

STable 3. gene category analysis of 1166 *dpum* regulators

Please note that only data colored in grey is considered statistically significant

Of these 1166 genes, 988 were assigned ro gene identifiers recognised by the DAVID tool.

Functional Annotation Clustering

Annotation Cluster 1 Enrichment Score: 8.113424315169704												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop	Tota	Fold Enri	Bonferroni	Benjamini FDR
GOTERM_BP_DIRECT	GO:0006367~transcription initiation from RNA polymerase II promoter	25	2.53	1.91E-12	FBGN0000617,	764	64	10996	5.6221	2.67E-09	1.34E-09	3.15E-09
GOTERM_BP_DIRECT	GO:0006357~regulation of transcription from RNA polymerase II prom	41	4.15	7.23E-12	FBGN0024330,	764	173	10996	3.411	1.01E-08	3.37E-09	1.19E-08
GOTERM_CC_DIRECT	GO:0016592~mediator complex	17	1.721	2.99E-10	FBGN0024330,	753	33	10026	6.8591	1.22E-07	6.12E-08	4.18E-07
GOTERM_MF_DIRECT	GO:0001104~RNA polymerase II transcription cofactor activity	17	1.721	3.35E-10	FBGN0024330,	677	34	9284	6.8567	1.77E-07	1.77E-07	4.86E-07
GOTERM_BP_DIRECT	GO:0007406~negative regulation of neuroblast proliferation	9	0.911	3.51E-04	FBGN0032833,	764	27	10996	4.7976	0.3880274	0.02847	0.577
GOTERM_CC_DIRECT	GO:0070847~core mediator complex	6	0.607	4.29E-04	FBGN0024330,	753	10	10026	7.9888	0.1614252	0.01167	0.59927

Annotation Cluster 2 Enrichment Score: 4.836687716120325												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop	Tota	Fold Enri	Bonferroni	Benjamini FDR
GOTERM_CC_DIRECT	GO:0000502--proteasome complex	16	1.619	2.42E-07	FBGN0050382,	753	43	10026	4.9543	9.91E-05	2.48E-05	3.38E-04
GOTERM_CC_DIRECT	GO:0005839--proteasome core complex	10	1.012	1.01E-06	FBGN0050382,	753	17	10026	7.8322	4.13E-04	6.88E-05	0.00141
GOTERM_BP_DIRECT	GO:0043161--proteasome-mediated ubiquitin-dependent protein catat	20	2.024	7.19E-06	FBGN0050382,	764	88	10996	3.2711	0.0099988	0.00112	0.01184
GOTERM_MF_DIRECT	GO:0004298--threonine-type endopeptidase activity	11	1.113	1.06E-05	FBGN0050382,	677	27	9284	5.587	0.0055667	0.00112	0.01537
GOTERM_MF_DIRECT	GO:0004175--endopeptidase activity	13	1.316	2.91E-05	FBGN0037022,	677	42	9284	4.2446	0.0152376	0.00256	0.04226
GOTERM_CC_DIRECT	GO:0019774--proteasome core complex, beta-subunit complex	4	0.405	0.0176857	FBGN0026380,	753	8	10026	6.6574	0.9993352	0.22297	22.103

Annotation Cluster 3 Enrichment Score: 4.136060022912842												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop	Tota	Fold Enri	Bonferroni	Benjamini FDR
GOTERM_CC_DIRECT	GO:0005704~polytene chromosome band	13	1.316	2.88E-07	FBGN0039169,	753	28	10026	6.1818	1.18E-04	2.36E-05	4.03E-04
GOTERM_BP_DIRECT	GO:0007526~larval somatic muscle development	16	1.619	1.09E-06	FBGN0030855,	764	51	10996	4.5153	0.0015285	2.18E-04	0.0018
GOTERM_CC_DIRECT	GO:0000788~nuclear nucleosome	18	1.822	5.98E-06	FBGN0053812,	753	67	10026	3.5771	0.0024503	2.73E-04	0.00838
GOTERM_BP_DIRECT	GO:0006334~nucleosome assembly	24	2.429	2.08E-05	FBGN0034975,	764	128	10996	2.6986	0.0286025	0.00263	0.03419
GOTERM_CC_DIRECT	GO:0000790~nuclear chromatin	19	1.923	4.64E-05	FBGN0037751,	753	85	10026	2.9762	0.0188264	0.00173	0.06487
GOTERM_BP_DIRECT	GO:0006325~chromatin organization	15	1.518	5.59E-05	FBGN0029094,	764	61	10996	3.5392	0.075222	0.006	0.09211
GOTERM_CC_DIRECT	GO:0005694~chromosome	17	1.721	7.47E-04	FBGN0010278,	753	88	10026	2.5722	0.2639168	0.01786	1.0407
GOTERM_CC_DIRECT	GO:0000786~nucleosome	20	2.024	0.0010629	FBGN0034975,	753	117	10026	2.276	0.3533954	0.02393	1.47763
GOTERM_MF_DIRECT	GO:0046982~protein heterodimerization activity	30	3.036	0.0020731	FBGN0000370,	677	227	9284	1.8123	0.6650023	0.08711	2.96561
GOTERM_BP_DIRECT	GO:0006342~chromatin silencing	17	1.721	0.0261004	FBGN0003732,	764	136	10996	1.7991	1	0.52978	35.3178

Annotation Cluster 4 Enrichment Score: 4.012981884441554												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop	Tota	Fold Enri	Bonferroni	Benjamini FDR
GOTERM_BP_DIRECT	GO:0035195~gene silencing by miRNA	8	0.81	4.95E-05	FBGN0033062,	764	16	10996	7.1963	0.066861	0.00575	0.08151
GOTERM_BP_DIRECT	GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense	8	0.81	7.91E-05	FBGN0033378,	764	17	10996	6.773	0.1047253	0.00787	0.13027
GOTERM_BP_DIRECT	GO:0016246~RNA interference	10	1.012	2.33E-04	FBGN0033062,	764	32	10996	4.4977	0.2784505	0.02019	0.38383

Annotation Cluster 5 Enrichment Score: 2.9487415014398084												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop	Tota	Fold Enri	Bonferroni	Benjamini FDR
GOTERM_CC_DIRECT	GO:0005665--DNA-directed RNA polymerase II, core complex	8	0.81	4.90E-05	FBGN0004855,	753	15	10026	7.1012	0.0198841	0.00167	0.06855
GOTERM_MF_DIRECT	GO:0003899--DNA-directed RNA polymerase activity	10	1.012	1.07E-04	FBGN0004855,	677	28	9284	4.8977	0.0547643	0.00801	0.15492
GOTERM_BP_DIRECT	GO:0006360--transcription from RNA polymerase I promoter	6	0.607	0.0012774	FBGN0033929,	764	13	10996	6.6428	0.8325404	0.08158	2.08377
GOTERM_BP_DIRECT	GO:0006383--transcription from RNA polymerase III promoter	6	0.607	0.0026527	FBGN0037121,	764	15	10996	5.7571	0.9756072	0.13803	4.28153
GOTERM_CC_DIRECT	GO:0005666--DNA-directed RNA polymerase III complex	6	0.607	0.0088138	FBGN0037121,	753	18	10026	4.4382	0.9734753	0.15209	11.6553
GOTERM_CC_DIRECT	GO:0005736--DNA-directed RNA polymerase I complex	5	0.506	0.0129852	FBGN0037121,	753	13	10026	5.1211	0.9952934	0.20784	16.7198

Annotation Cluster 6 Enrichment Score: 2.6044976246466724												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop	Tota	Fold Enri	Bonferroni	Benjamini FDR
GOTERM_BP_DIRECT	GO:0006378~mRNA polyadenylation	8	0.81	6.91E-04	FBGN0015949,	764	23	10996	5.0061	0.6193119	0.04956	1.1316
GOTERM_CC_DIRECT	GO:0005847~mRNA cleavage and polyadenylation specificity factor c	5	0.506	0.0045711	FBGN0027873,	753	10	10026	6.6574	0.8471752	0.08557	6.21209
GOTERM_BP_DIRECT	GO:0006379~mRNA cleavage	6	0.607	0.004867	FBGN0027873,	764	17	10996	5.0798	0.9989091	0.19196	7.72291

