

Acp-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:0008154 actin polymerization and or depolymerization	CG10724	FBgn0036357		5.30E-10	21	10	47.6%
GO:0008154 actin polymerization and or depolymerization	CG12530	FBgn0010341	Cdc42	5.30E-10	21	10	47.6%
GO:0008154 actin polymerization and or depolymerization	CG17158	FBgn0011570	capping protein beta	5.30E-10	21	10	47.6%
GO:0008154 actin polymerization and or depolymerization	CG4254	FBgn0011726	twinstar	5.30E-10	21	10	47.6%
GO:0008154 actin polymerization and or depolymerization	CG4560	FBgn0038369		5.30E-10	21	10	47.6%
GO:0008154 actin polymerization and or depolymerization	CG5061	FBgn0028388	capulet	5.30E-10	21	10	47.6%
GO:0008154 actin polymerization and or depolymerization	CG5972	FBgn0031781		5.30E-10	21	10	47.6%
GO:0008154 actin polymerization and or depolymerization	CG8936	FBgn0065032		5.30E-10	21	10	47.6%
GO:0008154 actin polymerization and or depolymerization	CG9553	FBgn0000308	chickadee	5.30E-10	21	10	47.6%
GO:0008154 actin polymerization and or depolymerization	CG9901	FBgn0011742	Actin-related protein 14D	5.30E-10	21	10	47.6%
GO:0051258 protein polymerization	CG12530	FBgn0010341	Cdc42	2.33E-09	18	9	50.0%
GO:0051258 protein polymerization	CG3401	FBgn0003888	beta-Tubulin at 60D	2.33E-09	18	9	50.0%
GO:0051258 protein polymerization	CG4560	FBgn0038369		2.33E-09	18	9	50.0%
GO:0051258 protein polymerization	CG4869	FBgn0003890	beta-Tubulin at 97EF	2.33E-09	18	9	50.0%
GO:0051258 protein polymerization	CG5972	FBgn0031781		2.33E-09	18	9	50.0%
GO:0051258 protein polymerization	CG8936	FBgn0065032		2.33E-09	18	9	50.0%
GO:0051258 protein polymerization	CG9277	FBgn0003887	beta-Tubulin at 56D	2.33E-09	18	9	50.0%
GO:0051258 protein polymerization	CG9476	FBgn0003886	alpha-Tubulin at 85E	2.33E-09	18	9	50.0%
GO:0051258 protein polymerization	CG9553	FBgn0000308	chickadee	2.33E-09	18	9	50.0%
GO:0030029 actin filament-based process	CG10545	FBgn0001105	G protein beta-subunit 13F	8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG10701	FBgn0011661	Moesin	8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG10724	FBgn0036357		8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG11341	FBgn0035533		8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG12530	FBgn0010341	Cdc42	8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG17158	FBgn0011570	capping protein beta	8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG1768	FBgn0011202	diaphanous	8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG1977	FBgn0003470	alpha Spectrin	8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG4254	FBgn0011726	twinstar	8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG4560	FBgn0038369		8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG5061	FBgn0028388	capulet	8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG5972	FBgn0031781		8.04E-08	92	16	17.4%

Age-specific age-related GO terms in Cluster 1

GO:0030029 actin filament-based process	CG8416	FBgn0014020		8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG8936	FBgn0065032		8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG9553	FBgn0000308	chickadee	8.04E-08	92	16	17.4%
GO:0030029 actin filament-based process	CG9901	FBgn0011742	Actin-related protein 14D	8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG10545	FBgn0001105	G protein beta-subunit 13F	8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG10701	FBgn0011661	Moesin	8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG10724	FBgn0036357		8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG11341	FBgn0035533		8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG12530	FBgn0010341	Cdc42	8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG17158	FBgn0011570	capping protein beta	8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG1768	FBgn0011202	diaphanous	8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG1977	FBgn0003470	alpha Spectrin	8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG4254	FBgn0011726	twinstar	8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG4560	FBgn0038369		8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG5061	FBgn0028388	capulet	8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG5972	FBgn0031781		8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG8416	FBgn0014020		8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG8936	FBgn0065032		8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG9553	FBgn0000308	chickadee	8.04E-08	92	16	17.4%
GO:0030036 actin cytoskeleton organization and biogenesis	CG9901	FBgn0011742	Actin-related protein 14D	8.04E-08	92	16	17.4%
GO:0035152 regulation of tracheal tube architecture	CG11949	FBgn0010434	coracle	2.58E-07	21	8	38.1%
GO:0035152 regulation of tracheal tube architecture	CG12210	FBgn0003660	Synaptobrevin	2.58E-07	21	8	38.1%
GO:0035152 regulation of tracheal tube architecture	CG12369	FBgn0010238	Lachesin	2.58E-07	21	8	38.1%
GO:0035152 regulation of tracheal tube architecture	CG14779	FBgn0013720	pickel	2.58E-07	21	8	38.1%

