

Brain-specific age-related GO terms in Cluster 1 (Upregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0007269 neurotransmitter secretion	CG12532	FBgn0010380	Beta Adaptin	9.04E-04	104	9	8.7%
GO:0007269 neurotransmitter secretion	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	9.04E-04	104	9	8.7%
GO:0007269 neurotransmitter secretion	CG5081	FBgn0033583	Syntaxin 7	9.04E-04	104	9	8.7%
GO:0007269 neurotransmitter secretion	CG5341	FBgn0034367		9.04E-04	104	9	8.7%
GO:0007269 neurotransmitter secretion	CG5675	FBgn0026313		9.04E-04	104	9	8.7%
GO:0007269 neurotransmitter secretion	CG7576	FBgn0005586	Rab-protein 3	9.04E-04	104	9	8.7%
GO:0007269 neurotransmitter secretion	CG8639	FBgn0033313		9.04E-04	104	9	8.7%
GO:0007269 neurotransmitter secretion	CG9778	FBgn0037233		9.04E-04	104	9	8.7%
GO:0007269 neurotransmitter secretion	CG9931	NA	NA	9.04E-04	104	9	8.7%
GO:0045055 regulated secretory pathway	CG12532	FBgn0010380	Beta Adaptin	9.04E-04	104	9	8.7%
GO:0045055 regulated secretory pathway	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	9.04E-04	104	9	8.7%
GO:0045055 regulated secretory pathway	CG5081	FBgn0033583	Syntaxin 7	9.04E-04	104	9	8.7%
GO:0045055 regulated secretory pathway	CG5341	FBgn0034367		9.04E-04	104	9	8.7%
GO:0045055 regulated secretory pathway	CG5675	FBgn0026313		9.04E-04	104	9	8.7%
GO:0045055 regulated secretory pathway	CG7576	FBgn0005586	Rab-protein 3	9.04E-04	104	9	8.7%
GO:0045055 regulated secretory pathway	CG8639	FBgn0033313		9.04E-04	104	9	8.7%
GO:0045055 regulated secretory pathway	CG9778	FBgn0037233		9.04E-04	104	9	8.7%
GO:0045055 regulated secretory pathway	CG9931	NA	NA	9.04E-04	104	9	8.7%
GO:0016579 protein deubiquitination	CG15817	FBgn0028476		1.46E-03	21	4	19.0%
GO:0016579 protein deubiquitination	CG3431	FBgn0011327	Ubiquitin C-terminal hydrolase	1.46E-03	21	4	19.0%
GO:0016579 protein deubiquitination	CG5384	FBgn0032216		1.46E-03	21	4	19.0%

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GO:0016579 protein deubiquitination	CG8494	FBgn0033916		1.46E-03	21	4	19.0%
GO:0007268 synaptic transmission	CG10693	FBgn0003429	slowpoke	1.58E-03	208	13	6.3%
GO:0007268 synaptic transmission	CG11340	FBgn0039840		1.58E-03	208	13	6.3%
GO:0007268 synaptic transmission	CG12532	FBgn0010380	Beta Adaptin	1.58E-03	208	13	6.3%
GO:0007268 synaptic transmission	CG12559	FBgn0003256	rolled	1.58E-03	208	13	6.3%
GO:0007268 synaptic transmission	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	1.58E-03	208	13	6.3%
GO:0007268 synaptic transmission	CG5081	FBgn0033583	Syntaxin 7	1.58E-03	208	13	6.3%
GO:0007268 synaptic transmission	CG5341	FBgn0034367		1.58E-03	208	13	6.3%
GO:0007268 synaptic transmission	CG5675	FBgn0026313		1.58E-03	208	13	6.3%
GO:0007268 synaptic transmission	CG7576	FBgn0005586	Rab-protein 3	1.58E-03	208	13	6.3%
GO:0007268 synaptic transmission	CG8082	NA	NA	1.58E-03	208	13	6.3%
GO:0007268 synaptic transmission	CG8639	FBgn0033313		1.58E-03	208	13	6.3%
GO:0007268 synaptic transmission	CG9778	FBgn0037233		1.58E-03	208	13	6.3%
GO:0007268 synaptic transmission	CG9931	NA	NA	1.58E-03	208	13	6.3%
GO:0001505 regulation of neurotransmitter levels	CG12532	FBgn0010380	Beta Adaptin	1.96E-03	116	9	7.8%
GO:0001505 regulation of neurotransmitter levels	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	1.96E-03	116	9	7.8%
GO:0001505 regulation of neurotransmitter levels	CG5081	FBgn0033583	Syntaxin 7	1.96E-03	116	9	7.8%
GO:0001505 regulation of neurotransmitter levels	CG5341	FBgn0034367		1.96E-03	116	9	7.8%
GO:0001505 regulation of neurotransmitter levels	CG5675	FBgn0026313		1.96E-03	116	9	7.8%
GO:0001505 regulation of neurotransmitter levels	CG7576	FBgn0005586	Rab-protein 3	1.96E-03	116	9	7.8%
GO:0001505 regulation of neurotransmitter levels	CG8639	FBgn0033313		1.96E-03	116	9	7.8%
GO:0001505 regulation of neurotransmitter levels	CG9778	FBgn0037233		1.96E-03	116	9	7.8%
GO:0001505 regulation of neurotransmitter levels	CG9931	NA	NA	1.96E-03	116	9	7.8%