Annotation Cluster 7 Enrichment Score: 2.369762841850479												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop	Tota	Fold Enri	Bonferroni	Benjamini FDR
GOTERM_BP_DIRECT	GO:0035195~gene silencing by miRNA	8	0.81	4.95E-05	FBGN0033062,	764	16	10996	7.1963	0.066861	0.00575	0.08151
GOTERM_BP_DIRECT	GO:0045071~negative regulation of viral genome replication	3	0.304	0.0262597	FBGN0033062,	764	4	10996	10.795	1	0.52481	35.4919
GOTERM_BP_DIRECT	GO:0031053~primary miRNA processing	3	0.304	0.0598172	FBGN0033062,	764	6	10996	7.1963	1	0.72391	63.8003

Annotation Cluster 8 Enrichment Score: 2.2463626594349453												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop	Tota	Fold Enri	Bonferroni	Benjamini FDR
GOTERM_CC_DIRECT	GO:0022625~cytosolic large ribosomal subunit	17	1.721	3.44E-06	FBGN0086710,	753	58	10026	3.9026	0.001411	1.76E-04	0.00482
GOTERM_CC_DIRECT	GO:0005840~ribosome	20	2.024	1.03E-04	FBGN0086710,	753	98	10026	2.7173	0.0411683	0.00323	0.14343
GOTERM_BP_DIRECT	GO:0002181~cytoplasmic translation	18	1.822	4.78E-04	FBGN0086710,	764	100	10996	2.5907	0.4871489	0.03642	0.7838
GOTERM_CC_DIRECT	GO:0022626~cytosolic ribosome	14	1.417	0.361353	FBGN0086710,	753	153	10026	1.2183	1	0.94345	99.8121
GOTERM_MF_DIRECT	GO:0003735~structural constituent of ribosome	24	2.429	0.5520483	FBGN0086710,	677	319	9284	1.0317	1	0.99819	99.9991
GOTERM_BP_DIRECT	GO:0006412~translation	30	3.036	0.9885137	FBGN0031980,	764	601	10996	0.7184	1	1	100

Annotation Cluster 9 Enrichment Score: 1.8867645444801537												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop	Tota	Fold Enri	Bonferroni	Benjamini FDR
GOTERM_BP_DIRECT	GO:0000398--mRNA splicing, via spliceosome	28	2.834	0.0039038	FBGN0017457,	764	226	10996	1.7832	0.995781	0.16663	6.24039
GOTERM_CC_DIRECT	GO:0071011--precatalytic spliceosome	20	2.024	0.0166665	FBGN0016978,	753	150	10026	1.7753	0.9989829	0.23282	20.964
GOTERM_CC_DIRECT	GO:0071013--catalytic step 2 spliceosome	17	1.721	0.0336029	FBGN0033378,	753	130	10026	1.7412	0.9999992	0.35463	38.0266

Annotation Cluster 10 Enrichment Score: 1.7504109536406758												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop	Tota	Fold Enri	Bonferroni	Benjamini FDR
GOTERM_BP_DIRECT	GO:0034472~snRNA 3'-end processing	6	0.607	0.0018745	FBGN0031314,	764	14	10996	6.1683	0.9274189	0.10778	3.04368
GOTERM_CC_DIRECT	GO:0032039~integrator complex	5	0.506	0.0171203	FBGN0031314,	753	14	10026	4.7553	0.9991583	0.23066	21.473