Age-specific age-related GO terms in Cluster 1

GO:0035152 regulation of tracheal tube architecture	CG5670	FBgn0002921	Na pump alpha subunit	2.58E-07	21	8	38.1%
GO:0035152 regulation of tracheal tube architecture	CG6827	FBgn0013997	Neurexin IV	2.58E-07	21	8	38.1%
GO:0035152 regulation of tracheal tube architecture	CG8416	FBgn0014020		2.58E-07	21	8	38.1%
GO:0035152 regulation of tracheal tube architecture	CG9261	FBgn0015777	nervana 2	2.58E-07	21	8	38.1%
GO:0000902 cellular morphogenesis	CG10701	FBgn0011661	Moesin	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG1084	FBgn0037240	Contactin	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG11949	FBgn0010434	coracle	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG12530	FBgn0010341	Cdc42	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG15792	FBgn0005634	zipper	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG18319	FBgn0000173	bendless	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG1977	FBgn0003470	alpha Spectrin	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG2275	FBgn0001291	Jun-related antigen	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG3637	FBgn0025865	Cortactin	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG4006	FBgn0010379		1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG1956	FBgn0004636	Roughened	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG5061	FBgn0028388	capulet	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG5670	FBgn0002921	Na pump alpha subunit	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG5972	FBgn0031781		1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG6383	FBgn0000368	crumbs	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG6827	FBgn0013997	Neurexin IV	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG6831	FBgn0020254	rhea	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG10939	FBgn0010620	SRY interacting protein 1	1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG8056	FBgn0052177		1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG8416	FBgn0014020		1.26E-06	215	23	10.7%
GO:0000902 cellular morphogenesis	CG9968	FBgn0030749	Annexin B11	1.26E-06	215	23	10.7%
GO:0002009 morphogenesis of an epithelium	CG10701	FBgn0011661	Moesin	4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG11949	FBgn0010434	coracle	4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG12530	FBgn0010341	Cdc42	4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG15792	FBgn0005634	zipper	4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG5248	FBgn0020278	locomotion defects	4.14E-06	122	16	13.1%

GO:0002009 morphogenesis of an epithelium	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG2275	FBgn0001291	Jun-related antigen	4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG3595	FBgn0003514	spaghetti squash	4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG1956	FBgn0004636	Roughened	4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG5562	FBgn0024234	glass bottom boat	4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG6383	FBgn0000368	crumbs	4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG6827	FBgn0013997	Neurexin IV	4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG8056	FBgn0052177		4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG8416	FBgn0014020		4.14E-06	122	16	13.1%
GO:0002009 morphogenesis of an epithelium	CG9553	FBgn0000308	chickadee	4.14E-06	122	16	13.1%
GO:0006928 cell motility	CG10724	FBgn0036357		5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG10838	FBgn0028570		5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG11081	FBgn0025741	plexin A	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG12530	FBgn0010341	Cdc42	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG15792	FBgn0005634	zipper	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG18061	NA	NA	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG3171	FBgn0046687	trapped in endoderm-1	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG3401	FBgn0003888	beta-Tubulin at 60D	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG3595	FBgn0003514	spaghetti squash	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG3637	FBgn0025865	Cortactin	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG4254	FBgn0011726	twinstar	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG4869	FBgn0003890	beta-Tubulin at 97EF	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG5803	FBgn0000636	Fasciclin 3	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG5972	FBgn0031781		5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG6831	FBgn0020254	rhea	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG7555	FBgn0036736		5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG8076	NA	NA	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG8416	FBgn0014020		5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG8440	FBgn0015754	Lissencephaly-1	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG9277	FBgn0003887	beta-Tubulin at 56D	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG9476	FBgn0003886	alpha-Tubulin at 85E	5.45E-06	234	23	9.8%
GO:0006928 cell motility	CG9755	FBgn0003165	pumilio	5.45E-06	234	23	9.8%
GO:0035151 regulation of tracheal tube size	CG11949	FBgn0010434	coracle	6.31E-06	15	6	40.0%
GO:0035151 regulation of tracheal tube size	CG12369	FBgn0010238	Lachesin	6.31E-06	15	6	40.0%
GO:0035151 regulation of tracheal tube size	CG14779	FBgn0013720	pickel	6.31E-06	15	6	40.0%
GO:0035151 regulation of tracheal tube size	CG5670	FBgn0002921	Na pump alpha subunit	6.31E-06	15	6	40.0%
GO:0035151 regulation of tracheal tube size	CG6827	FBgn0013997	Neurexin IV	6.31E-06	15	6	40.0%
GO:0035151 regulation of tracheal tube size	CG9261	FBgn0015777	nervana 2	6.31E-06	15	6	40.0%
GO:0040011 locomotion	CG10724	FBgn0036357		7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG10838	FBgn0028570		7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG11081	FBgn0025741	plexin A	7.77E-06	239	23	9.6%