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GO:0007369 gastrulation	CG12532	FBgn0010380	Beta Adaptin	4.44E-03	45	5	11.1%
GO:0007369 gastrulation	CG12559	FBgn0003256	rolled	4.44E-03	45	5	11.1%
GO:0007369 gastrulation	CG12653	FBgn0000233	buttonhead	4.44E-03	45	5	11.1%
GO:0007369 gastrulation	CG9358	FBgn0035089	Pherokine 3	4.44E-03	45	5	11.1%
GO:0007369 gastrulation	CG9635	FBgn0023172		4.44E-03	45	5	11.1%
GO:0016079 synaptic vesicle exocytosis	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	4.44E-03	45	5	11.1%
GO:0016079 synaptic vesicle exocytosis	CG5081	FBgn0033583	Syntaxin 7	4.44E-03	45	5	11.1%
GO:0016079 synaptic vesicle exocytosis	CG5341	FBgn0034367		4.44E-03	45	5	11.1%
GO:0016079 synaptic vesicle exocytosis	CG5675	FBgn0026313		4.44E-03	45	5	11.1%
GO:0016079 synaptic vesicle exocytosis	CG9931	NA	NA	4.44E-03	45	5	11.1%
GO:0008360 regulation of cell shape	CG10295	FBgn0014001	PAK-kinase	4.73E-03	86	7	8.1%
GO:0008360 regulation of cell shape	CG8201	FBgn0026193		4.73E-03	86	7	8.1%
GO:0008360 regulation of cell shape	CG12007	FBgn0037293		4.73E-03	86	7	8.1%
GO:0008360 regulation of cell shape	CG1720	NA	NA	4.73E-03	86	7	8.1%
GO:0008360 regulation of cell shape	CG6831	FBgn0020254	rhea	4.73E-03	86	7	8.1%
GO:0008360 regulation of cell shape	CG7323	FBgn0036943		4.73E-03	86	7	8.1%
GO:0008360 regulation of cell shape	CG9635	FBgn0023172		4.73E-03	86	7	8.1%
GO:0009792 embryonic development (sensu Metazoa)	CG10295	FBgn0014001	PAK-kinase	5.20E-03	159	10	6.3%
GO:0009792 embryonic development (sensu Metazoa)	CG1064	FBgn0011715	Snf5-related 1	5.20E-03	159	10	6.3%
GO:0009792 embryonic development (sensu Metazoa)	CG12532	FBgn0010380	Beta Adaptin	5.20E-03	159	10	6.3%
GO:0009792 embryonic development (sensu Metazoa)	CG12559	FBgn0003256	rolled	5.20E-03	159	10	6.3%
GO:0009792 embryonic development (sensu Metazoa)	CG12653	FBgn0000233	buttonhead	5.20E-03	159	10	6.3%
GO:0009792 embryonic development (sensu Metazoa)	CG1388	NA	NA	5.20E-03	159	10	6.3%

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GO:0009792 embryonic development (sensu Metazoa)	CG1720	NA	NA	5.20E-03	159	10	6.3%
GO:0009792 embryonic development (sensu Metazoa)	CG8978	FBgn0001961	Suppressor of profilin 2	5.20E-03	159	10	6.3%
GO:0009792 embryonic development (sensu Metazoa)	CG9358	FBgn0035089	Pherokine 3	5.20E-03	159	10	6.3%
GO:0009792 embryonic development (sensu Metazoa)	CG9635	FBgn0023172		5.20E-03	159	10	6.3%
GO:0007264 small GTPase mediated signal transduction	CG10295	FBgn0014001	PAK-kinase	6.04E-03	113	8	7.1%
GO:0007264 small GTPase mediated signal transduction	CG12156	FBgn0029959		6.04E-03	113	8	7.1%
GO:0007264 small GTPase mediated signal transduction	CG15069	FBgn0034357		6.04E-03	113	8	7.1%
GO:0007264 small GTPase mediated signal transduction	CG16828	NA	NA	6.04E-03	113	8	7.1%
GO:0007264 small GTPase mediated signal transduction	CG6860	FBgn0032633		6.04E-03	113	8	7.1%
GO:0007264 small GTPase mediated signal transduction	CG7576	FBgn0005586	Rab-protein 3	6.04E-03	113	8	7.1%
GO:0007264 small GTPase mediated signal transduction	CG7605	FBgn0037072		6.04E-03	113	8	7.1%
GO:0007264 small GTPase mediated signal transduction	CG9358	FBgn0035089	Pherokine 3	6.04E-03	113	8	7.1%
GO:0007411 axon guidance	CG10295	FBgn0014001	PAK-kinase	6.82E-03	70	6	8.6%
GO:0007411 axon guidance	CG14334	FBgn0038498	beaten path IIa	6.82E-03	70	6	8.6%
GO:0007411 axon guidance	CG5580	FBgn0010575	scribbler	6.82E-03	70	6	8.6%
GO:0007411 axon guidance	CG7555	FBgn0036736		6.82E-03	70	6	8.6%
GO:0007411 axon guidance	CG8168	NA	NA	6.82E-03	70	6	8.6%
GO:0007411 axon guidance	CG8581	FBgn0011592	frazzled	6.82E-03	70	6	8.6%
GO:0007409 axonogenesis	CG10295	FBgn0014001	PAK-kinase	8.11E-03	95	7	7.4%
GO:0007409 axonogenesis	CG14334	FBgn0038498	beaten path IIa	8.11E-03	95	7	7.4%
GO:0007409 axonogenesis	CG5580	FBgn0010575	scribbler	8.11E-03	95	7	7.4%
GO:0007409 axonogenesis	CG7555	FBgn0036736		8.11E-03	95	7	7.4%
GO:0007409 axonogenesis	CG8168	NA	NA	8.11E-03	95	7	7.4%

GO:0007409 axonogenesis	CG8581	FBgn0011592	frazzled	8.11E-03	95	7	7.4%
GO:0007409 axonogenesis	CG8978	FBgn0001961	Suppressor of profilin 2	8.11E-03	95	7	7.4%
GO:0007034 vacuolar transport	CG12156	FBgn0029959		1.02E-02	19	3	15.8%
GO:0007034 vacuolar transport	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	1.02E-02	19	3	15.8%
GO:0007034 vacuolar transport	CG5081	FBgn0033583	Syntaxin 7	1.02E-02	19	3	15.8%
GO:0007041 lysosomal transport	CG12156	FBgn0029959		1.02E-02	19	3	15.8%
GO:0007041 lysosomal transport	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	1.02E-02	19	3	15.8%
GO:0007041 lysosomal transport	CG5081	FBgn0033583	Syntaxin 7	1.02E-02	19	3	15.8%
GO:0048489 synaptic vesicle transport	CG12532	FBgn0010380	Beta Adaptin	1.21E-02	79	6	7.6%
GO:0048489 synaptic vesicle transport	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	1.21E-02	79	6	7.6%
GO:0048489 synaptic vesicle transport	CG5081	FBgn0033583	Syntaxin 7	1.21E-02	79	6	7.6%
GO:0048489 synaptic vesicle transport	CG5341	FBgn0034367		1.21E-02	79	6	7.6%
GO:0048489 synaptic vesicle transport	CG5675	FBgn0026313		1.21E-02	79	6	7.6%
GO:0048489 synaptic vesicle transport	CG9931	NA	NA	1.21E-02	79	6	7.6%
GO:0008407 bristle morphogenesis	CG6780	NA	NA	1.36E-02	21	3	14.3%
GO:0008407 bristle morphogenesis	CG1720	NA	NA	1.36E-02	21	3	14.3%
GO:0008407 bristle morphogenesis	CG8978	FBgn0001961	Suppressor of profilin 2	1.36E-02	21	3	14.3%
GO:0016081 synaptic vesicle docking during exocytosis	CG5081	FBgn0033583	Syntaxin 7	1.36E-02	21	3	14.3%
GO:0016081 synaptic vesicle docking during exocytosis	CG5341	FBgn0034367		1.36E-02	21	3	14.3%
GO:0016081 synaptic vesicle docking during exocytosis	CG5675	FBgn0026313		1.36E-02	21	3	14.3%
GO:0000902 cellular morphogenesis	CG10295	FBgn0014001	PAK-kinase	1.53E-02	215	11	5.1%
GO:0000902 cellular morphogenesis	CG8201	FBgn0026193		1.53E-02	215	11	5.1%