GOTERM_BP_DIRECT	GO:0016180~snRNA processing	3	0.304	0.174729	FBGN0039691,	764	11	10996	3.9253	1	0.92621	95.773
Annotation Cluster 11	Enrichment Score: 1.7245142310644581											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_BP_DIRECT	GO:0006368~transcription elongation from RNA polymerase II promot	7	0.709	0.0091978	FBGN0019949,	764	27	10996	3.7314	0.9999975	0.30151	14.1204
GOTERM_BP_DIRECT	GO:0016570~histone modification	5	0.506	0.0131346	FBGN0035205,	764	14	10996	5.1402	1	0.3629	19.5722
GOTERM_CC_DIRECT	GO:0016593~Cdc73/Paf1 complex	4	0.405	0.0555082	FBGN0035205,	753	12	10026	4.4382	1	0.47816	55.0407
Annotation Cluster 12	Enrichment Score: 1.6475724158809963											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_BP_DIRECT	GO:0016573~histone acetylation	10	1.012	0.012668	FBGN0034975,	764	55	10996	2.6168	1	0.36682	18.9435
GOTERM_BP_DIRECT	GO:0043486~histone exchange	5	0.506	0.0264626	FBGN0000046,	764	17	10996	4.2331	1	0.52057	35.713
GOTERM_CC_DIRECT	GO:0035267~NuA4 histone acetyltransferase complex	5	0.506	0.0340362	FBGN0000046,	753	17	10026	3.9161	0.9999993	0.34136	38.4144
Annotation Cluster 13	Enrichment Score: 1.4873313256014422											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_CC_DIRECT	GO:0005675~holo TFIIF complex	5	0.506	0.0045711	FBGN0033929,	753	10	10026	6.6574	0.8471752	0.08557	6.21209
GOTERM_BP_DIRECT	GO:0001113~transcriptional open complex formation at RNA polymer	4	0.405	0.0094268	FBGN0033929,	764	7	10996	8.2244	0.9999982	0.30084	14.4469
GOTERM_BP_DIRECT	GO:0001111~promoter clearance from RNA polymerase II promoter	4	0.405	0.0143123	FBGN0033929,	764	8	10996	7.1963	1	0.38111	21.1388
GOTERM_MF_DIRECT	GO:0000990~transcription factor activity, core RNA polymerase bindir	4	0.405	0.0231653	FBGN0033929,	677	9	9284	6.0949	0.9999957	0.51644	28.8237
GOTERM_CC_DIRECT	GO:0000439~core TFIIF complex	3	0.304	0.0688246	FBGN0033929,	753	6	10026	6.6574	1	0.5853	63.1449
GOTERM_BP_DIRECT	GO:0006289~nucleotide-excision repair	4	0.405	0.1410546	FBGN0033929,	764	19	10996	3.03	1	0.88824	91.8311
GOTERM_BP_DIRECT	GO:0009411~response to UV	3	0.304	0.2796486	FBGN0033929,	764	15	10996	2.8785	1	0.97669	99.55
Annotation Cluster 14	Enrichment Score: 1.4742675218646217											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_CC_DIRECT	GO:0005838~proteasome regulatory particle	6	0.607	0.0173644	FBGN0028684,	753	21	10026	3.8042	0.9992398	0.22624	21.7456
GOTERM_MF_DIRECT	GO:0017025~TBP-class protein binding	5	0.506	0.019911	FBGN0036224,	677	15	9284	4.5711	0.9999751	0.48441	25.3052
GOTERM_BP_DIRECT	GO:0045899~positive regulation of RNA polymerase II transcriptional	4	0.405	0.0203756	FBGN0036224,	764	9	10996	6.3967	1	0.46508	28.7611
GOTERM_MF_DIRECT	GO:0036402~proteasome-activating ATPase activity	4	0.405	0.0231653	FBGN0036224,	677	9	9284	6.0949	0.9999957	0.51644	28.8237
GOTERM_CC_DIRECT	GO:0031597~cytosolic proteasome complex	4	0.405	0.0250713	FBGN0036224,	753	9	10026	5.9177	0.9999699	0.28525	29.9126
GOTERM_CC_DIRECT	GO:0031595~nuclear proteasome complex	4	0.405	0.0338571	FBGN0036224,	753	10	10026	5.3259	0.9999993	0.34815	38.2543
GOTERM_CC_DIRECT	GO:0008540~proteasome regulatory particle, base subcomplex	4	0.405	0.0822138	FBGN0036224,	753	14	10026	3.8042	1	0.5672	69.9081
GOTERM_BP_DIRECT	GO:0030433~ER-associated ubiquitin-dependent protein catabolic prc	4	0.405	0.1410546	FBGN0036224,	764	19	10996	3.03	1	0.88824	91.8311
Annotation Cluster 15	Enrichment Score: 1.4256013880954497											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_BP_DIRECT	GO:1901409~positive regulation of phosphorylation of RNA polymera	4	0.405	0.005678	FBGN0040394,	764	6	10996	9.5951	0.999651	0.21434	8.95393
GOTERM_MF_DIRECT	GO:0016538~cyclin-dependent protein serine/threonine kinase regula	4	0.405	0.0634909	FBGN0040394,	677	13	9284	4.2195	1	0.74912	61.3875
GOTERM_CC_DIRECT	GO:0000307~cyclin-dependent protein kinase holoenzyme complex	3	0.304	0.0688246	FBGN0040394,	753	6	10026	6.6574	1	0.51853	63.1449
GOTERM_BP_DIRECT	GO:0045737~positive regulation of cyclin-dependent protein serine/thi	3	0.304	0.0799734	FBGN0040394,	764	7	10996	6.1683	1	0.79293	74.6689
Annotation Cluster 16	Enrichment Score: 1.2064808029886938											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_BP_DIRECT	GO:0006402~mRNA catabolic process	6	0.607	0.0081469	FBGN0031047,	764	19	10996	4.5451	0.9999892	0.27873	12.6075
GOTERM_BP_DIRECT	GO:0017148~negative regulation of translation	6	0.607	0.1305463	FBGN0031047,	764	39	10996	2.2143	1	0.87513	90.0194
GOTERM_CC_DIRECT	GO:0030014~CCR4-NOT complex	3	0.304	0.2258386	FBGN0031047,	753	12	10026	3.3287	1	0.86196	97.2213
Annotation Cluster 17	Enrichment Score: 1.033449820259569											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_BP_DIRECT	GO:0016575~histone deacetylation	4	0.405	0.0564096	FBGN0025825,	764	13	10996	4.4285	1	0.71315	61.5773
GOTERM_MF_DIRECT	GO:0032041~NAD-dependent histone deacetylase activity (H3-K14 s	3	0.304	0.0870359	FBGN0025825,	677	7	9284	5.8772	1	0.81983	73.3126
GOTERM_MF_DIRECT	GO:0004407~histone deacetylase activity	3	0.304	0.1616588	FBGN0025825,	677	10	9284	4.114	1	0.91331	92.254
Annotation Cluster 18	Enrichment Score: 0.9376591879883236											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_BP_DIRECT	GO:0048067~cuticle pigmentation	5	0.506	0.045714	FBGN0036504,	764	20	10996	3.5982	1	0.65781	53.7376
GOTERM_BP_DIRECT	GO:0042438~melanin biosynthetic process	4	0.405	0.0810283	FBGN0033367,	764	15	10996	3.838	1	0.79301	75.1431
GOTERM_MF_DIRECT	GO:0016853~isomerase activity	4	0.405	0.4152752	FBGN0036504,	677	32	9284	1.7142	1	0.993	99.9584
Annotation Cluster 19	Enrichment Score: 0.8126855983354536											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_MF_DIRECT	GO:0017056~structural constituent of nuclear pore	4	0.405	0.1219862	FBGN0010660,	677	17	9284	3.2267	1	0.86687	84.8511
GOTERM_MF_DIRECT	GO:0008139~nuclear localization sequence binding	4	0.405	0.1219862	FBGN0010660,	677	17	9284	3.2267	1	0.86687	84.8511
GOTERM_BP_DIRECT	GO:0006405~RNA export from nucleus	3	0.304	0.174729	FBGN0010660,	764	11	10996	3.9253	1	0.92621	95.773
GOTERM_MF_DIRECT	GO:0005487~nucleocytoplasmic transporter activity	3	0.304	0.2159092	FBGN0010660,	677	12	9284	3.4284	1	0.94926	97.0651
Annotation Cluster 20	Enrichment Score: 0.7414066943519563											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_CC_DIRECT	GO:0033181~plasma membrane proton-transporting V-type ATPase c	4	0.405	0.1303364	FBGN0027779,	753	17	10026	3.1329	1	0.71983	85.8411
GOTERM_CC_DIRECT	GO:0000221~vacuolar proton-transporting V-type ATPase, V1 domair	3	0.304	0.1424142	FBGN0027779,	753	9	10026	4.4382	1	0.74573	88.3585
GOTERM_MF_DIRECT	GO:0046961~proton-transporting ATPase activity, rotational mechanis	6	0.607	0.1752609	FBGN0027779,	677	41	9284	2.0068	1	0.92103	93.8904
GOTERM_BP_DIRECT	GO:0015991~ATP hydrolysis coupled proton transport	5	0.506	0.3327126	FBGN0027779,	764	42	10996	1.7134	1	0.98484	99.8724
Annotation Cluster 21	Enrichment Score: 0.7021014351600119											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_MF_DIRECT	GO:0017056~structural constituent of nuclear pore	4	0.405	0.1219862	FBGN0010660,	677	17	9284	3.2267	1	0.86687	84.8511
GOTERM_BP_DIRECT	GO:0007184~SMAD protein import into nucleus	3	0.304	0.2267439	FBGN0010660,	764	13	10996	3.3214	1	0.95963	98.5537
GOTERM_CC_DIRECT	GO:0005643~nuclear pore	5	0.506	0.2830409	FBGN0010660,	753	36	10026	1.8493	1	0.90483	99.0512
Annotation Cluster 22	Enrichment Score: 0.6747314653843575											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_BP_DIRECT	GO:0007010~cytoskeleton organization	6	0.607	0.1008839	FBGN0000046,	764	36	10996	2.3988	1	0.84407	82.6552
GOTERM_MF_DIRECT	GO:0005200~structural constituent of cytoskeleton	6	0.607	0.2838905	FBGN0000046,	677	49	9284	1.6792	1	0.97635	99.2126