Age-specific age-related GO terms in Cluster 1

GO:0040011 locomotion	CG12530	FBgn0010341	Cdc42	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG15792	FBgn0005634	zipper	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG18061	NA	NA	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG3171	FBgn0046687	trapped in endoderm-1	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG3401	FBgn0003888	beta-Tubulin at 60D	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG3595	FBgn0003514	spaghetti squash	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG3637	FBgn0025865	Cortactin	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG4254	FBgn0011726	twinstar	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG4869	FBgn0003890	beta-Tubulin at 97EF	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG5803	FBgn0000636	Fasciclin 3	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG5972	FBgn0031781		7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG6831	FBgn0020254	rhea	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG7555	FBgn0036736		7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG8076	NA	NA	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG8416	FBgn0014020		7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG8440	FBgn0015754	Lissencephaly-1	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG9277	FBgn0003887	beta-Tubulin at 56D	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG9476	FBgn0003886	alpha-Tubulin at 85E	7.77E-06	239	23	9.6%
GO:0040011 locomotion	CG9755	FBgn0003165	pumilio	7.77E-06	239	23	9.6%
GO:0035150 regulation of tube size	CG11949	FBgn0010434	coracle	1.47E-05	17	6	35.3%
GO:0035150 regulation of tube size	CG12369	FBgn0010238	Lachesin	1.47E-05	17	6	35.3%
GO:0035150 regulation of tube size	CG14779	FBgn0013720	pickel	1.47E-05	17	6	35.3%
GO:0035150 regulation of tube size	CG5670	FBgn0002921	Na pump alpha subunit	1.47E-05	17	6	35.3%
GO:0035150 regulation of tube size	CG6827	FBgn0013997	Neurexin IV	1.47E-05	17	6	35.3%
GO:0035150 regulation of tube size	CG9261	FBgn0015777	nervana 2	1.47E-05	17	6	35.3%
GO:0042306 regulation of protein-nucleus import	CG2048	FBgn0002413	discs overgrown	1.88E-05	11	5	45.5%
GO:0042306 regulation of protein-nucleus import	CG4006	FBgn0010379		1.88E-05	11	5	45.5%
GO:0042306 regulation of protein-nucleus import	CG4057	FBgn0041582		1.88E-05	11	5	45.5%
GO:0042306 regulation of protein-nucleus import	CG5848	FBgn0000250	cactus	1.88E-05	11	5	45.5%
GO:0042306 regulation of protein-nucleus import	CG9426	FBgn0032485		1.88E-05	11	5	45.5%
GO:0007163 establishment and or maintenance of cell polarity	CG10701	FBgn0011661	Moesin	2.15E-05	69	11	15.9%
GO:0007163 establishment and or maintenance of cell polarity	CG1084	FBgn0037240	Contactin	2.15E-05	69	11	15.9%
GO:0007163 establishment and or maintenance of cell polarity	CG11949	FBgn0010434	coracle	2.15E-05	69	11	15.9%
GO:0007163 establishment and or maintenance of cell polarity	CG15792	FBgn0005634	zipper	2.15E-05	69	11	15.9%
GO:0007163 establishment and or maintenance of cell polarity	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	2.15E-05	69	11	15.9%