GO:0000902 cellular morphogenesis	CG12007	FBgn0037293		1.53E-02	215	11	5.1%
GO:0000902 cellular morphogenesis	CG12559	FBgn0003256	rolled	1.53E-02	215	11	5.1%
GO:0000902 cellular morphogenesis	CG1388	NA	NA	1.53E-02	215	11	5.1%
GO:0000902 cellular morphogenesis	CG1720	NA	NA	1.53E-02	215	11	5.1%
GO:0000902 cellular morphogenesis	CG5580	FBgn0010575	scribbler	1.53E-02	215	11	5.1%
GO:0000902 cellular morphogenesis	CG5675	FBgn0026313		1.53E-02	215	11	5.1%
GO:0000902 cellular morphogenesis	CG6831	FBgn0020254	rhea	1.53E-02	215	11	5.1%
GO:0000902 cellular morphogenesis	CG7323	FBgn0036943		1.53E-02	215	11	5.1%
GO:0000902 cellular morphogenesis	CG9635	FBgn0023172		1.53E-02	215	11	5.1%
GO:0006897 endocytosis	CG12156	FBgn0029959		2.06E-02	114	7	6.1%
GO:0006897 endocytosis	CG12532	FBgn0010380	Beta Adaptin	2.06E-02	114	7	6.1%
GO:0006897 endocytosis	CG15298	NA	NA	2.06E-02	114	7	6.1%
GO:0006897 endocytosis	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	2.06E-02	114	7	6.1%
GO:0006897 endocytosis	CG7576	FBgn0005586	Rab-protein 3	2.06E-02	114	7	6.1%
GO:0006897 endocytosis	CG7605	FBgn0037072		2.06E-02	114	7	6.1%
GO:0006897 endocytosis	CG9635	FBgn0023172		2.06E-02	114	7	6.1%
GO:0007398 ectoderm development	CG11182	FBgn0025334	Putative homeodomain protein	2.08E-02	225	11	4.9%
GO:0007398 ectoderm development	CG12532	FBgn0010380	Beta Adaptin	2.08E-02	225	11	4.9%
GO:0007398 ectoderm development	CG13898	FBgn0035161		2.08E-02	225	11	4.9%
GO:0007398 ectoderm development	CG1720	NA	NA	2.08E-02	225	11	4.9%
GO:0007398 ectoderm development	CG1848	FBgn0041203	LIM-kinase1	2.08E-02	225	11	4.9%
GO:0007398 ectoderm development	CG2380	FBgn0042696	Nuclear factor I	2.08E-02	225	11	4.9%
GO:0007398 ectoderm development	CG3629	FBgn0000157	Distal-less	2.08E-02	225	11	4.9%
GO:0007398 ectoderm development	CG6883	FBgn0003749	trachealess	2.08E-02	225	11	4.9%

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GO:0007398 ectoderm development	CG8168	NA	NA	2.08E-02	225	11	4.9%
GO:0007398 ectoderm development	CG8240	NA	NA	2.08E-02	225	11	4.9%
GO:0007398 ectoderm development	CG8581	FBgn0011592	frazzled	2.08E-02	225	11	4.9%
GO:0031175 neurite morphogenesis	CG10295	FBgn0014001	PAK-kinase	2.15E-02	115	7	6.1%
GO:0031175 neurite morphogenesis	CG14334	FBgn0038498	beaten path IIa	2.15E-02	115	7	6.1%
GO:0031175 neurite morphogenesis	CG5580	FBgn0010575	scribbler	2.15E-02	115	7	6.1%
GO:0031175 neurite morphogenesis	CG7555	FBgn0036736		2.15E-02	115	7	6.1%
GO:0031175 neurite morphogenesis	CG8168	NA	NA	2.15E-02	115	7	6.1%
GO:0031175 neurite morphogenesis	CG8581	FBgn0011592	frazzled	2.15E-02	115	7	6.1%
GO:0031175 neurite morphogenesis	CG8978	FBgn0001961	Suppressor of profilin 2	2.15E-02	115	7	6.1%
GO:0007033 vacuole organization and biogenesis	CG12156	FBgn0029959		2.43E-02	26	3	11.5%
GO:0007033 vacuole organization and biogenesis	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	2.43E-02	26	3	11.5%
GO:0007033 vacuole organization and biogenesis	CG5081	FBgn0033583	Syntaxin 7	2.43E-02	26	3	11.5%
GO:0007040 lysosome organization and biogenesis	CG12156	FBgn0029959		2.43E-02	26	3	11.5%
GO:0007040 lysosome organization and biogenesis	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	2.43E-02	26	3	11.5%
GO:0007040 lysosome organization and biogenesis	CG5081	FBgn0033583	Syntaxin 7	2.43E-02	26	3	11.5%
GO:0006887 exocytosis	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	2.86E-02	122	7	5.7%
GO:0006887 exocytosis	CG5081	FBgn0033583	Syntaxin 7	2.86E-02	122	7	5.7%
GO:0006887 exocytosis	CG5341	FBgn0034367		2.86E-02	122	7	5.7%
GO:0006887 exocytosis	CG5675	FBgn0026313		2.86E-02	122	7	5.7%
GO:0006887 exocytosis	CG7576	FBgn0005586	Rab-protein 3	2.86E-02	122	7	5.7%
GO:0006887 exocytosis	CG7605	FBgn0037072		2.86E-02	122	7	5.7%
GO:0006887 exocytosis	CG9931	NA	NA	2.86E-02	122	7	5.7%

