	0.588937	0.039604	1.89703
GOTERM CC	DIRECT GO:0005730--nucleolus	82	6.119403	0.002929	ACOX1, Z	1269	897	18224	1.37409	0.871699	0.085408	4.327316
GOTERM CC	DIRECT GO:0031083--BLOC-1 complex	6	0.447761	0.003697	BLOC1S4,	1269	16	18224	5.385343	0.925156	0.102386	5.431802
GOTERM CC	DIRECT GO:0005905--clathrin-coated pit	11	0.820896	0.004229	APP, API1	1269	55	18224	2.872183	0.948529	0.111899	6.191501
GOTERM CC	DIRECT GO:0005776--autophagosome	12	0.895522	0.004336	ORAI1, TI	1269	64	18224	2.692671	0.952243	0.110402	6.342737
GOTERM CC	DIRECT GO:0043209--myelin sheath	21	1.567164	0.00399	LDHB, GE	1269	152	18224	1.984074	0.954315	0.108006	6.432158
GOTERM CC	DIRECT GO:0032154--cleavage furrow	10	0.746269	0.004567	RAB11FIP	1269	47	18224	3.055514	0.959398	0.108122	6.669642
GOTERM CC	DIRECT GO:0032588--trans-Golgi network membrane	14	1.044776	0.004648	TGOLN2,	1269	83	18224	2.422323	0.961647	0.106354	6.784151
GOTERM CC	DIRECT GO:0005813--centrosome	45	3.358209	0.005606	CEP97, KI	1269	426	18224	1.516998	0.980456	0.122931	8.12823
GOTERM CC	DIRECT GO:0016604--nuclear body	8	0.597015	0.006691	SUMO1, N	1269	33	18224	3.481434	0.990902	0.14067	9.629148
GOTERM CC	DIRECT GO:0015630--microtubule cytoskeleton	19	1.41791	0.006774	HYPC, CK	1269	137	18224	1.99166	0.991414	0.138151	9.741855
GOTERM CC	DIRECT GO:0030496--midbody	18	1.343284	0.008106	KIF23, TR	1269	129	18224	2.003848	0.996645	0.158563	11.55065
GOTERM CC	DIRECT GO:0043234--protein complex	43	3.208955	0.008338	CEP97, OI	1269	412	18224	1.498833	0.997151	0.158337	11.86172
GOTERM CC	DIRECT GO:1904115--axon cytoplasm	8	0.597015	0.009331	BLOC1S4,	1269	35	18224	3.282495	0.998588	0.170976	13.18452
GOTERM CC	DIRECT GO:0010008--endosome membrane	23	1.716418	0.009633	ATPGV0E,	1269	185	18224	1.785411	0.998859	0.171562	13.58194
GOTERM CC	DIRECT GO:0032587--ruffle membrane	13	0.970149	0.010944	DLC1, SPI	1269	82	18224	2.27673	0.999548	0.18794	15.29071
GOTERM CC	DIRECT GO:0005802--trans-Golgi network	18	1.343284	0.013414	TGOLN2,	1269	136	18224	1.900709	0.999922	0.220244	18.42623
GOTERM CC	DIRECT GO:0031252--cell leading edge	8	0.597015	0.016771	GBF1, SLI	1269	39	18224	2.945829	0.999993	0.261817	22.5127
GOTERM CC	DIRECT GO:0005662--DNA replication factor A complex	5	0.373134	0.017134	RPA2, PLI	1269	15	18224	4.786971	0.999994	0.260984	22.94293
GOTERM CC	DIRECT GO:0000151--ubiquitin ligase complex	15	1.119403	0.017549	RNF216, T	1269	108	18224	1.994571	0.999996	0.260862	23.43217
GOTERM CC	DIRECT GO:0030670--phagocytic vesicle membrane	10	0.746269	0.020023	ATPGV0E,	1269	59	18224	2.434053	0.999999	0.286166	26.28952
GOTERM CC	DIRECT GO:0005819--spindle	16	1.19403	0.020774	KIF23, M	1269	121	18224	1.898964	1	0.289473	27.13703
GOTERM CC	DIRECT GO:0030424--axon	25	1.865672	0.021108	TNFRSF21	1269	222	18224	1.61722	1	0.2878	27.51002
GOTERM CC	DIRECT GO:0042470--melanosome	14	1.044776	0.022765	HSP90AB,	1269	101	18224	1.990622	1	0.30108	29.33943
GOTERM CC	DIRECT GO:0005801--cis-Golgi network	8	0.597015	0.024572	MPPE1, R	1269	42	18224	2.735412	1	0.315179	31.28447
GOTERM CC	DIRECT GO:0005643--nuclear pore	11	0.820896	0.026281	MAD1L1,	1269	72	18224	2.194029	1	0.332963	33.63451