GO:0007163 establishment and or maintenance of cell polarity	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	2.15E-05	69	11	15.9%
GO:0007163 establishment and or maintenance of cell polarity	CG2275	FBgn0001291	Jun-related antigen	2.15E-05	69	11	15.9%
GO:0007163 establishment and or maintenance of cell polarity	CG6383	FBgn0000368	crumbs	2.15E-05	69	11	15.9%
GO:0007163 establishment and or maintenance of cell polarity	CG6827	FBgn0013997	Neurexin IV	2.15E-05	69	11	15.9%
GO:0007163 establishment and or maintenance of cell polarity	CG8056	FBgn0052177		2.15E-05	69	11	15.9%
GO:0007163 establishment and or maintenance of cell polarity	CG8416	FBgn0014020		2.15E-05	69	11	15.9%
GO:0007015 actin filament organization	CG10545	FBgn0001105	G protein beta-subunit 13F	2.53E-05	58	10	17.2%
GO:0007015 actin filament organization	CG12530	FBgn0010341	Cdc42	2.53E-05	58	10	17.2%
GO:0007015 actin filament organization	CG17158	FBgn0011570	capping protein beta	2.53E-05	58	10	17.2%
GO:0007015 actin filament organization	CG1768	FBgn0011202	diaphanous	2.53E-05	58	10	17.2%
GO:0007015 actin filament organization	CG1977	FBgn0003470	alpha Spectrin	2.53E-05	58	10	17.2%
GO:0007015 actin filament organization	CG4254	FBgn0011726	twinstar	2.53E-05	58	10	17.2%
GO:0007015 actin filament organization	CG5061	FBgn0028388	capulet	2.53E-05	58	10	17.2%
GO:0007015 actin filament organization	CG8416	FBgn0014020		2.53E-05	58	10	17.2%
GO:0007015 actin filament organization	CG8936	FBgn0065032		2.53E-05	58	10	17.2%
GO:0007015 actin filament organization	CG9553	FBgn0000308	chickadee	2.53E-05	58	10	17.2%
GO:0051223 regulation of protein transport	CG2048	FBgn0002413	discs overgrown	3.13E-05	12	5	41.7%
GO:0051223 regulation of protein transport	CG4006	FBgn0010379		3.13E-05	12	5	41.7%
GO:0051223 regulation of protein transport	CG4057	FBgn0041582		3.13E-05	12	5	41.7%
GO:0051223 regulation of protein transport	CG5848	FBgn0000250	cactus	3.13E-05	12	5	41.7%
GO:0051223 regulation of protein transport	CG9426	FBgn0032485		3.13E-05	12	5	41.7%
GO:0008360 regulation of cell shape	CG12530	FBgn0010341	Cdc42	3.62E-05	86	12	14.0%
GO:0008360 regulation of cell shape	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	3.62E-05	86	12	14.0%
GO:0008360 regulation of cell shape	CG1977	FBgn0003470	alpha Spectrin	3.62E-05	86	12	14.0%
GO:0008360 regulation of cell shape	CG3637	FBgn0025865	Cortactin	3.62E-05	86	12	14.0%
GO:0008360 regulation of cell shape	CG4006	FBgn0010379		3.62E-05	86	12	14.0%
GO:0008360 regulation of cell shape	CG1956	FBgn0004636	Roughened	3.62E-05	86	12	14.0%
GO:0008360 regulation of cell shape	CG5061	FBgn0028388	capulet	3.62E-05	86	12	14.0%
GO:0008360 regulation of cell shape	CG5670	FBgn0002921	Na pump alpha subunit	3.62E-05	86	12	14.0%
GO:0008360 regulation of cell shape	CG5972	FBgn0031781		3.62E-05	86	12	14.0%
GO:0008360 regulation of cell shape	CG6831	FBgn0020254	rhea	3.62E-05	86	12	14.0%
GO:0008360 regulation of cell shape	CG10939	FBgn0010620	SRY interacting protein 1	3.62E-05	86	12	14.0%
GO:0008360 regulation of cell shape	CG9968	FBgn0030749	Annexin B11	3.62E-05	86	12	14.0%

GO:0007424 tracheal system development (sensu Insecta)	CG11949	FBgn0010434	coracle	3.70E-05	100	13	13.0%
GO:0007424 tracheal system development (sensu Insecta)	CG12210	FBgn0003660	Synaptobrevin	3.70E-05	100	13	13.0%
GO:0007424 tracheal system development (sensu Insecta)	CG12369	FBgn0010238	Lachesin	3.70E-05	100	13	13.0%
GO:0007424 tracheal system development (sensu Insecta)	CG13221	FBgn0041174	von Hippel-Lindau	3.70E-05	100	13	13.0%
GO:0007424 tracheal system development (sensu Insecta)	CG14665	NA	NA	3.70E-05	100	13	13.0%
GO:0007424 tracheal system development (sensu Insecta)	CG14779	FBgn0013720	pickel	3.70E-05	100	13	13.0%
GO:0007424 tracheal system development (sensu Insecta)	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	3.70E-05	100	13	13.0%
GO:0007424 tracheal system development (sensu Insecta)	CG4006	FBgn0010379		3.70E-05	100	13	13.0%
GO:0007424 tracheal system development (sensu Insecta)	CG4859	FBgn0035049	Matrix metalloproteinase 1	3.70E-05	100	13	13.0%
GO:0007424 tracheal system development (sensu Insecta)	CG5670	FBgn0002921	Na pump alpha subunit	3.70E-05	100	13	13.0%
GO:0007424 tracheal system development (sensu Insecta)	CG6827	FBgn0013997	Neurexin IV	3.70E-05	100	13	13.0%
GO:0007424 tracheal system development (sensu Insecta)	CG8416	FBgn0014020		3.70E-05	100	13	13.0%
GO:0007424 tracheal system development (sensu Insecta)	CG9261	FBgn0015777	nervana 2	3.70E-05	100	13	13.0%
GO:0046822 regulation of nucleocytoplasmic transport	CG2048	FBgn0002413	discs overgrown	4.94E-05	13	5	38.5%
GO:0046822 regulation of nucleocytoplasmic transport	CG4006	FBgn0010379		4.94E-05	13	5	38.5%
GO:0046822 regulation of nucleocytoplasmic transport	CG4057	FBgn0041582		4.94E-05	13	5	38.5%
GO:0046822 regulation of nucleocytoplasmic transport	CG5848	FBgn0000250	cactus	4.94E-05	13	5	38.5%
GO:0046822 regulation of nucleocytoplasmic transport	CG9426	FBgn0032485		4.94E-05	13	5	38.5%
GO:0016331 morphogenesis of embryonic epithelium	CG11949	FBgn0010434	coracle	6.95E-05	78	11	14.1%
GO:0016331 morphogenesis of embryonic epithelium	CG12530	FBgn0010341	Cdc42	6.95E-05	78	11	14.1%
GO:0016331 morphogenesis of embryonic epithelium	CG15792	FBgn0005634	zipper	6.95E-05	78	11	14.1%