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GO:0045045 secretory pathway	CG12532	FBgn0010380	Beta Adaptin	3.15E-02	210	10	4.8%
GO:0045045 secretory pathway	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	3.15E-02	210	10	4.8%
GO:0045045 secretory pathway	CG5081	FBgn0033583	Syntaxin 7	3.15E-02	210	10	4.8%
GO:0045045 secretory pathway	CG5341	FBgn0034367		3.15E-02	210	10	4.8%
GO:0045045 secretory pathway	CG5675	FBgn0026313		3.15E-02	210	10	4.8%
GO:0045045 secretory pathway	CG7576	FBgn0005586	Rab-protein 3	3.15E-02	210	10	4.8%
GO:0045045 secretory pathway	CG7605	FBgn0037072		3.15E-02	210	10	4.8%
GO:0045045 secretory pathway	CG8639	FBgn0033313		3.15E-02	210	10	4.8%
GO:0045045 secretory pathway	CG9778	FBgn0037233		3.15E-02	210	10	4.8%
GO:0045045 secretory pathway	CG9931	NA	NA	3.15E-02	210	10	4.8%
GO:0006904 vesicle docking during exocytosis	CG5081	FBgn0033583	Syntaxin 7	3.24E-02	29	3	10.3%
GO:0006904 vesicle docking during exocytosis	CG5341	FBgn0034367		3.24E-02	29	3	10.3%
GO:0006904 vesicle docking during exocytosis	CG5675	FBgn0026313		3.24E-02	29	3	10.3%
GO:0048278 vesicle docking	CG5081	FBgn0033583	Syntaxin 7	3.24E-02	29	3	10.3%
GO:0048278 vesicle docking	CG5341	FBgn0034367		3.24E-02	29	3	10.3%
GO:0048278 vesicle docking	CG5675	FBgn0026313		3.24E-02	29	3	10.3%
GO:0016082 synaptic vesicle priming	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	3.30E-02	12	2	16.7%
GO:0016082 synaptic vesicle priming	CG9931	NA	NA	3.30E-02	12	2	16.7%
GO:0006511 ubiquitin-dependent protein catabolism	CG15817	FBgn0028476		3.35E-02	74	5	6.8%
GO:0006511 ubiquitin-dependent protein catabolism	CG3416	FBgn0002787	Mov34	3.35E-02	74	5	6.8%
GO:0006511 ubiquitin-dependent protein catabolism	CG3431	FBgn0011327	Ubiquitin C-terminal hydrolase	3.35E-02	74	5	6.8%
GO:0006511 ubiquitin-dependent protein catabolism	CG5384	FBgn0032216		3.35E-02	74	5	6.8%

GO:0006511 ubiquitin-dependent protein catabolism	CG8494	FBgn0033916		3.35E-02	74	5	6.8%
GO:0006512 ubiquitin cycle	CG15817	FBgn0028476		3.38E-02	183	9	4.9%
GO:0006512 ubiquitin cycle	CG3431	FBgn0011327	Ubiquitin C-terminal hydrolase	3.38E-02	183	9	4.9%
GO:0006512 ubiquitin cycle	CG5384	FBgn0032216		3.38E-02	183	9	4.9%
GO:0006512 ubiquitin cycle	CG6256	NA	NA	3.38E-02	183	9	4.9%
GO:0006512 ubiquitin cycle	CG6613	FBgn0034694		3.38E-02	183	9	4.9%
GO:0006512 ubiquitin cycle	CG6720	FBgn0015320	Ubiquitin conjugating enzyme 2	3.38E-02	183	9	4.9%
GO:0006512 ubiquitin cycle	CG7555	FBgn0036736		3.38E-02	183	9	4.9%
GO:0006512 ubiquitin cycle	CG8494	FBgn0033916		3.38E-02	183	9	4.9%
GO:0006512 ubiquitin cycle	CG9041	NA	NA	3.38E-02	183	9	4.9%
GO:0019941 modification-dependent protein catabolism	CG15817	FBgn0028476		3.69E-02	76	5	6.6%
GO:0019941 modification-dependent protein catabolism	CG3416	FBgn0002787	Mov34	3.69E-02	76	5	6.6%
GO:0019941 modification-dependent protein catabolism	CG3431	FBgn0011327	Ubiquitin C-terminal hydrolase	3.69E-02	76	5	6.6%
GO:0019941 modification-dependent protein catabolism	CG5384	FBgn0032216		3.69E-02	76	5	6.6%
GO:0019941 modification-dependent protein catabolism	CG8494	FBgn0033916		3.69E-02	76	5	6.6%
GO:0006720 isoprenoid metabolism	CG12389	FBgn0025373	Farnesyl pyrophosphate synthase	3.84E-02	13	2	15.4%
GO:0006720 isoprenoid metabolism	CG5919	FBgn0038876		3.84E-02	13	2	15.4%
GO:0030166 proteoglycan biosynthesis	CG10067	FBgn0000044	Actin 57B	3.84E-02	13	2	15.4%
GO:0030166 proteoglycan biosynthesis	CG8433	NA	NA	3.84E-02	13	2	15.4%
GO:0007600 sensory perception	CG11390	FBgn0011695	Ejaculatory bulb protein III	4.38E-02	192	9	4.7%
GO:0007600 sensory perception	CG13495	FBgn0041238	Gustatory receptor 58b	4.38E-02	192	9	4.7%
GO:0007600 sensory perception	CG15860	FBgn0060296	painless	4.38E-02	192	9	4.7%
GO:0007600 sensory perception	CG17885	FBgn0029521	Odorant receptor 1a	4.38E-02	192	9	4.7%
GO:0007600 sensory perception	CG6618	FBgn0029137		4.38E-02	192	9	4.7%