GOTERM CC	DIRECT GO:0000790--nuclear chromatin	22	1.641791	0.027766	POLR3G, I	1269	93	18224	1.636995	1	0.336784	34.60063
GOTERM CC	DIRECT GO:0000813--ESCRT I complex	4	0.298507	0.027851	TSV101, V	1269	10	18224	5.744366	1	0.332094	34.69266
GOTERM CC	DIRECT GO:0031901--early endosome membrane	15	1.119403	0.030553	CAV1, RA	1269	116	18224	1.857015	1	0.352358	37.3714
GOTERM CC	DIRECT GO:0005901--caveola	10	0.746269	0.035254	DLC1, MA	1269	65	18224	2.209371	1	0.388976	41.79828
GOTERM CC	DIRECT GO:0009986--cell surface	50	3.731343	0.03531	PVR, HSP	1269	542	18224	1.324808	1	0.38364	41.84905
GOTERM CC	DIRECT GO:0031985--Golgi cisterna	4	0.298507	0.036362	RAB30, R	1269	11	18224	5.222151	1	0.386881	42.79749
GOTERM CC	DIRECT GO:0042612--MHC class I protein complex	4	0.298507	0.036362	HLA-A, H	1269	11	18224	5.222151	1	0.386881	42.79749
GOTERM CC	DIRECT GO:1990316--ATG1/ULK1 kinase complex	3	0.223881	0.041998	ULK1, RB	1269	5	18224	8.616548	1	0.426604	47.64048
GOTERM CC	DIRECT GO:0005874--microtubule	31	2.313433	0.043626	KIF23, DY	1269	311	18224	1.431474	1	0.433181	48.96661
GOTERM CC	DIRECT GO:0005844--polysome	7	0.522388	0.045697	EIF4H, EII	1269	38	18224	2.645432	1	0.442713	50.60796
GOTERM CC	DIRECT GO:0005667--transcription factor complex	21	1.567164	0.048124	E2F2, E2F	1269	193	18224	1.562587	1	0.454302	52.4687
GOTERM CC	DIRECT GO:0000792--heterochromatin	5	0.373134	0.053997	SUMO1, N	1269	21	18224	3.419265	1	0.488261	56.70423
GOTERM CC	DIRECT GO:0005721--pericentric heterochromatin	4	0.298507	0.056834	DNMT3, C	1269	13	18224	4.418743	1	0.500539	58.62188
GOTERM CC	DIRECT GO:0005739--mitochondrion	108	8.059701	0.059609	HCCS, LD	1269	1331	18224	1.165273	1	0.511802	60.42036
GOTERM CC	DIRECT GO:0001940--male pronucleus	3	0.223881	0.060132	TET3, CB	1269	6	18224	7.180457	1	0.50917	60.75077
GOTERM CC	DIRECT GO:0035749--myelin sheath adaxonal region	3	0.223881	0.060132	STX4, MP	1269	6	18224	7.180457	1	0.50917	60.75077
GOTERM CC	DIRECT GO:0070062--extracellular exosome	216	16.1194	0.062468	PVR, LDH	1269	2811	18224	1.103507	1	0.517262	62.19666
GOTERM CC	DIRECT GO:0005720--nuclear heterochromatin	5	0.373134	0.062499	CBX3, FO	1269	22	18224	3.263844	1	0.511824	62.21512
GOTERM CC	DIRECT GO:0072686--mitotic spindle	7	0.522388	0.062541	KIF23, M	1269	41	18224	2.451863	1	0.506568	62.24091
GOTERM CC	DIRECT GO:0005765--lysosomal membrane	27	2.014925	0.066776	HSP90AB,	1269	274	18224	1.415127	1	0.524917	64.7332
GOTERM CC	DIRECT GO:0000974--Prp19 complex	4	0.298507	0.068712	PLRG1, IS	1269	14	18224	4.103118	1	0.529994	65.82035
GOTERM CC	DIRECT GO:0090575--RNA polymerase II transcription fact	6	0.447761	0.075873	NONO, HI	1269	33	18224	2.611075	1	0.561495	69.57608
GOTERM CC	DIRECT GO:0005739--mitochondrion	13	0.970149	0.080372	AP1G1, R	1269	110	18224	1.697199	1	0.577894	71.73482
GOTERM CC	DIRECT GO:0000779--condensed chromosome, centromeric	3	0.223881	0.080381	CBX3, AU	1269	7	18224	6.154677	1	0.572629	71.73917
GOTERM CC	DIRECT GO:0045121--membrane raft	21	1.567164	0.082077	LDHB, CA	1269	206	18224	1.463977	1	0.575322	72.51525