GO:0016331 morphogenesis of embryonic epithelium	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	6.95E-05	78	11	14.1%
GO:0016331 morphogenesis of embryonic epithelium	CG2275	FBgn0001291	Jun-related antigen	6.95E-05	78	11	14.1%
GO:0016331 morphogenesis of embryonic epithelium	CG1956	FBgn0004636	Roughened	6.95E-05	78	11	14.1%
GO:0016331 morphogenesis of embryonic epithelium	CG5562	FBgn0024234	glass bottom boat	6.95E-05	78	11	14.1%
GO:0016331 morphogenesis of embryonic epithelium	CG6383	FBgn0000368	crumbs	6.95E-05	78	11	14.1%
GO:0016331 morphogenesis of embryonic epithelium	CG6827	FBgn0013997	Neurexin IV	6.95E-05	78	11	14.1%
GO:0016331 morphogenesis of embryonic epithelium	CG8416	FBgn0014020		6.95E-05	78	11	14.1%
GO:0016331 morphogenesis of embryonic epithelium	CG9553	FBgn0000308	chickadee	6.95E-05	78	11	14.1%
GO:0017038 protein import	CG10174	FBgn0032680	Nuclear transport factor-2-related	7.32E-05	53	9	17.0%
GO:0017038 protein import	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	7.32E-05	53	9	17.0%
GO:0017038 protein import	CG1740	FBgn0031145	Nuclear transport factor-2	7.32E-05	53	9	17.0%
GO:0017038 protein import	CG2048	FBgn0002413	discs overgrown	7.32E-05	53	9	17.0%
GO:0017038 protein import	CG4006	FBgn0010379		7.32E-05	53	9	17.0%
GO:0017038 protein import	CG4057	FBgn0041582		7.32E-05	53	9	17.0%
GO:0017038 protein import	CG4663	FBgn0033812		7.32E-05	53	9	17.0%
GO:0017038 protein import	CG5848	FBgn0000250	cactus	7.32E-05	53	9	17.0%
GO:0017038 protein import	CG9426	FBgn0032485		7.32E-05	53	9	17.0%
GO:0006606 protein-nucleus import	CG10174	FBgn0032680	Nuclear transport factor-2-related	1.33E-04	45	8	17.8%
GO:0006606 protein-nucleus import	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	1.33E-04	45	8	17.8%
GO:0006606 protein-nucleus import	CG1740	FBgn0031145	Nuclear transport factor-2	1.33E-04	45	8	17.8%
GO:0006606 protein-nucleus import	CG2048	FBgn0002413	discs overgrown	1.33E-04	45	8	17.8%
GO:0006606 protein-nucleus import	CG4006	FBgn0010379		1.33E-04	45	8	17.8%
GO:0006606 protein-nucleus import	CG4057	FBgn0041582		1.33E-04	45	8	17.8%
GO:0006606 protein-nucleus import	CG5848	FBgn0000250	cactus	1.33E-04	45	8	17.8%
GO:0006606 protein-nucleus import	CG9426	FBgn0032485		1.33E-04	45	8	17.8%
GO:0030707 ovarian follicle cell development (sensu Insecta)	CG12530	FBgn0010341	Cdc42	1.47E-04	114	13	11.4%