GOTERM_CC_DIRECT	GO:0005884~actin filament	4	0.405	0.3302424	FBGN0000046,	753	27	10026	1.9726	1	0.9294	99.6343
Annotation Cluster 23	Enrichment Score: 0.653438915592703											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_MF_DIRECT	GO:0003743~translation initiation factor activity	9	0.911	0.0484654	FBGN0034654,	677	56	9284	2.2039	1	0.71255	51.3583
GOTERM_CC_DIRECT	GO:0016282~eukaryotic 43S preinitiation complex	3	0.304	0.4488624	FBGN0034654,	753	20	10026	1.9972	1	0.96638	99.9761
GOTERM_BP_DIRECT	GO:0001731~formation of translation preinitiation complex	3	0.304	0.5036614	FBGN0034654,	764	24	10996	1.7991	1	0.99754	99.999
Annotation Cluster 24	Enrichment Score: 0.6301013782617502											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_MF_DIRECT	GO:0005484~SNAP receptor activity	5	0.506	0.1042792	FBGN0039212,	677	25	9284	2.7427	1	0.83694	79.7617
GOTERM_BP_DIRECT	GO:0048278~vesicle docking	3	0.304	0.1495192	FBGN0037084,	764	10	10996	4.3178	1	0.89608	93.0608
GOTERM_MF_DIRECT	GO:0000149~SNARE binding	5	0.506	0.1858826	FBGN0039212,	677	31	9284	2.2118	1	0.92888	94.9377
GOTERM_BP_DIRECT	GO:0016081~synaptic vesicle docking	4	0.405	0.1931788	FBGN0037084,	764	22	10996	2.6168	1	0.94105	97.0875
GOTERM_BP_DIRECT	GO:0006906~vesicle fusion	4	0.405	0.2301859	FBGN0037084,	764	24	10996	2.3988	1	0.9607	98.6562
GOTERM_CC_DIRECT	GO:0031201~SNARE complex	5	0.506	0.2659278	FBGN0039212,	753	35	10026	1.9021	1	0.9002	98.68
GOTERM_BP_DIRECT	GO:0007269~neurotransmitter secretion	8	0.81	0.4229143	FBGN0000346,	764	89	10996	1.2937	1	0.99464	99.9883
GOTERM_CC_DIRECT	GO:0098793~presynapse	5	0.506	0.6280604	FBGN0039774,	753	57	10026	1.168	1	0.99244	99.9999
Annotation Cluster 25	Enrichment Score: 0.3098311395278172											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_BP_DIRECT	GO:0000413~protein peptidyl-prolyl isomerization	3	0.304	0.3581967	FBGN0036207,	764	18	10996	2.3988	1	0.98917	99.9328
GOTERM_BP_DIRECT	GO:0006457~protein folding	9	0.911	0.4773894	FBGN0036207,	764	108	10996	1.1994	1	0.99679	99.9977
GOTERM_MF_DIRECT	GO:0003755~peptidyl-prolyl cis-trans isomerase activity	3	0.304	0.6878793	FBGN0036207,	677	32	9284	1.2856	1	0.99938	100
Annotation Cluster 26	Enrichment Score: 0.2648556496671683											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_CC_DIRECT	GO:0019005~SCF ubiquitin ligase complex	7	0.709	0.3610959	FBGN0038566,	753	65	10026	1.4339	1	0.94583	99.811
GOTERM_BP_DIRECT	GO:0031146~SCF-dependent proteasomal ubiquitin-dependent proteolysis	4	0.405	0.6425312	FBGN0038566,	764	47	10996	1.2249	1	0.9995	100
GOTERM_BP_DIRECT	GO:0016567~protein ubiquitination	10	1.012	0.6916976	FBGN0038566,	764	146	10996	0.9858	1	0.99971	100
Annotation Cluster 27	Enrichment Score: 0.21204216999006045											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_CC_DIRECT	GO:0019005~SCF ubiquitin ligase complex	7	0.709	0.3610959	FBGN0038566,	753	65	10026	1.4339	1	0.94583	99.811
GOTERM_BP_DIRECT	GO:0042787~protein ubiquitination involved in ubiquitin-dependent proteolysis	6	0.607	0.7016495	FBGN0040291,	764	84	10996	1.028	1	0.99975	100
GOTERM_MF_DIRECT	GO:0004842~ubiquitin-protein transferase activity	10	1.012	0.9122854	FBGN0038566,	677	179	9284	0.7661	1	1	100
Annotation Cluster 28	Enrichment Score: 0.1493318492312938											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_MF_DIRECT	GO:0008017~microtubule binding	9	0.911	0.5115339	FBGN0001202,	677	106	9284	1.1643	1	0.99726	99.9969
GOTERM_CC_DIRECT	GO:0005871~kinesin complex	3	0.304	0.7039009	FBGN0004381,	753	32	10026	1.2483	1	0.99718	100
GOTERM_MF_DIRECT	GO:0003777~microtubule motor activity	3	0.304	0.748882	FBGN0004381,	677	36	9284	1.1428	1	0.99975	100
GOTERM_BP_DIRECT	GO:0007018~microtubule-based movement	4	0.405	0.9372886	FBGN0004381,	764	84	10996	0.6854	1	1	100
Annotation Cluster 29	Enrichment Score: 0.1259756760089817											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_BP_DIRECT	GO:0006468~protein phosphorylation	18	1.822	0.6742697	FBGN0029970,	764	266	10996	0.9739	1	0.99964	100
GOTERM_MF_DIRECT	GO:0004674~protein serine/threonine kinase activity	11	1.113	0.7082115	FBGN0041203,	677	156	9284	0.967	1	0.99952	100
GOTERM_MF_DIRECT	GO:0004672~protein kinase activity	9	0.911	0.8771551	FBGN0041203,	677	153	9284	0.8067	1	0.99999	100
Annotation Cluster 30	Enrichment Score: 0.11463557599085497											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_MF_DIRECT	GO:0008010~structural constituent of chitin-based larval cuticle	8	0.81	0.6608066	FBGN0020644,	677	106	9284	1.035	1	0.99919	100
GOTERM_MF_DIRECT	GO:0042302~structural constituent of cuticle	8	0.81	0.7163032	FBGN0020644,	677	112	9284	0.9795	1	0.99956	100
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	9	0.911	0.8449459	FBGN0020644,	753	142	10026	0.8439	1	0.99973	100
GOTERM_BP_DIRECT	GO:0040003~chitin-based cuticle development	9	0.911	0.8698763	FBGN0020644,	764	159	10996	0.8147	1	1	100
Annotation Cluster 31	Enrichment Score: 0.09228945423908888											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_BP_DIRECT	GO:0032482~Rab protein signal transduction	3	0.304	0.6938906	FBGN0016701,	764	34	10996	1.2699	1	0.99971	100
GOTERM_MF_DIRECT	GO:0003924~GTPase activity	9	0.911	0.7618787	FBGN0003886,	677	133	9284	0.928	1	0.9998	100
GOTERM_CC_DIRECT	GO:0045202~synapse	6	0.607	0.8940689	FBGN0001202,	753	103	10026	0.7756	1	0.99992	100
GOTERM_CC_DIRECT	GO:0031982~vesicle	3	0.304	0.9042622	FBGN0016701,	753	51	10026	0.7832	1	0.99994	100
Annotation Cluster 32	Enrichment Score: 0.028904186706984126											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_MF_DIRECT	GO:0005549~odorant binding	7	0.709	0.8343851	FBGN0062565,	677	112	9284	0.8571	1	0.99996	100
GOTERM_CC_DIRECT	GO:0032590~dendrite membrane	3	0.304	0.9583177	FBGN0062565,	753	64	10026	0.6241	1	0.99999	100
GOTERM_BP_DIRECT	GO:0050911~detection of chemical stimulus involved in sensory perception	3	0.304	0.9644908	FBGN0062565,	764	72	10996	0.5997	1	1	100
GOTERM_MF_DIRECT	GO:0004984~olfactory receptor activity	4	0.405	0.9935943	FBGN0052693,	677	119	9284	0.461	1	1	100
Annotation Cluster 33	Enrichment Score: 0.014790441734365816											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_MF_DIRECT	GO:0016705~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	5	0.506	0.9062324	FBGN0038680,	677	91	9284	0.7535	1	1	100
GOTERM_MF_DIRECT	GO:0004497~monooxygenase activity	4	0.405	0.9599886	FBGN0038680,	677	88	9284	0.6233	1	1	100
GOTERM_CC_DIRECT	GO:0031090~organelle membrane	3	0.304	0.9846227	FBGN0031182,	753	79	10026	0.5056	1	1	100
GOTERM_MF_DIRECT	GO:0020037~heme binding	5	0.506	0.989	FBGN0038680,	677	132	9284	0.5194	1	1	100
GOTERM_MF_DIRECT	GO:0005506~iron ion binding	5	0.506	0.9955797	FBGN0038680,	677	148	9284	0.4633	1	1	100

Functional Annotation Chart

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enri	Bonferroni	Benjamini FDR	
GOTERM_CC_DIRECT	GO:0005634~nucleus	225	22.77	8.60E-16	FBGN0040465,	753	1832	10026	1.6353	3.64E-13	3.64E-13	1.24E-12
GOTERM_BP_DIRECT	GO:0006366~transcription from RNA polymerase II promoter	26	2.63	7.52E-13	FBGN0000617,	764	67	10996	5.5852	1.05E-09	1.05E-09	1.24E-09