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GO:0007600 sensory perception	CG6642	FBgn0011293	antennal protein 10	4.38E-02	192	9	4.7%
GO:0007600 sensory perception	CG7000	FBgn0038867		4.38E-02	192	9	4.7%
GO:0007600 sensory perception	CG9358	FBgn0035089	Pherokine 3	4.38E-02	192	9	4.7%
GO:0007600 sensory perception	CG9668	FBgn0003250	Rhodopsin 4	4.38E-02	192	9	4.7%
GO:0006029 proteoglycan metabolism	CG10067	FBgn0000044	Actin 57B	4.41E-02	14	2	14.3%
GO:0006029 proteoglycan metabolism	CG8433	NA	NA	4.41E-02	14	2	14.3%
GO:0046903 secretion	CG12532	FBgn0010380	Beta Adaptin	4.46E-02	223	10	4.5%
GO:0046903 secretion	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	4.46E-02	223	10	4.5%
GO:0046903 secretion	CG5081	FBgn0033583	Syntaxin 7	4.46E-02	223	10	4.5%
GO:0046903 secretion	CG5341	FBgn0034367		4.46E-02	223	10	4.5%
GO:0046903 secretion	CG5675	FBgn0026313		4.46E-02	223	10	4.5%
GO:0046903 secretion	CG7576	FBgn0005586	Rab-protein 3	4.46E-02	223	10	4.5%
GO:0046903 secretion	CG7605	FBgn0037072		4.46E-02	223	10	4.5%
GO:0046903 secretion	CG8639	FBgn0033313		4.46E-02	223	10	4.5%
GO:0046903 secretion	CG9778	FBgn0037233		4.46E-02	223	10	4.5%
GO:0046903 secretion	CG9931	NA	NA	4.46E-02	223	10	4.5%
GO:0008293 torso signaling pathway	CG12559	FBgn0003256	rolled	4.51E-02	33	3	9.1%
GO:0008293 torso signaling pathway	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	4.51E-02	33	3	9.1%
GO:0008293 torso signaling pathway	CG9358	FBgn0035089	Pherokine 3	4.51E-02	33	3	9.1%
GO:0007507 heart development	CG10067	FBgn0000044	Actin 57B	4.91E-02	57	4	7.0%
GO:0007507 heart development	CG12532	FBgn0010380	Beta Adaptin	4.91E-02	57	4	7.0%
GO:0007507 heart development	CG12559	FBgn0003256	rolled	4.91E-02	57	4	7.0%
GO:0007507 heart development	CG1720	NA	NA	4.91E-02	57	4	7.0%

Brain-specific age-related GO terms in Cluster 1

Brain-specific age-related GO terms in Cluster 2 (Upregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0006458 'de novo' protein folding	CG6719	FBgn0037893		1.26E-02	11	2	18.2%
GO:0006458 'de novo' protein folding	CG7235	FBgn0031728		1.26E-02	11	2	18.2%
GO:0008103 oocyte microtubule cytoskeleton polarization	CG4909	FBgn0040294	Plenty of SH3s	1.74E-02	13	2	15.4%
GO:0008103 oocyte microtubule cytoskeleton polarization	CG9401	FBgn0002736	mago nashi	1.74E-02	13	2	15.4%
GO:0006270 DNA replication initiation	CG3658	FBgn0026143		2.01E-02	14	2	14.3%
GO:0006270 DNA replication initiation	CG4206	FBgn0024332	Minichromosome maintenance 3	2.01E-02	14	2	14.3%
GO:0006406 mRNA-nucleus export	CG12752	FBgn0028411	NTF2-related export protein 1	2.60E-02	16	2	12.5%
GO:0006406 mRNA-nucleus export	CG9401	FBgn0002736	mago nashi	2.60E-02	16	2	12.5%
GO:0009967 positive regulation of signal transduction	CG5031	NA	NA	2.60E-02	16	2	12.5%
GO:0009967 positive regulation of signal transduction	CG3929	FBgn0000524	deltex	2.60E-02	16	2	12.5%
GO:0051028 mRNA transport	CG12752	FBgn0028411	NTF2-related export protein 1	2.60E-02	16	2	12.5%
GO:0051028 mRNA transport	CG9401	FBgn0002736	mago nashi	2.60E-02	16	2	12.5%
GO:0006512 ubiquitin cycle	CG14472	FBgn0011230	purity of essence	2.62E-02	183	7	3.8%
GO:0006512 ubiquitin cycle	CG3929	FBgn0000524	deltex	2.62E-02	183	7	3.8%
GO:0006512 ubiquitin cycle	CG4909	FBgn0040294	Plenty of SH3s	2.62E-02	183	7	3.8%
GO:0006512 ubiquitin cycle	CG5555	FBgn0038686		2.62E-02	183	7	3.8%
GO:0006512 ubiquitin cycle	CG6759	FBgn0025781		2.62E-02	183	7	3.8%
GO:0006512 ubiquitin cycle	CG7220	FBgn0033544		2.62E-02	183	7	3.8%
GO:0006512 ubiquitin cycle	CG9041	NA	NA	2.62E-02	183	7	3.8%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG3381	FBgn0051961		2.73E-02	72	4	5.6%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG4909	FBgn0040294	Plenty of SH3s	2.73E-02	72	4	5.6%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG8339	FBgn0020251	sulfateless	2.73E-02	72	4	5.6%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG9401	FBgn0002736	mago nashi	2.73E-02	72	4	5.6%
GO:0006260 DNA replication	CG12176	FBgn0030506	Ligase4	2.94E-02	109	5	4.6%
GO:0006260 DNA replication	CG3658	FBgn0026143		2.94E-02	109	5	4.6%
GO:0006260 DNA replication	CG4206	FBgn0024332	Minichromosome maintenance 3	2.94E-02	109	5	4.6%
GO:0006260 DNA replication	CG4337	FBgn0010438	mitochondrial single stranded DNA-binding protein	2.94E-02	109	5	4.6%
GO:0006260 DNA replication	CG6019	FBgn0002905	mutagen-sensitive 308	2.94E-02	109	5	4.6%