GOTERM CC	DIRECT GO:0045171--intercellular bridge	7	0.522388	0.082593	KIF23, SP	1269	44	18224	2.284691	1	0.572543	72.74725
GOTERM CC	DIRECT GO:0055038--recycling endosome membrane	7	0.522388	0.082593	RAB11FIP	1269	44	18224	2.284691	1	0.5	

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferroni	Benjamini	FDR
GOTERM	GO:0005515~protein binding	804	60	1.79E-24	LDHB, CF	1221	8785	16881	1.26531	2.22E-21	2.22E-21	2.90E-21
GOTERM	GO:0031625~ubiquitin protein ligase binding	48	3.58209	1.01E-07	TRIOBP, I	1221	287	16881	2.312288	1.26E-04	6.29E-05	1.64E-04
GOTERM	GO:0019901~protein kinase binding	54	4.029851	2.09E-06	E2F1, HSF	1221	376	16881	1.985585	0.002598	8.67E-04	0.003393
GOTERM	GO:0004672~protein kinase activity	52	3.880597	2.58E-06	CDK19, N	1221	359	16881	2.002587	0.003212	8.04E-04	0.004197
GOTERM	GO:0044822~poly(A) RNA binding	119	8.880597	2.50E-05	MKRN1, I	1221	1129	16881	1.457255	0.030688	0.006214	0.040651
GOTERM	GO:0004674~protein serine/threonine kinase activit	50	3.731343	4.18E-05	CDK19, N	1221	376	16881	1.838504	0.050744	0.008642	0.06791
GOTERM	GO:0008134~transcription factor binding	39	2.910448	1.69E-04	E2F1, E2F	1221	284	16881	1.898579	0.189492	0.029568	0.273688
GOTERM	GO:0003700~transcription factor activity, sequence	100	7.462687	1.95E-04	REST, RO	1221	961	16881	1.438663	0.215942	0.029951	0.316841
GOTERM	GO:0003677~DNA binding	158	11.79104	3.16E-04	BBX, INO	1221	1674	16881	1.304921	0.325188	0.042761	0.511764
GOTERM	GO:0042826~histone deacetylase binding	19	1.41791	3.44E-04	HSP90AB	1221	102	16881	2.575348	0.348678	0.041969	0.557734
GOTERM	GO:0046872~metal ion binding	189	14.10448	4.07E-04	HCCS, MF	1221	2069	16881	1.262943	0.397438	0.045007	0.658622
GOTERM	GO:0004842~ubiquitin-protein transferase activity	42	3.134328	4.43E-04	MKRN1, I	1221	329	16881	1.764964	0.423709	0.04489	0.716375
GOTERM	GO:0019903~protein phosphatase binding	14	1.044776	4.80E-04	HMGB2, H	1221	63	16881	3.072545	0.450066	0.044955	0.776987
GOTERM	GO:0046332~SMAD binding	11	0.820896	7.95E-04	ACVR1B,	1221	43	16881	3.536769	0.62867	0.068316	1.283985
GOTERM	GO:0005524~ATP binding	140	10.44776	0.001029	DYNCL1L	1221	1495	16881	1.294701	0.722319	0.081872	1.65751
GOTERM	GO:0004702~receptor signaling protein serine/thre	12	0.895522	0.00122	PAK6, AC	1221	53	16881	3.130314	0.781205	0.090605	1.962789
GOTERM	GO:0042802~identical protein binding	77	5.746269	0.001606	CEP72, LI	1221	749	16881	1.421319	0.864743	0.111021	2.575953
GOTERM	GO:0001047~core promoter binding	13	0.970149	0.001886	E2F1, NOI	1221	64	16881	2.808315	0.904651	0.122402	3.019274
GOTERM	GO:0098641~cadherin binding involved in cell-cell	36	2.686567	0.001948	HSP90AB	1221	290	16881	1.716276	0.911785	0.119961	3.117614
GOTERM	GO:0003707~steroid hormone receptor activity	12	0.895522	0.001953	NR1H2, P	1221	56	16881	2.962618	0.912324	0.114591	3.125361
GOTERM	GO:0003682~chromatin binding	45	3.358209	0.002277	MORF4L1	1221	391	16881	1.591176	0.941466	0.126415	3.634591
GOTERM	GO:0000981~RNA polymerase II transcription fact	24	1.791045	0.002862	ZMYM1, I	1221	171	16881	1.940428	0.971802	0.149732	4.548332
GOTERM	GO:0003727~single-stranded RNA binding	10	0.746269	0.003134	HMGB1, I	1221	43	16881	3.215245	0.979929	0.15628	4.970748