GO:0030707 ovarian follicle cell development (sensu Insecta)	CG15792	FBgn0005634	zipper	1.47E-04	114	13	11.4%
GO:0030707 ovarian follicle cell development (sensu Insecta)	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	1.47E-04	114	13	11.4%
GO:0030707 ovarian follicle cell development (sensu Insecta)	CG5248	FBgn0020278	locomotion defects	1.47E-04	114	13	11.4%
GO:0030707 ovarian follicle cell development (sensu Insecta)	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	1.47E-04	114	13	11.4%
GO:0030707 ovarian follicle cell development (sensu Insecta)	CG1977	FBgn0003470	alpha Spectrin	1.47E-04	114	13	11.4%
GO:0030707 ovarian follicle cell development (sensu Insecta)	CG2275	FBgn0001291	Jun-related antigen	1.47E-04	114	13	11.4%
GO:0030707 ovarian follicle cell development (sensu Insecta)	CG3595	FBgn0003514	spaghetti squash	1.47E-04	114	13	11.4%
GO:0030707 ovarian follicle cell development (sensu Insecta)	CG3637	FBgn0025865	Cortactin	1.47E-04	114	13	11.4%
GO:0030707 ovarian follicle cell development (sensu Insecta)	CG4254	FBgn0011726	twinstar	1.47E-04	114	13	11.4%
GO:0030707 ovarian follicle cell development (sensu Insecta)	CG1956	FBgn0004636	Roughened	1.47E-04	114	13	11.4%
GO:0030707 ovarian follicle cell development (sensu Insecta)	CG5803	FBgn0000636	Fasciclin 3	1.47E-04	114	13	11.4%
GO:0030707 ovarian follicle cell development (sensu Insecta)	CG5848	FBgn0000250	cactus	1.47E-04	114	13	11.4%
GO:0043297 apical junction assembly	CG11949	FBgn0010434	coracle	1.54E-04	16	5	31.3%
GO:0043297 apical junction assembly	CG5670	FBgn0002921	Na pump alpha subunit	1.54E-04	16	5	31.3%
GO:0043297 apical junction assembly	CG6383	FBgn0000368	crumbs	1.54E-04	16	5	31.3%
GO:0043297 apical junction assembly	CG6827	FBgn0013997	Neurexin IV	1.54E-04	16	5	31.3%
GO:0043297 apical junction assembly	CG9261	FBgn0015777	nervana 2	1.54E-04	16	5	31.3%
GO:0051170 nuclear import	CG10174	FBgn0032680	Nuclear transport factor-2-related	1.56E-04	46	8	17.4%
GO:0051170 nuclear import	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	1.56E-04	46	8	17.4%
GO:0051170 nuclear import	CG1740	FBgn0031145	Nuclear transport factor-2	1.56E-04	46	8	17.4%
GO:0051170 nuclear import	CG2048	FBgn0002413	discs overgrown	1.56E-04	46	8	17.4%
GO:0051170 nuclear import	CG4006	FBgn0010379		1.56E-04	46	8	17.4%
GO:0051170 nuclear import	CG4057	FBgn0041582		1.56E-04	46	8	17.4%
GO:0051170 nuclear import	CG5848	FBgn0000250	cactus	1.56E-04	46	8	17.4%
GO:0051170 nuclear import	CG9426	FBgn0032485		1.56E-04	46	8	17.4%
GO:0007349 cellularization	CG12530	FBgn0010341	Cdc42	1.67E-04	25	6	24.0%
GO:0007349 cellularization	CG1768	FBgn0011202	diaphanous	1.67E-04	25	6	24.0%