Brain-specific age-related GO terms in Cluster 2

GO:0016325 oocyte microtubule cytoskeleton organization	CG4909	FBgn0040294	Plenty of SH3s	3.59E-02	19	2	10.5%
GO:0016325 oocyte microtubule cytoskeleton organization	CG9401	FBgn0002736	mago nashi	3.59E-02	19	2	10.5%
GO:0030951 establishment and or maintenance of microtubule cytoskeleton polarity	CG4909	FBgn0040294	Plenty of SH3s	3.59E-02	19	2	10.5%
GO:0030951 establishment and or maintenance of microtubule cytoskeleton polarity	CG9401	FBgn0002736	mago nashi	3.59E-02	19	2	10.5%
GO:0030952 establishment and or maintenance of cytoskeleton polarity	CG4909	FBgn0040294	Plenty of SH3s	3.59E-02	19	2	10.5%
GO:0030952 establishment and or maintenance of cytoskeleton polarity	CG9401	FBgn0002736	mago nashi	3.59E-02	19	2	10.5%
GO:0006405 RNA-nucleus export	CG12752	FBgn0028411	NTF2-related export protein 1	3.95E-02	20	2	10.0%
GO:0006405 RNA-nucleus export	CG9401	FBgn0002736	mago nashi	3.95E-02	20	2	10.0%
GO:0009063 amino acid catabolism	CG17691	FBgn0039993		4.25E-02	49	3	6.1%
GO:0009063 amino acid catabolism	CG5241	FBgn0036564		4.25E-02	49	3	6.1%
GO:0009063 amino acid catabolism	CG7399	FBgn0001208	Henna	4.25E-02	49	3	6.1%
GO:0009310 amine catabolism	CG17691	FBgn0039993		4.93E-02	52	3	5.8%
GO:0009310 amine catabolism	CG5241	FBgn0036564		4.93E-02	52	3	5.8%
GO:0009310 amine catabolism	CG7399	FBgn0001208	Henna	4.93E-02	52	3	5.8%

Brain-specific age-related GO terms in Cluster 3 (Downregulated)							
GO term	CG ID	FB ID	Full name	P-value	Total gene	Changed gene	% of change
GO:0031109 microtubule polymerization or depolymerization	CG17566	FBgn0010097	gamma-Tubulin at 37C	1.13E-03	13	3	23.1%
GO:0031109 microtubule polymerization or depolymerization	CG18637	FBgn0030549		1.13E-03	13	3	23.1%
GO:0031109 microtubule polymerization or depolymerization	CG8308	FBgn0004236	alpha-Tubulin at 67C	1.13E-03	13	3	23.1%
GO:0006413 translational initiation	CG10124	FBgn0035709		2.45E-03	57	5	8.8%
GO:0006413 translational initiation	CG10161	FBgn0040227	Eukaryotic initiation factor 3 p66 subunit	2.45E-03	57	5	8.8%
GO:0006413 translational initiation	CG17737	FBgn0035423		2.45E-03	57	5	8.8%
GO:0006413 translational initiation	CG2677	FBgn0024996		2.45E-03	57	5	8.8%
GO:0006413 translational initiation	CG8900	FBgn0010411	Ribosomal protein S18	2.45E-03	57	5	8.8%
GO:0007067 mitosis	CG1618	FBgn0000346	comatose	1.07E-02	220	9	4.1%
GO:0007067 mitosis	CG1625	FBgn0033447		1.07E-02	220	9	4.1%
GO:0007067 mitosis	CG17081	FBgn0036480		1.07E-02	220	9	4.1%
GO:0007067 mitosis	CG17493	FBgn0040010		1.07E-02	220	9	4.1%
GO:0007067 mitosis	CG17566	FBgn0010097	gamma-Tubulin at 37C	1.07E-02	220	9	4.1%
GO:0007067 mitosis	CG2210	FBgn0000150	abnormal wing discs	1.07E-02	220	9	4.1%
GO:0007067 mitosis	CG3068	FBgn0000147	aurora	1.07E-02	220	9	4.1%
GO:0007067 mitosis	CG5692	FBgn0040080	rapsynoid	1.07E-02	220	9	4.1%
GO:0007067 mitosis	CG8308	FBgn0004236	alpha-Tubulin at 67C	1.07E-02	220	9	4.1%
GO:0000087 M phase of mitotic cell cycle	CG1618	FBgn0000346	comatose	1.11E-02	221	9	4.1%
GO:0000087 M phase of mitotic cell cycle	CG1625	FBgn0033447		1.11E-02	221	9	4.1%
GO:0000087 M phase of mitotic cell cycle	CG17081	FBgn0036480		1.11E-02	221	9	4.1%
GO:0000087 M phase of mitotic cell cycle	CG17493	FBgn0040010		1.11E-02	221	9	4.1%
GO:0000087 M phase of mitotic cell cycle	CG17566	FBgn0010097	gamma-Tubulin at 37C	1.11E-02	221	9	4.1%
GO:0000087 M phase of mitotic cell cycle	CG2210	FBgn0000150	abnormal wing discs	1.11E-02	221	9	4.1%
GO:0000087 M phase of mitotic cell cycle	CG3068	FBgn0000147	aurora	1.11E-02	221	9	4.1%
GO:0000087 M phase of mitotic cell cycle	CG5692	FBgn0040080	rapsynoid	1.11E-02	221	9	4.1%
GO:0000087 M phase of mitotic cell cycle	CG8308	FBgn0004236	alpha-Tubulin at 67C	1.11E-02	221	9	4.1%
GO:0050790 regulation of enzyme activity	CG2835	FBgn0001123	G protein salpha 60A	1.19E-02	29	3	10.3%
GO:0050790 regulation of enzyme activity	CG4237	FBgn0020655	GTPase-activating protein 69C	1.19E-02	29	3	10.3%
GO:0050790 regulation of enzyme activity	CG7508	FBgn0010433	atonal	1.19E-02	29	3	10.3%
GO:0006123 mitochondrial electron transport cytochrome c to oxygen	CG11015	FBgn0031830		1.37E-02	11	2	18.2%
GO:0006123 mitochondrial electron transport cytochrome c to oxygen	CG17280	FBgn0034877		1.37E-02	11	2	18.2%
GO:0035146 tube fusion	CG17750	NA	NA	1.37E-02	11	2	18.2%
GO:0035146 tube fusion	CG18637	FBgn0030549		1.37E-02	11	2	18.2%
GO:0035147 tracheal branch fusion	CG17750	NA	NA	1.37E-02	11	2	18.2%
GO:0035147 tracheal branch fusion	CG18637	FBgn0030549		1.37E-02	11	2	18.2%