GOTERM_BP_DIRECT	GO:0006367~transcription initiation from RNA polymerase II promoter	25	2.53	1.91E-12	FBGN0000617,	764	64	10996	5.6221	2.67E-09	1.34E-09	3.15E-09
GOTERM_BP_DIRECT	GO:0006357~regulation of transcription from RNA polymerase II prom	41	4.15	7.23E-12	FBGN0024330,	764	173	10996	3.411	1.01E-08	3.37E-09	1.19E-08
GOTERM_CC_DIRECT	GO:0016592~mediator complex	17	1.72	2.99E-10	FBGN0024330,	753	33	10026	6.8591	1.22E-07	6.12E-08	4.18E-07
GOTERM_MF_DIRECT	GO:0001104~RNA polymerase II transcription cofactor activity	17	1.72	3.35E-10	FBGN0024330,	677	34	9284	6.8567	1.77E-07	1.77E-07	4.86E-07
GOTERM_BP_DIRECT	GO:0051298~centrosome duplication	29	2.94	6.50E-10	FBGN0003886,	764	108	10996	3.8647	9.09E-07	2.27E-07	1.07E-06
GOTERM_BP_DIRECT	GO:0022008~neurogenesis	77	7.79	1.20E-08	FBGN0032262,	764	565	10996	1.9615	1.68E-05	3.35E-06	1.98E-05
GOTERM_MF_DIRECT	GO:0003677~DNA binding	78	7.89	1.67E-08	FBGN0002914,	677	555	9284	1.9273	8.78E-06	4.39E-06	2.42E-05
GOTERM_CC_DIRECT	GO:0005700~polytene chromosome	37	3.74	4.15E-08	FBGN0002914,	753	180	10026	2.7369	1.70E-05	5.68E-06	5.82E-05
GOTERM_BP_DIRECT	GO:0006351~transcription, DNA-templated	55	5.57	2.15E-07	FBGN0045852,	764	376	10996	2.1053	3.01E-04	5.01E-05	3.54E-04
GOTERM_CC_DIRECT	GO:0000502~proteasome complex	16	1.62	2.42E-07	FBGN0050382,	753	43	10026	4.9543	9.91E-05	2.48E-05	3.38E-04
GOTERM_CC_DIRECT	GO:0005704~polytene chromosome band	13	1.32	2.88E-07	FBGN0039169,	753	28	10026	6.1818	1.18E-04	2.36E-05	4.03E-04
GOTERM_MF_DIRECT	GO:0003723~RNA binding	44	4.45	8.43E-07	FBGN0017457,	677	271	9284	2.2265	4.44E-04	1.48E-04	0.00122
GOTERM_CC_DIRECT	GO:0005839~proteasome core complex	10	1.01	1.01E-06	FBGN0050382,	753	17	10026	7.8322	4.13E-04	6.88E-05	0.00141
GOTERM_BP_DIRECT	GO:0007526~larval somatic muscle development	16	1.62	1.09E-06	FBGN0030855,	764	51	10996	4.5153	0.0015285	2.18E-04	0.0018
GOTERM_BP_DIRECT	GO:0007095~mitotic G2 DNA damage checkpoint	9	0.92	1.34E-06	FBGN0037121,	764	72	10996	3.7981	0.0018666	2.34E-04	0.0022
GOTERM_CC_DIRECT	GO:0035060~brahma complex	19	1.91	1.93E-06	FBGN0011715,	753	14	10026	8.5595	7.91E-04	1.13E-04	0.0027
GOTERM_MF_DIRECT	GO:0005515~protein binding	80	8.10	2.38E-06	FBGN0040465,	677	647	9284	1.6956	0.0012539	3.14E-04	0.00345
GOTERM_CC_DIRECT	GO:0022625~cytosolic large ribosomal subunit	17	1.72	3.44E-06	FBGN0086710,	753	58	10026	3.9026	0.001411	1.76E-04	0.00482
GOTERM_CC_DIRECT	GO:0000788~nuclear nucleosome	18	1.82	5.98E-06	FBGN0053812,	753	67	10026	3.5771	0.0024503	2.73E-04	0.00838
GOTERM_BP_DIRECT	GO:0043161~proteasome-mediated ubiquitin-dependent protein cata	20	2.02	7.19E-06	FBGN0050382,	764	88	10996	3.2711	0.0099988	0.00112	0.01184
GOTERM_MF_DIRECT	GO:0004298~threonine-type endopeptidase activity	11	1.11	1.06E-05	FBGN0050382,	677	27	9284	5.587	0.0055667	0.00112	0.01537
GOTERM_BP_DIRECT	GO:0006355~regulation of transcription, DNA-templated	52	5.26	1.68E-05	FBGN0045852,	764	401	10996	1.8664	0.0232489	0.00235	0.02772
GOTERM_CC_DIRECT	GO:0005811~lipid particle	42	4.25	1.93E-05	FBGN0000046,	753	277	10026	2.0188	0.00789	7.92E-04	0.02704
GOTERM_BP_DIRECT	GO:0006334~nucleosome assembly	24	2.43	2.08E-05	FBGN0034975,	764	128	10996	2.6986	0.0286025	0.00263	0.03419
GOTERM_MF_DIRECT	GO:0004175~endopeptidase activity	13	1.32	2.91E-05	FBGN0037022,	677	42	9284	4.2446	0.0152376	0.00256	0.04226
GOTERM_CC_DIRECT	GO:0000790~nuclear chromatin	19	1.92	4.64E-05	FBGN0037751,	753	85	10026	2.9762	0.0188264	0.00173	0.06487
GOTERM_CC_DIRECT	GO:0005665~DNA-directed RNA polymerase II, core complex	8	0.81	4.90E-05	FBGN0004855,	753	15	10026	7.1012	0.0198841	0.00167	0.06855
GOTERM_BP_DIRECT	GO:0035195~gene silencing by miRNA	8	0.81	4.95E-05	FBGN0033062,	764	16	10996	7.1963	0.066861	0.00575	0.08151
GOTERM_BP_DIRECT	GO:0006325~chromatin organization	15	1.52	5.59E-05	FBGN0029094,	764	61	10996	3.5392	0.075222	0.006	0.09211
GOTERM_BP_DIRECT	GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense	8	0.81	7.91E-05	FBGN0033378,	764	17	10996	6.773	0.1047253	0.00787	0.13027
GOTERM_CC_DIRECT	GO:0005840~ribosome	20	2.02	1.03E-04	FBGN0086710,	753	98	10026	2.7173	0.0411683	0.00323	0.14343
GOTERM_MF_DIRECT	GO:0003899~DNA-directed RNA polymerase activity	10	1.01	1.07E-04	FBGN0004855,	677	28	9284	4.8977	0.0547643	0.00801	0.15492
GOTERM_BP_DIRECT	GO:0007067~mitotic nuclear division	23	2.33	2.20E-04	FBGN0002914,	764	139	10996	2.3815	0.2644642	0.02027	0.36129
GOTERM_BP_DIRECT	GO:0016246~RNA interference	10	1.01	2.33E-04	FBGN0033062,	764	32	10996	4.4977	0.2784505	0.02019	0.38383
GOTERM_MF_DIRECT	GO:0003729~mRNA binding	27	2.73	2.54E-04	FBGN0004237,	677	171	9284	2.1653	0.1253201	0.0166	0.3679
GOTERM_MF_DIRECT	GO:0000166~nucleotide binding	31	3.14	3.20E-04	FBGN0004237,	677	212	9284	2.0053	0.1553018	0.01858	0.46352
GOTERM_CC_DIRECT	GO:0030529~intracellular ribonucleoprotein complex	9	0.91	3.30E-04	FBGN0004237,	753	25	10026	4.7933	0.126722	0.00963	0.46156
GOTERM_BP_DIRECT	GO:0007406~negative regulation of neuroblast proliferation	9	0.91	3.51E-04	FBGN0032833,	764	27	10996	4.7976	0.3880274	0.02847	0.577
GOTERM_CC_DIRECT	GO:0070847~core mediator complex	6	0.61	4.29E-04	FBGN0024330,	753	10	10026	7.9888	0.1614252	0.01167	0.59927
GOTERM_BP_DIRECT	GO:0002181~cytoplasmic translation	18	1.82	4.78E-04	FBGN0086710,	764	100	10996	2.5907	0.4871489	0.03642	0.7838
GOTERM_CC_DIRECT	GO:0005875~microtubule associated complex	40	4.05	5.01E-04	FBGN0000043,	753	300	10026	1.7753	0.1858456	0.01277	0.69952