Age-specific age-related GO terms in Cluster 1

GO:0007349 cellularization	CG3595	FBgn0003514	spaghetti squash	1.67E-04	25	6	24.0%
GO:0007349 cellularization	CG4173	FBgn0014029	Septin-2	1.67E-04	25	6	24.0%
GO:0007349 cellularization	CG5771	FBgn0015790	Rab-protein 11	1.67E-04	25	6	24.0%
GO:0007349 cellularization	CG8416	FBgn0014020		1.67E-04	25	6	24.0%
GO:0007391 dorsal closure	CG11949	FBgn0010434	coracle	1.70E-04	72	10	13.9%
GO:0007391 dorsal closure	CG12530	FBgn0010341	Cdc42	1.70E-04	72	10	13.9%
GO:0007391 dorsal closure	CG15792	FBgn0005634	zipper	1.70E-04	72	10	13.9%
GO:0007391 dorsal closure	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	1.70E-04	72	10	13.9%
GO:0007391 dorsal closure	CG2275	FBgn0001291	Jun-related antigen	1.70E-04	72	10	13.9%
GO:0007391 dorsal closure	CG1956	FBgn0004636	Roughened	1.70E-04	72	10	13.9%
GO:0007391 dorsal closure	CG5562	FBgn0024234	glass bottom boat	1.70E-04	72	10	13.9%
GO:0007391 dorsal closure	CG6827	FBgn0013997	Neurexin IV	1.70E-04	72	10	13.9%
GO:0007391 dorsal closure	CG8416	FBgn0014020		1.70E-04	72	10	13.9%
GO:0007391 dorsal closure	CG9553	FBgn0000308	chickadee	1.70E-04	72	10	13.9%
GO:0007043 intercellular junction assembly	CG11949	FBgn0010434	coracle	2.12E-04	17	5	29.4%
GO:0007043 intercellular junction assembly	CG5670	FBgn0002921	Na pump alpha subunit	2.12E-04	17	5	29.4%
GO:0007043 intercellular junction assembly	CG6383	FBgn0000368	crumbs	2.12E-04	17	5	29.4%
GO:0007043 intercellular junction assembly	CG6827	FBgn0013997	Neurexin IV	2.12E-04	17	5	29.4%
GO:0007043 intercellular junction assembly	CG9261	FBgn0015777	nervana 2	2.12E-04	17	5	29.4%
GO:0000910 cytokinesis	CG15792	FBgn0005634	zipper	2.25E-04	61	9	14.8%
GO:0000910 cytokinesis	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	2.25E-04	61	9	14.8%
GO:0000910 cytokinesis	CG1768	FBgn0011202	diaphanous	2.25E-04	61	9	14.8%
GO:0000910 cytokinesis	CG3595	FBgn0003514	spaghetti squash	2.25E-04	61	9	14.8%
GO:0000910 cytokinesis	CG4173	FBgn0014029	Septin-2	2.25E-04	61	9	14.8%
GO:0000910 cytokinesis	CG4254	FBgn0011726	twinstar	2.25E-04	61	9	14.8%
GO:0000910 cytokinesis	CG1956	FBgn0004636	Roughened	2.25E-04	61	9	14.8%
GO:0000910 cytokinesis	CG8416	FBgn0014020		2.25E-04	61	9	14.8%
GO:0000910 cytokinesis	CG9553	FBgn0000308	chickadee	2.25E-04	61	9	14.8%
GO:0046785 microtubule polymerization	CG3401	FBgn0003888	beta-Tubulin at 60D	2.52E-04	10	4	40.0%
GO:0046785 microtubule polymerization	CG4869	FBgn0003890	beta-Tubulin at 97EF	2.52E-04	10	4	40.0%
GO:0046785 microtubule polymerization	CG9277	FBgn0003887	beta-Tubulin at 56D	2.52E-04	10	4	40.0%
GO:0046785 microtubule polymerization	CG9476	FBgn0003886	alpha-Tubulin at 85E	2.52E-04	10	4	40.0%
GO:0035239 tube morphogenesis	CG11949	FBgn0010434	coracle	3.26E-04	64	9	14.1%
GO:0035239 tube morphogenesis	CG12210	FBgn0003660	Synaptobrevin	3.26E-04	64	9	14.1%
GO:0035239 tube morphogenesis	CG12369	FBgn0010238	Lachesin	3.26E-04	64	9	14.1%
GO:0035239 tube morphogenesis	CG14779	FBgn0013720	pickel	3.26E-04	64	9	14.1%
GO:0035239 tube morphogenesis	CG15792	FBgn0005634	zipper	3.26E-04	64	9	14.1%
GO:0035239 tube morphogenesis	CG5670	FBgn0002921	Na pump alpha subunit	3.26E-04	64	9	14.1%
GO:0035239 tube morphogenesis	CG6827	FBgn0013997	Neurexin IV	3.26E-04	64	9	14.1%
GO:0035239 tube morphogenesis	CG8416	FBgn0014020		3.26E-04	64	9	14.1%
GO:0035239 tube morphogenesis	CG9261	FBgn0015777	nervana 2	3.26E-04	64	9	14.1%