GO:0043085 positive regulation of enzyme activity	CG2835	FBgn0001123	G protein salpha 60A	1.90E-02	13	2	15.4%
GO:0043085 positive regulation of enzyme activity	CG7508	FBgn0010433	atonal	1.90E-02	13	2	15.4%
GO:0000278 mitotic cell cycle	CG1618	FBgn0000346	comatose	2.04E-02	245	9	3.7%
GO:0000278 mitotic cell cycle	CG1625	FBgn0033447		2.04E-02	245	9	3.7%
GO:0000278 mitotic cell cycle	CG17081	FBgn0036480		2.04E-02	245	9	3.7%
GO:0000278 mitotic cell cycle	CG17493	FBgn0040010		2.04E-02	245	9	3.7%
GO:0000278 mitotic cell cycle	CG17566	FBgn0010097	gamma-Tubulin at 37C	2.04E-02	245	9	3.7%
GO:0000278 mitotic cell cycle	CG2210	FBgn0000150	abnormal wing discs	2.04E-02	245	9	3.7%
GO:0000278 mitotic cell cycle	CG3068	FBgn0000147	aurora	2.04E-02	245	9	3.7%
GO:0000278 mitotic cell cycle	CG5692	FBgn0040080	rapsynoid	2.04E-02	245	9	3.7%
GO:0000278 mitotic cell cycle	CG8308	FBgn0004236	alpha-Tubulin at 67C	2.04E-02	245	9	3.7%
GO:0007539 primary sex determination soma	CG6315	FBgn0000662	female lethal d	2.19E-02	14	2	14.3%
GO:0007539 primary sex determination soma	CG8704	FBgn0010109	deadpan	2.19E-02	14	2	14.3%
GO:0008105 asymmetric protein localization	CG10701	FBgn0011661	Moesin	2.31E-02	37	3	8.1%
GO:0008105 asymmetric protein localization	CG3068	FBgn0000147	aurora	2.31E-02	37	3	8.1%
GO:0008105 asymmetric protein localization	CG5692	FBgn0040080	rapsynoid	2.31E-02	37	3	8.1%
GO:0007538 primary sex determination	CG6315	FBgn0000662	female lethal d	2.83E-02	16	2	12.5%
GO:0007538 primary sex determination	CG8704	FBgn0010109	deadpan	2.83E-02	16	2	12.5%
GO:0007017 microtubule-based process	CG17566	FBgn0010097	gamma-Tubulin at 37C	3.08E-02	181	7	3.9%
GO:0007017 microtubule-based process	CG17866	FBgn0001313	male fertility factor kl2	3.08E-02	181	7	3.9%
GO:0007017 microtubule-based process	CG18637	FBgn0030549		3.08E-02	181	7	3.9%
GO:0007017 microtubule-based process	CG2210	FBgn0000150	abnormal wing discs	3.08E-02	181	7	3.9%
GO:0007017 microtubule-based process	CG3068	FBgn0000147	aurora	3.08E-02	181	7	3.9%
GO:0007017 microtubule-based process	CG5692	FBgn0040080	rapsynoid	3.08E-02	181	7	3.9%
GO:0007017 microtubule-based process	CG8308	FBgn0004236	alpha-Tubulin at 67C	3.08E-02	181	7	3.9%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG17566	FBgn0010097	gamma-Tubulin at 37C	3.14E-02	72	4	5.6%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG18637	FBgn0030549		3.14E-02	72	4	5.6%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG5692	FBgn0040080	rapsynoid	3.14E-02	72	4	5.6%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG8308	FBgn0004236	alpha-Tubulin at 67C	3.14E-02	72	4	5.6%
GO:0006614 SRP-dependent cotranslational protein-membrane targeting	CG5064	FBgn0035947		3.17E-02	17	2	11.8%
GO:0006614 SRP-dependent cotranslational protein-membrane targeting	CG5417	FBgn0038808		3.17E-02	17	2	11.8%
GO:0006605 protein targeting	CG1625	FBgn0033447		3.19E-02	223	8	3.6%
GO:0006605 protein targeting	CG17081	FBgn0036480		3.19E-02	223	8	3.6%
GO:0006605 protein targeting	CG17866	FBgn0001313	male fertility factor kl2	3.19E-02	223	8	3.6%
GO:0006605 protein targeting	CG2852	FBgn0034753		3.19E-02	223	8	3.6%
GO:0006605 protein targeting	CG3511	FBgn0035027		3.19E-02	223	8	3.6%
GO:0006605 protein targeting	CG5064	FBgn0035947		3.19E-02	223	8	3.6%
GO:0006605 protein targeting	CG5417	FBgn0038808		3.19E-02	223	8	3.6%
GO:0006605 protein targeting	CG5692	FBgn0040080	rapsynoid	3.19E-02	223	8	3.6%