GOTERM_MF_DIRECT	GO:0003713~transcription coactivator activity	13	1.32	6.79E-04	FBGN0020496,	677	57	9284	3.1276	0.3007839	0.03515	0.98008
GOTERM_BP_DIRECT	GO:0006378~mRNA polyadenylation	8	0.81	6.91E-04	FBGN0015949,	764	23	10996	5.0061	0.6193119	0.04956	1.1316
GOTERM_CC_DIRECT	GO:0005694~chromosome	17	1.72	7.47E-04	FBGN0010278,	753	88	10026	2.5722	0.2639168	0.01786	1.0407
GOTERM_CC_DIRECT	GO:0000786~nucleosome	20	2.02	0.0010629	FBGN0034975,	753	117	10026	2.276	0.3533954	0.02393	1.47763
GOTERM_CC_DIRECT	GO:0031523~Myb complex	6	0.61	0.0011884	FBGN0002914,	753	12	10026	6.6574	0.3858677	0.02533	1.65079
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymeras	30	3.04	0.0010903	FBGN00000370,	764	228	10996	1.8938	0.7823937	0.07342	1.78106
GOTERM_BP_DIRECT	GO:0006360~transcription from RNA polymerase I promoter	6	0.61	0.0012774	FBGN0033929,	764	13	10996	6.6428	0.8325404	0.08158	2.08377
GOTERM_MF_DIRECT	GO:0008134~transcription factor binding	16	1.62	0.0013997	FBGN0020496,	677	87	9284	2.522	0.5220095	0.0649	2.01146
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription from RNA polymeras	22	2.23	0.0014371	FBGN0020496,	764	149	10996	2.1251	0.8660742	0.08733	2.34126
GOTERM_BP_DIRECT	GO:0034472~snRNA 3'-end processing	6	0.61	0.0018745	FBGN0031314,	764	14	10996	6.1683	0.9274189	0.10778	3.04368
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	8	0.81	0.0019605	FBGN0025463,	764	27	10996	4.2645	0.9356543	0.10802	3.18118
GOTERM_MF_DIRECT	GO:0046982~protein heterodimerization activity	30	3.04	0.0020731	FBGN00000370,	677	227	9284	1.8123	0.6650023	0.08711	2.96561
GOTERM_BP_DIRECT	GO:0006383~transcription from RNA polymerase III promoter	6	0.61	0.0026527	FBGN0037121,	764	15	10996	5.7571	0.9756072	0.13803	4.28153
GOTERM_BP_DIRECT	GO:0016569~covalent chromatin modification	8	0.81	0.0030518	FBGN0029755,	764	29	10996	3.9704	0.9860601	0.15155	4.91057
GOTERM_BP_DIRECT	GO:0045893~positive regulation of transcription, DNA-templated	18	1.82	0.0034067	FBGN0004892,	764	119	10996	2.177	0.9915261	0.16196	5.46669
GOTERM_BP_DIRECT	GO:0045892~negative regulation of transcription, DNA-templated	18	1.82	0.0037203	FBGN0020496,	764	120	10996	2.1589	0.9945417	0.1698	5.9554
GOTERM_BP_DIRECT	GO:0030261~chromosome condensation	8	0.81	0.0037467	FBGN0002914,	764	30	10996	3.838	0.9947403	0.16553	5.99646
GOTERM_CC_DIRECT	GO:0019013~viral nucleocapsid	4	0.40	0.0037469	FBGN0004237,	753	5	10026	10.652	0.7854254	0.07407	5.11909
GOTERM_BP_DIRECT	GO:0000398~mRNA splicing, via spliceosome	28	2.83	0.0039038	FBGN0017457,	764	226	10996	1.7832	0.995781	0.16663	6.24039
GOTERM_MF_DIRECT	GO:0008353~RNA polymerase II carboxy-terminal domain kinase acti	5	0.51	0.0041019	FBGN0019949,	677	10	9284	6.8567	0.8853845	0.15349	5.78858
GOTERM_BP_DIRECT	GO:0000278~mitotic cell cycle	11	1.11	0.0041078	FBGN0002914,	764	55	10996	2.8785	0.9968316	0.16942	6.56525
GOTERM_CC_DIRECT	GO:0005847~mRNA cleavage and polyadenylation specificity factor c	5	0.51	0.0045711	FBGN0027873,	753	10	10026	6.6574	0.8471752	0.08557	6.21209
GOTERM_CC_DIRECT	GO:0005675~holo TFIIF complex	5	0.51	0.0045711	FBGN0033929,	753	10	10026	6.6574	0.8471752	0.08557	6.21209
GOTERM_BP_DIRECT	GO:0006379~mRNA cleavage	6	0.61	0.004867	FBGN0027873,	764	17	10996	5.0798	0.9989091	0.19196	7.72291
GOTERM_BP_DIRECT	GO:1901409~positive regulation of phosphorylation of RNA polymeras	4	0.40	0.005678	FBGN0040394,	764	6	10996	9.5951	0.999651	0.21434	8.95393
GOTERM_BP_DIRECT	GO:0006974~cellular response to DNA damage stimulus	16	1.62	0.0057527	FBGN0050382,	764	105	10996	2.1932	0.9996858	0.21118	9.06655
GOTERM_BP_DIRECT	GO:0006402~mRNA catabolic process	6	0.61	0.0081469	FBGN0031047,	764	19	10996	4.5451	0.9998982	0.27873	12.6075
GOTERM_CC_DIRECT	GO:0005666~DNA-directed RNA polymerase III complex	6	0.61	0.0088138	FBGN0037121,	753	18	10026	4.4382	0.9734753	0.15209	11.6553
GOTERM_MF_DIRECT	GO:0003676~nucleic acid binding	46	4.66	0.0089446	FBGN0026263,	677	432	9284	1.4602	0.9912178	0.28696	12.2205
GOTERM_BP_DIRECT	GO:0006368~transcription elongation from RNA polymerase II promot	7	0.71	0.0091978	FBGN0019949,	764	27	10996	3.7314	0.9999975	0.30151	14.1204
GOTERM_BP_DIRECT	GO:0001113~transcriptional open complex formation at RNA polymer	4	0.40	0.0094268	FBGN0033929,	764	7	10996	8.2244	0.9999982	0.30084	14.4469
GOTERM_BP_DIRECT	GO:0007030~Golgi organization	13	1.32	0.0106113	FBGN0002914,	764	82	10996	2.2818	0.9999997	0.32461	16.1167
GOTERM_BP_DIRECT	GO:0016573~histone acetylation	10	1.01	0.012668	FBGN0034975,	764	55	10996	2.6168	1	0.36682	18.9435
GOTERM_BP_DIRECT	GO:0007307~eggshell chorion gene amplification	6	0.61	0.0127062	FBGN0002914,	764	21	10996	4.1122	1	0.36041	18.9951
GOTERM_CC_DIRECT	GO:0005736~DNA-directed RNA polymerase I complex	5	0.51	0.0129852	FBGN0037121,	753	13	10026	5.1211	0.9952934	0.20784	16.7198
GOTERM_BP_DIRECT	GO:0016570~histone modification	5	0.51	0.0131346	FBGN0035205,	764	14	10996	5.1402	1	0.3629	19.5722
GOTERM_CC_DIRECT	GO:0000228~nuclear chromosome	10	1.01	0.01423	FBGN0011715,	753	52	10026	2.5605	0.9971946	0.21717	18.1781
GOTERM_BP_DIRECT	GO:0001111~promoter clearance from RNA polymerase II promoter	4	0.40	0.0143123	FBGN0033929,	764	8	10996	7.1963	1	0.38111	21.1388
GOTERM_CC_DIRECT	GO:0097255~R2TP complex	3	0.30	0.0160157	FBGN0040078,	753	3	10026	13.315	0.998666	0.23263	20.2286
GOTERM_MF_DIRECT	GO:0031208~POZ domain binding	4	0.40	0.0163137	FBGN0026263,	677	8	9284	6.8567	0.999828	0.43891	21.228
GOTERM_BP_DIRECT	GO:0006338~chromatin remodeling	9	0.91	0.0164512	FBGN0015268,	764	48					