GOTERM	GO:0004709~MAP kinase kinase kinase activity	7	0.522388	0.003838	MAP3K5,	1221	22	16881	4.39904	0.991671	0.18086	6.054782
GOTERM	GO:0070411~I-SMAD binding	5	0.373134	0.005934	SMAD7, S	1221	11	16881	6.284342	0.999394	0.25649	9.21291
GOTERM	GO:0043130~ubiquitin binding	13	0.970149	0.009856	ADRM1, I	1221	78	16881	2.304259	0.999996	0.377667	14.85877
GOTERM	GO:0001046~core promoter sequence-specific DN	9	0.671642	0.010889	USP3, KLI	1221	43	16881	2.89372	0.999999	0.396422	16.29094
GOTERM	GO:0004725~protein tyrosine phosphatase activity	15	1.119403	0.012626	SSH2, PT	1221	100	16881	2.073833	1	0.431622	18.64571
GOTERM	GO:0042803~protein homodimerization activity	70	5.223881	0.012794	PVR, GRP	1221	730	16881	1.325738	1	0.424667	18.87069
GOTERM	GO:0004879~RNA polymerase II transcription fact	8	0.597015	0.01326	NR1H2, P	1221	36	16881	3.072345	1	0.425342	19.49063
GOTERM	GO:0017048~Rho GTPase binding	7	0.522388	0.013372	FMN1B, F	1221	28	16881	3.456388	1	0.417639	19.63874
GOTERM	GO:0035035~histone acetyltransferase binding	7	0.522388	0.013372	ZBTB7A,	1221	28	16881	3.456388	1	0.417639	19.63874
GOTERM	GO:0002134~UTP binding	3	0.223881	0.014904	HSP90AB	1221	3	16881	13.82555	1	0.442461	21.64133
GOTERM	GO:0017098~sulfonurylurea receptor binding	3	0.223881	0.014904	HSP90AB	1221	3	16881	13.82555	1	0.442461	21.64133
GOTERM	GO:0004713~protein tyrosine kinase activity	18	1.343284	0.015343	TWF1, NR	1221	133	16881	1.871127	1	0.441971	22.20684
GOTERM	GO:0019904~protein domain specific binding	25	1.865672	0.01551	HMGB2, I	1221	208	16881	1.661725	1	0.435816	22.42001
GOTERM	GO:0035197~siRNA binding	4	0.298507	0.016007	DICER1, M	1221	8	16881	6.912776	1	0.436725	23.05378
GOTERM	GO:0019899~enzyme binding	36	2.686567	0.016436	CDK19, A	1221	333	16881	1.494654	1	0.43625	23.59753
GOTERM	GO:0001228~transcriptional activator activity, RN	14	1.044776	0.018935	MAFB, TF	1221	95	16881	2.03745	1	0.474423	26.68995
GOTERM	GO:0001077~transcriptional activator activity, RN	27	2.014925	0.020845	CAMTA1,	1221	236	16881	1.581737	1	0.49851	28.97359
GOTERM	GO:0004675~transmembrane receptor protein serin	4	0.298507	0.022737	ACVR1B,	1221	9	16881	6.14469	1	0.520112	31.16946
GOTERM	GO:0034713~type I transforming growth factor bet	4	0.298507	0.022737	SMAD7, S	1221	9	16881	6.14469	1	0.520112	31.16946
GOTERM	GO:0032403~protein complex binding	24	1.791045	0.024821	RWY1, UC	1221	206	16881	1.610744	1	0.542651	33.51548
GOTERM	GO:0003723~RNA binding	53	3.955224	0.02564	TALF1, RF	1221	547	16881	1.339587	1	0.545581	34.41634
GOTERM	GO:0051082~unfolded protein binding	15	1.119403	0.027043	PTGES3, I	1221	110	16881	1.885303	1	0.556325	35.9331
GOTERM	GO:0051434~BH3 domain binding	3	0.223881	0.028383	MCL1, BA	1221	4	16881	10.36916	1	0.56555	37.35139
GOTERM	GO:0004843~thiol-dependent ubiquitin-specific pr	12	0.895522	0.028485	OTUD4, C	1221	80	16881	2.073833	1	0.558559	37.4586
GOTERM	GO:0051015~actin filament binding	17	1.268657	0.028644	TRIOBP, I	1221	132	16881	1.780564	1	0.552489	37.6241
GOTERM	GO:0003725~double-stranded RNA binding	10	0.746269	0.030263	HSP90AB	1221	61	16881	2.266484	1	0.564703	39.29145