Brain-specific age-related GO terms in Cluster 3

GO:0006613 cotranslational protein-membrane targeting	CG5064	FBgn0035947		3.53E-02	18	2	11.1%
GO:0006613 cotranslational protein-membrane targeting	CG5417	FBgn0038808		3.53E-02	18	2	11.1%
GO:0018993 somatic sex determination	CG6315	FBgn0000662	female lethal d	3.53E-02	18	2	11.1%
GO:0018993 somatic sex determination	CG8704	FBgn0010109	deadpan	3.53E-02	18	2	11.1%
GO:0045047 protein-ER targeting	CG5064	FBgn0035947		3.53E-02	18	2	11.1%
GO:0045047 protein-ER targeting	CG5417	FBgn0038808		3.53E-02	18	2	11.1%
GO:0051258 protein polymerization	CG17566	FBgn0010097	gamma-Tubulin at 37C	3.53E-02	18	2	11.1%
GO:0051258 protein polymerization	CG8308	FBgn0004236	alpha-Tubulin at 67C	3.53E-02	18	2	11.1%
GO:0007530 sex determination	CG3726	FBgn0029824		3.62E-02	44	3	6.8%
GO:0007530 sex determination	CG6315	FBgn0000662	female lethal d	3.62E-02	44	3	6.8%
GO:0007530 sex determination	CG8704	FBgn0010109	deadpan	3.62E-02	44	3	6.8%
GO:0007059 chromosome segregation	CG11330	FBgn0000351	cortex	3.71E-02	111	5	4.5%
GO:0007059 chromosome segregation	CG17493	FBgn0040010		3.71E-02	111	5	4.5%
GO:0007059 chromosome segregation	CG17566	FBgn0010097	gamma-Tubulin at 37C	3.71E-02	111	5	4.5%
GO:0007059 chromosome segregation	CG3068	FBgn0000147	aurora	3.71E-02	111	5	4.5%
GO:0007059 chromosome segregation	CG8308	FBgn0004236	alpha-Tubulin at 67C	3.71E-02	111	5	4.5%
GO:0016071 mRNA metabolism	CG10466	FBgn0032822		3.76E-02	189	7	3.7%
GO:0016071 mRNA metabolism	CG2163	FBgn0005648		3.76E-02	189	7	3.7%
GO:0016071 mRNA metabolism	CG2925	FBgn0014366	noisette	3.76E-02	189	7	3.7%
GO:0016071 mRNA metabolism	CG4555	NA	NA	3.76E-02	189	7	3.7%
GO:0016071 mRNA metabolism	CG4901	FBgn0032194		3.76E-02	189	7	3.7%
GO:0016071 mRNA metabolism	CG6315	FBgn0000662	female lethal d	3.76E-02	189	7	3.7%
GO:0016071 mRNA metabolism	CG6615	NA	NA	3.76E-02	189	7	3.7%
GO:0006612 protein-membrane targeting	CG5064	FBgn0035947		4.29E-02	20	2	10.0%
GO:0006612 protein-membrane targeting	CG5417	FBgn0038808		4.29E-02	20	2	10.0%
GO:0051128 regulation of cell organization and biogenesis	CG15112	FBgn0000578	enabled	4.29E-02	20	2	10.0%
GO:0051128 regulation of cell organization and biogenesis	CG18637	FBgn0030549		4.29E-02	20	2	10.0%

Brain-specific age-related GO terms in Cluster 4 (Downregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0050830 defense response to Gram-positive bacteria	CG1385	FBgn0010385	Defensin	1.15E-02	12	2	16.7%
GO:0050830 defense response to Gram-positive bacteria	CG6134	FBgn0003495	spatzle	1.15E-02	12	2	16.7%
GO:0006979 response to oxidative stress	CG4026	FBgn0032147	Inositol 1,4,5-triphosphate kinase 1	1.78E-02	15	2	13.3%
GO:0006979 response to oxidative stress	disp	FBgn0029088	dispatched	1.78E-02	15	2	13.3%
GO:0006099 tricarboxylic acid cycle	CG3861	FBgn0026708		2.56E-02	46	3	6.5%
GO:0006099 tricarboxylic acid cycle	CG7010	FBgn0028325		2.56E-02	46	3	6.5%
GO:0006099 tricarboxylic acid cycle	CG7998	FBgn0038587		2.56E-02	46	3	6.5%
GO:0009060 aerobic respiration	CG3861	FBgn0026708		2.56E-02	46	3	6.5%
GO:0009060 aerobic respiration	CG7010	FBgn0028325		2.56E-02	46	3	6.5%
GO:0009060 aerobic respiration	CG7998	FBgn0038587		2.56E-02	46	3	6.5%
GO:0045333 cellular respiration	CG3861	FBgn0026708		2.56E-02	46	3	6.5%
GO:0045333 cellular respiration	CG7010	FBgn0028325		2.56E-02	46	3	6.5%
GO:0045333 cellular respiration	CG7998	FBgn0038587		2.56E-02	46	3	6.5%
GO:0046356 acetyl-CoA catabolism	CG3861	FBgn0026708		2.56E-02	46	3	6.5%
GO:0046356 acetyl-CoA catabolism	CG7010	FBgn0028325		2.56E-02	46	3	6.5%
GO:0046356 acetyl-CoA catabolism	CG7998	FBgn0038587		2.56E-02	46	3	6.5%
GO:0006084 acetyl-CoA metabolism	CG3861	FBgn0026708		2.71E-02	47	3	6.4%
GO:0006084 acetyl-CoA metabolism	CG7010	FBgn0028325		2.71E-02	47	3	6.4%
GO:0006084 acetyl-CoA metabolism	CG7998	FBgn0038587		2.71E-02	47	3	6.4%
GO:0009109 coenzyme catabolism	CG3861	FBgn0026708		2.71E-02	47	3	6.4%
GO:0009109 coenzyme catabolism	CG7010	FBgn0028325		2.71E-02	47	3	6.4%
GO:0009109 coenzyme catabolism	CG7998	FBgn0038587		2.71E-02	47	3	6.4%
GO:0051187 cofactor catabolism	CG3861	FBgn0026708		2.86E-02	48	3	6.3%
GO:0051187 cofactor catabolism	CG7010	FBgn0028325		2.86E-02	48	3	6.3%
GO:0051187 cofactor catabolism	CG7998	FBgn0038587		2.86E-02	48	3	6.3%
GO:0051128 regulation of cell organization and biogenesis	CG7558	FBgn0011744	Actin-related protein 66B	3.08E-02	20	2	10.0%
GO:0051128 regulation of cell organization and biogenesis	CG7859	NA	NA	3.08E-02	20	2	10.0%
GO:0042445 hormone metabolism	CG15106	FBgn0034406	Juvenile hormone epoxide hydrolase 3	3.68E-02	22	2	9.1%
GO:0042445 hormone metabolism	CG9122	FBgn0035187		3.68E-02	22	2	9.1%
GO:0007224 smoothened signaling pathway	disp	FBgn0029088	dispatched	3.99E-02	23	2	8.7%
GO:0007224 smoothened signaling pathway	fu	NA	NA	3.99E-02	23	2	8.7%
GO:0006092 main pathways of carbohydrate metabolism	CG3001	FBgn0001186	Hexokinase A	4.98E-02	100	4	4.0%
GO:0006092 main pathways of carbohydrate metabolism	CG3861	FBgn0026708		4.98E-02	100	4	4.0%

GO:0006092 main pathways of carbohydrate metabolism	CG7010	FBgn0028325		4.98E-02	100	4	4.0%
GO:0006092 main pathways of carbohydrate metabolism	CG7998	FBgn0038587		4.98E-02	100	4	4.0%