GOTERM_CC_DIRECT	GO:0032039~integrator complex	5	0.51	0.0171203	FBGN0031314,	753	14	10026	4.7553	0.9991583	0.23066	21.473
GOTERM_CC_DIRECT	GO:0000176~nuclear exosome (RNase complex)	5	0.51	0.0171203	FBGN0034879,	753	14	10026	4.7553	0.9991583	0.23066	21.473
GOTERM_CC_DIRECT	GO:0005838~proteasome regulatory particle	6	0.61	0.0173644	FBGN0028684,	753	21	10026	3.8042	0.9992398	0.22624	21.7456
GOTERM_CC_DIRECT	GO:0019774~proteasome core complex, beta-subunit complex	4	0.40	0.0176857	FBGN0026380,	753	8	10026	6.6574	0.9993352	0.22297	22.103
GOTERM_MF_DIRECT	GO:0008094~DNA-dependent ATPase activity	5	0.51	0.019911	FBGN0002542,	677	15	9284	4.5711	0.9999751	0.48441	25.3052
GOTERM_MF_DIRECT	GO:0017025~TBP-class protein binding	5	0.51	0.019911	FBGN0036224,	677	15	9284	4.5711	0.9999751	0.48441	25.3052
GOTERM_BP_DIRECT	GO:0051301~cell division	11	1.11	0.0200001	FBGN0025815,	764	69	10996	2.2945	1	0.46615	28.3099
GOTERM_BP_DIRECT	GO:0043044~ATP-dependent chromatin remodeling	4	0.40	0.0203756	FBGN0020496,	764	9	10996	6.3967	1	0.46508	28.7611
GOTERM_BP_DIRECT	GO:0045899~positive regulation of RNA polymerase II transcriptional	4	0.40	0.0203756	FBGN0036224,	764	9	10996	6.3967	1	0.46508	28.7611
GOTERM_BP_DIRECT	GO:0010906~regulation of glucose metabolic process	21	2.13	0.0209287	FBGN0050382,	764	177	10996	1.7076	1	0.46694	29.4207
GOTERM_BP_DIRECT	GO:0045926~negative regulation of growth	5	0.51	0.0213813	FBGN0036165,	764	16	10996	4.4977	1	0.46713	29.9564
GOTERM_CC_DIRECT	GO:0071004~U2-type prespliceosome	5	0.51	0.0219899	FBGN0016978,	753	15	10026	4.4382	0.9998902	0.26205	26.7472
GOTERM_MF_DIRECT	GO:0036402~proteasome-activating ATPase activity	4	0.40	0.0231653	FBGN0036224,	677	9	9284	6.0949	0.9999957	0.51644	28.8237
GOTERM_MF_DIRECT	GO:0000990~transcription factor activity, core RNA polymerase bindir	4	0.40	0.0231653	FBGN0033929,	677	9	9284	6.0949	0.9999957	0.51644	28.8237
GOTERM_CC_DIRECT	GO:0031597~cytosolic proteasome complex	4	0.40	0.0250713	FBGN0036224,	753	9	10026	5.9177	0.9999699	0.28525	29.9126
GOTERM_CC_DIRECT	GO:0070604~PBAF complex	4	0.40	0.0250713	FBGN0011715,	753	9	10026	5.9177	0.9999699	0.28525	29.9126
GOTERM_BP_DIRECT	GO:0006342~chromatin silencing	17	1.72	0.0261004	FBGN0003732,	764	136	10996	1.7991	1	0.52978	35.3178
GOTERM_BP_DIRECT	GO:0045071~negative regulation of viral genome replication	3	0.30	0.0262597	FBGN0033062,	764	4	10996	10.795	1	0.52481	35.4919
GOTERM_BP_DIRECT	GO:0070816~phosphorylation of RNA polymerase II C-terminal domai	3	0.30	0.0262597	FBGN0033929,	764	4	10996	10.795	1	0.52481	35.4919
GOTERM_BP_DIRECT	GO:0032784~regulation of DNA-templated transcription, elongation	3	0.30	0.0262597	FBGN0010422,	764	4	10996	10.795	1	0.52481	35.4919
GOTERM_BP_DIRECT	GO:0000492~box C/D snoRNP assembly	3	0.30	0.0262597	FBGN0040078,	764	4	10996	10.795	1	0.52481	35.4919
GOTERM_BP_DIRECT	GO:0043486~histone exchange	5	0.51	0.0264626	FBGN0000046,	764	17	10996	4.2331	1	0.52057	35.713
GOTERM_BP_DIRECT	GO:0007517~muscle organ development	12	1.21	0.0277918	FBGN0039039,	764	83	10996	2.0809	1	0.53128	37.1437
GOTERM_BP_DIRECT	GO:0000381~regulation of alternative mRNA splicing, via spliceosome	11	1.11	0.028558	FBGN0033378,	764	73	10996	2.1688	1	0.53432	37.9549
GOTERM_BP_DIRECT	GO:0048813~dendrite morphogenesis	21	2.13	0.0302469	FBGN0045852,	764	184	10996	1.6426	1	0.54848	39.7082
GOTERM_MF_DIRECT	GO:0000339~RNA cap binding	4	0.40	0.0313354	FBGN0039622,	677	10	9284	5.4854	0.9999999	0.60628	36.9885
GOTERM_BP_DIRECT	GO:0045727~positive regulation of translation	5	0.51	0.0322062	FBGN0027835,	764	18	10996	3.998	1	0.56486	41.6839
GOTERM_BP_DIRECT	GO:0006909~phagocytosis	23	2.33	0.0328186	FBGN0053526,	764	209	10996	1.5839	1	0.56527	42.2888
GOTERM_CC_DIRECT	GO:0071013~catalytic step 2 spliceosome	17	1.72	0.0336029	FBGN0033378,	753	130	10026	1.7412	0.9999992	0.35463	38.0266
GOTERM_CC_DIRECT	GO:0031595~nuclear proteasome complex	4	0.40	0.0338571	FBGN0036224,	753	10	10026	5.3259	0.9999993	0.34815	38.2543
GOTERM_CC_DIRECT	GO:0005721~pericentric heterochromatin	4	0.40	0.0338571	FBGN0026573,	753	10	10026	5.3259	0.9999993	0.34815	38.2543
GOTERM_CC_DIRECT	GO:0035267~NuA4 histone acetyltransferase complex	5	0.51	0.0340362	FBGN0000046,	753	17	10026	3.9161	0.9999993	0.34136	38.4144
GOTERM_BP_DIRECT	GO:2000134~negative regulation of G1/S transition of mitotic cell cycl	4	0.40	0.0360752	FBGN0001965,	764	11	10996	5.2337	1	0.5939	45.4079
GOTERM_MF_DIRECT	GO:0046872~metal ion binding	61	6.17	0.0373969	FBGN0039631,	677	656	9284	1.2752	1	0.65256	42.4731
GOTERM_BP_DIRECT	GO:0051297~centrosome organization	9	0.91	0.038217	FBGN0002914,	764	56	10996	2.3131	1	0.60907	47.3722
GOTERM_BP_DIRECT	GO:0008283~cell proliferation	10	1.01	0.0409314	FBGN0002914,	764	67	10996	2.1482	1	0.62852	49.7663
GOTERM_MF_DIRECT	GO:0019843~rRNA binding	6	0.61	0.0427113	FBGN0031419,	677	27	9284	3.0474	1	0.68342	46.9125
GOTERM_BP_DIRECT	GO:0042752~regulation of circadian rhythm	4	0.40	0.0456806	FBGN0002413,	764	12	10996	4.7976	1	0.66359	53.7109
GOTERM_BP_DIRECT	GO:0032007~negative regulation of TOR signaling	4	0.40	0.0456806	FBGN0016120,	764	12	10996	4.7976	1	0.66359	53.7109
GOTERM_BP_DIRECT	GO:0048067~cuticle pigmentation	5	0.51	0.045714	FBGN0036504,	764	20	10996	3.5982	1	0.65781	53.7376
GOTERM_BP_DIRECT	GO:0050808~synapse organization	9	0.91	0.0457437	FBGN0029992,	764	58	10996	2.2333	1	0.65208	53.7613
GOTERM_BP_DIRECT	GO:0007049~cell cycle	6	0.61	0.0470151	FBGN0037102,	764	29	10996	2.9778	1	0.65651	54.7658
GOTERM_MF_DIRECT	GO:0003743~translation initiation factor activity	9	0.91	0.0484654	FBGN0034654,	677	56	9284	2.2039	1	0.71255	51.3583