GOTERM	GO:0003743~translation initiation factor activity	10	0.746269	0.030263	E1F4G2, R	1221	61	16881	2.266484	1	0.564703	39.29145
GOTERM	GO:0005086~ARF guanyl-nucleotide exchange fac	6	0.447761	0.03087	GBL1, FN	1221	25	16881	3.318133	1	0.564215	39.90524
GOTERM	GO:0017137~Rab GTPase binding	17	1.268657	0.032366	TBC1D2B	1221	134	16881	1.753988	1	0.574022	41.39413
GOTERM	GO:0003684~damaged DNA binding	10	0.746269	0.036368	HMGB1, I	1221	63	16881	2.194532	1	0.609866	45.20931
GOTERM	GO:0008301~DNA binding, bending	5	0.373134	0.036727	TFAM, HN	1221	18	16881	3.840431	1	0.606122	45.53974
GOTERM	GO:0000978~RNA polymerase II core promoter pr	36	2.686567	0.037871	ZNF805, F	1221	355	16881	1.402028	1	0.610336	46.5813
GOTERM	GO:0042056~chemoattractant activity	6	0.447761	0.041665	HMGB1, I	1221	27	16881	3.072345	1	0.639022	49.90126
GOTERM	GO:0051721~protein phosphatase 2A binding	6	0.447761	0.041665	E1F4EBP1	1221	27	16881	3.072345	1	0.639022	49.90126
GOTERM	GO:0005525~GTP binding	38	2.835821	0.04488	HSP90AB	1221	384	16881	1.368154	1	0.65994	52.56162
GOTERM	GO:0015057~thrombin receptor activity	3	0.223881	0.045058	F2RL3, F2	1221	5	16881	8.295332	1	0.654571	52.70536
GOTERM	GO:0043621~protein self-association	8	0.597015	0.045659	ATXN1, C	1221	46	16881	2.404444	1	0.652812	53.18638
GOTERM	GO:0031267~small GTPase binding	5	0.373134	0.051891	GD12, RC	1221	20	16881	3.456388	1	0.694147	57.91149
GOTERM	GO:0005102~receptor binding	35	2.61194	0.052863	PVR, GLC	1221	353	16881	1.370806	1	0.694644	58.60702
GOTERM	GO:0042169~SH2 domain binding	6	0.447761	0.054474	DLC1, LA	1221	29	16881	2.860459	1	0.69952	59.73598
GOTERM	GO:0003713~transcription coactivator activity	26	1.940299	0.057217	TDRD3, P	1221	248	16881	1.449453	1	0.711564	61.59115
GOTERM	GO:0044212~transcription regulatory region DNA	23	1.716418	0.057441	TBL1XR1	1221	213	16881	1.4929	1	0.70698	61.73972
GOTERM	GO:0001227~transcriptional repressor activity, RN	9	0.671642	0.060781	ZNF280B,	1221	59	16881	2.108983	1	0.721916	63.88281
GOTERM	GO:1990226~histone methyltransferase binding	3	0.223881	0.064397	HSP90AB	1221	6	16881	6.912776	1	0.737277	66.07624
GOTERM	GO:0032947~protein complex scaffold	7	0.522388	0.065667	ISCU, CA	1221	40	16881	2.419472	1	0.738748	66.81606
GOTERM	GO:0003697~single-stranded DNA binding	12	0.895522	0.071705	PRIM1, HI	1221	93	16881	1.783942	1	0.764824	70.1326
GOTERM	GO:0046934~phosphatidylinositol-4,5-bisphosphat	9	0.671642	0.07692	NRG4, FG	1221	62	16881	2.006935	1	0.784127	72.7441
GOTERM	GO:0046982~protein heterodimerization activity	43	3.208955	0.079132	CAV1, PP	1221	465	16881	1.278492	1	0.788828	73.78545
GOTERM	GO:0008270~zinc ion binding	98	7.313433	0.083019	MKRN1, I	1221	1169	16881	1.159028	1	0.800208	75.52594
GOTERM	GO:0043565~sequence-specific DNA binding	47	3.507463	0.085697	E2F1, BAC	1221	518	16881	1.254442	1	0.806089	76.66158
GOTERM	GO:0004703~G-protein coupled receptor kinase act	3	0.223881	0.085929	GRK7, GR	1221	7	16881	5.925237	1	0.802331	76.75757
GOTERM	GO:0001222~transcription corepressor binding	3	0.223881	0.085929	HDGF, RC	1221	7	16881	5.925237	1	0.802331	76.7575