GOTERM_MF_DIRECT	GO:0000981~RNA polymerase II transcription factor activity, sequenc	10	1.01	0.0486319	FBGN00039169,	677	66	9284	2.0778	1	0.69706	51.4817
GOTERM_CC_DIRECT	GO:0017053~transcriptional repressor complex	5	0.51	0.0492439	FBGN0004837,	753	19	10026	3.5039	1	0.44653	50.6818
GOTERM_MF_DIRECT	GO:0003746~translation elongation factor activity	5	0.51	0.053006	FBGN0034967,	677	20	9284	3.4284	1	0.71289	54.6192
GOTERM_BP_DIRECT	GO:0000462~maturation of SSU-rRNA from tricistronic rRNA transcrip	6	0.61	0.053326	FBGN00029755,	764	30	10996	2.8785	1	0.69792	59.4556
GOTERM_CC_DIRECT	GO:0019773~proteasome core complex, alpha-subunit complex	4	0.40	0.0555082	FBGN0050382,	753	12	10026	4.4382	1	0.47816	55.0407
GOTERM_CC_DIRECT	GO:0005719~nuclear euchromatin	4	0.40	0.0555082	FBGN0002914,	753	12	10026	4.4382	1	0.47816	55.0407
GOTERM_CC_DIRECT	GO:0016593~Cdc73/Paf1 complex	4	0.40	0.0555082	FBGN0035205,	753	12	10026	4.4382	1	0.47816	55.0407
GOTERM_CC_DIRECT	GO:0031011~Ino80 complex	4	0.40	0.0555082	FBGN0000042,	753	12	10026	4.4382	1	0.47816	55.0407
GOTERM_BP_DIRECT	GO:0016575~histone deacetylation	4	0.40	0.0564096	FBGN0025825,	764	13	10996	4.4285	1	0.71315	61.5773
GOTERM_BP_DIRECT	GO:0007283~spermatogenesis	18	1.82	0.0569926	FBGN0016978,	764	162	10996	1.5992	1	0.71148	61.9665
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	18	1.82	0.0597394	FBGN0004237,	753	151	10026	1.5872	1	0.49469	57.7794
GOTERM_BP_DIRECT	GO:0031053~primary miRNA processing	3	0.30	0.0598172	FBGN0033062,	764	6	10996	7.1963	1	0.72391	63.8003
GOTERM_BP_DIRECT	GO:0006370~7-methylguanosine mRNA capping	3	0.30	0.0598172	FBGN0030556,	764	6	10996	7.1963	1	0.72391	63.8003
GOTERM_BP_DIRECT	GO:0006260~DNA replication	8	0.81	0.0608808	FBGN0025815,	764	51	10996	2.2577	1	0.7251	64.4691
GOTERM_CC_DIRECT	GO:0035327~transcriptionally active chromatin	6	0.61	0.0619709	FBGN0040022,	753	29	10026	2.7548	1	0.49855	59.1606
GOTERM_MF_DIRECT	GO:004386~helicase activity	8	0.81	0.0627129	FBGN0023157,	677	49	9284	2.2389	1	0.7588	60.9195
GOTERM_MF_DIRECT	GO:0016538~cyclin-dependent protein serine/threonine kinase regula	4	0.40	0.0634909	FBGN0040394,	677	13	9284	4.2195	1	0.74912	61.3875
GOTERM_MF_DIRECT	GO:0004003~ATP-dependent DNA helicase activity	4	0.40	0.0634909	FBGN0001179,	677	13	9284	4.2195	1	0.74912	61.3875
GOTERM_BP_DIRECT	GO:0007419~ventral cord development	11	1.11	0.0647483	FBGN00085424,	764	84	10996	1.8848	1	0.74238	66.8043
GOTERM_MF_DIRECT	GO:0043140~ATP-dependent 3'-5' DNA helicase activity	3	0.30	0.0652465	FBGN0001179,	677	6	9284	6.8567	1	0.74529	62.4243
GOTERM_BP_DIRECT	GO:0006333~chromatin assembly or disassembly	8	0.81	0.0663445	FBGN0053904,	764	52	10996	2.2143	1	0.74615	67.7254
GOTERM_CC_DIRECT	GO:0005685~U1 snRNP	5	0.51	0.0676049	FBGN0016978,	753	21	10026	3.1702	1	0.52092	62.4634
GOTERM_CC_DIRECT	GO:0000439~core TFIIH complex	3	0.30	0.0688246	FBGN0033929,	753	6	10026	6.6574	1	0.51853	63.1449
GOTERM_CC_DIRECT	GO:0000307~cyclin-dependent protein kinase holoenzyme complex	3	0.30	0.0688246	FBGN0040394,	753	6	10026	6.6574	1	0.51853	63.1449
GOTERM_BP_DIRECT	GO:0008380~RNA splicing	5	0.51	0.0710056	FBGN0033378,	764	23	10996	3.1288	1	0.76548	70.2796
GOTERM_BP_DIRECT	GO:0007275~multicellular organism development	17	1.72	0.0713303	FBGN0010453,	764	155	10996	1.5786	1	0.76233	70.4503
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	132	13.36	0.0723501	FBGN0000046,	753	1553	10026	1.1317	1	0.52811	65.0508
GOTERM_MF_DIRECT	GO:0005524~ATP binding	66	6.68	0.0753829	FBGN0000046,	677	751	9284	1.2052	1	0.78342	67.9215
GOTERM_BP_DIRECT	GO:0000281~mitotic cytokinesis	9	0.91	0.0793906	FBGN0002914,	764	65	10996	1.9928	1	0.79487	74.4032
GOTERM_BP_DIRECT	GO:0010591~regulation of lamellipodium assembly	3	0.30	0.0799734	FBGN0000578,	764	7	10996	6.1683	1	0.79293	74.6689
GOTERM_BP_DIRECT	GO:0045737~positive regulation of cyclin-dependent protein serine/thi	3	0.30	0.0799734	FBGN0040394,	764	7	10996	6.1683	1	0.79293	74.6689
GOTERM_BP_DIRECT	GO:0042438~melanin biosynthetic process	4	0.40	0.0810283	FBGN0033367,	764	15	10996	3.838	1	0.79301	75.1431
GOTERM_CC_DIRECT	GO:0008540~proteasome regulatory particle, base subcomplex	4	0.40	0.0822138	FBGN0036224,	753	14	10026	3.8042	1	0.5672	69.9081
GOTERM_BP_DIRECT	GO:0007274~neuromuscular synaptic transmission	9	0.91	0.0851478	FBGN00086901,	764	66	10996	1.9626	1	0.80544	76.9165
GOTERM_CC_DIRECT	GO:0005730~nucleolus	19	1.92	0.0861664	FBGN0010278,	753	170	10026	1.4881	1	0.57648	71.6723
GOTERM_MF_DIRECT	GO:0032041~NAD-dependent histone deacetylase activity (H3-K14 s	3	0.30	0.0870359	FBGN0025825,	677	7	9284	5.8772	1	0.81983	73.3126
GOTERM_BP_DIRECT	GO:0006281~DNA repair	11	1.11	0.0880628	FBGN0033929,	764	89	10996	1.7789	1	0.81244	78.0987
GOTERM_BP_DIRECT	GO:0030036~actin cytoskeleton organization	7	0.71	0.0889111	FBGN0041203,	764	45	10996	2.2389	1	0.81155	78.4319
GOTERM_MF_DIRECT	GO:0004693~cyclin-dependent protein serine/threonine kinase activity	4	0.40	0.0907552	FBGN0019949,	677	15	9284	3.6569	1	0.82253	78.4747
GOTERM_BP_DIRECT	GO:0032436~positive regulation of proteasomal ubiquitin-dependent r	4	0.40	0.094793	FBGN0033669,	764	16	10996	3.5982	1	0.82837	80.6171
GOTERM_MF_DIRECT	GO:0003705~transcription factor activity, RNA polymerase II distal enl	8	0.81	0.0951438	FBGN0039039,	677	54	9284	2.0316	1	0.82732	76.552

GOTERM_MF_DIRECT	GO:0030170~pyridoxal phosphate binding	6	0.61	0.0974964	FBGN0000422,	677	34	9284	2.42	1	0.82516	77.4211
GOTERM_CC_DIRECT	GO:0005703~polytene chromosome puff	7	0.71	0.0997383	FBGN0004237,	753	43	10026	2.1675	1	0.62434	77.0255