Age-specific age-related GO terms in Cluster 1

GO:0045216 intercellular junction assembly and or maintenance	CG11949	FBgn0010434	coracle	3.77E-04	19	5	26.3%
GO:0045216 intercellular junction assembly and or maintenance	CG5670	FBgn0002921	Na pump alpha subunit	3.77E-04	19	5	26.3%
GO:0045216 intercellular junction assembly and or maintenance	CG6383	FBgn0000368	crumbs	3.77E-04	19	5	26.3%
GO:0045216 intercellular junction assembly and or maintenance	CG6827	FBgn0013997	Neurexin IV	3.77E-04	19	5	26.3%
GO:0045216 intercellular junction assembly and or maintenance	CG9261	FBgn0015777	nervana 2	3.77E-04	19	5	26.3%
GO:0009795 embryonic morphogenesis	CG11949	FBgn0010434	coracle	4.31E-04	127	13	10.2%
GO:0009795 embryonic morphogenesis	CG12530	FBgn0010341	Cdc42	4.31E-04	127	13	10.2%
GO:0009795 embryonic morphogenesis	CG15792	FBgn0005634	zipper	4.31E-04	127	13	10.2%
GO:0009795 embryonic morphogenesis	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	4.31E-04	127	13	10.2%
GO:0009795 embryonic morphogenesis	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	4.31E-04	127	13	10.2%
GO:0009795 embryonic morphogenesis	CG2275	FBgn0001291	Jun-related antigen	4.31E-04	127	13	10.2%
GO:0009795 embryonic morphogenesis	CG1956	FBgn0004636	Roughened	4.31E-04	127	13	10.2%
GO:0009795 embryonic morphogenesis	CG5562	FBgn0024234	glass bottom boat	4.31E-04	127	13	10.2%
GO:0009795 embryonic morphogenesis	CG6383	FBgn0000368	crumbs	4.31E-04	127	13	10.2%
GO:0009795 embryonic morphogenesis	CG6827	FBgn0013997	Neurexin IV	4.31E-04	127	13	10.2%
GO:0009795 embryonic morphogenesis	CG7123	FBgn0002527	Laminin B1	4.31E-04	127	13	10.2%
GO:0009795 embryonic morphogenesis	CG8416	FBgn0014020		4.31E-04	127	13	10.2%
GO:0009795 embryonic morphogenesis	CG9553	FBgn0000308	chickadee	4.31E-04	127	13	10.2%
GO:0051128 regulation of cell organization and biogenesis	CG17158	FBgn0011570	capping protein beta	4.88E-04	20	5	25.0%
GO:0051128 regulation of cell organization and biogenesis	CG4560	FBgn0038369		4.88E-04	20	5	25.0%
GO:0051128 regulation of cell organization and biogenesis	CG8076	NA	NA	4.88E-04	20	5	25.0%
GO:0051128 regulation of cell organization and biogenesis	CG8936	FBgn0065032		4.88E-04	20	5	25.0%
GO:0051128 regulation of cell organization and biogenesis	CG9901	FBgn0011742	Actin-related protein 14D	4.88E-04	20	5	25.0%
GO:0008064 regulation of actin polymerization and or depolymerization	CG17158	FBgn0011570	capping protein beta	7.90E-04	13	4	30.8%
GO:0008064 regulation of actin polymerization and or depolymerization	CG4560	FBgn0038369		7.90E-04	13	4	30.8%
GO:0008064 regulation of actin polymerization and or depolymerization	CG8936	FBgn0065032		7.90E-04	13	4	30.8%
GO:0008064 regulation of actin polymerization and or depolymerization	CG9901	FBgn0011742	Actin-related protein 14D	7.90E-04	13	4	30.8%

Age-specific age-related GO terms in Cluster 1

GO:0030832 regulation of actin filament length	CG17158	FBgn0011570	capping protein beta	7.90E-04	13	4	30.8%
GO:0030832 regulation of actin filament length	CG4560	FBgn0038369		7.90E-04	13	4	30.8%
GO:0030832 regulation of actin filament length	CG8936	FBgn0065032		7.90E-04	13	4	30.8%
GO:0030832 regulation of actin filament length	CG9901	FBgn0011742	Actin-related protein 14D	7.90E-04	13	4	30.8%
GO:0031109 microtubule polymerization or depolymerization	CG3401	FBgn0003888	beta-Tubulin at 60D	7.90E-04	13	4	30.8%
GO:0031109 microtubule polymerization or depolymerization	CG4869	FBgn0003890	beta-Tubulin at 97EF	7.90E-04	13	4	30.8%
GO:0031109 microtubule polymerization or depolymerization	CG9277	FBgn0003887	beta-Tubulin at 56D	7.90E-04	13	4	30.8%
GO:0031109 microtubule polymerization or depolymerization	CG9476	FBgn0003886	alpha-Tubulin at 85E	7.90E-04	13	4	30.8%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG11254	FBgn0016034	maelstrom	7.93E-04	72	9	12.5%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG17870	FBgn0004907		7.93E-04	72	9	12.5%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG3381	FBgn0051961		7.93E-04	72	9	12.5%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG3401	FBgn0003888	beta-Tubulin at 60D	7.93E-04	72	9	12.5%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG4869	FBgn0003890	beta-Tubulin at 97EF	7.93E-04	72	9	12.5%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG5061	FBgn0028388	capulet	7.93E-04	72	9	12.5%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG5771	FBgn0015790	Rab-protein 11	7.93E-04	72	9	12.5%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG9277	FBgn0003887	beta-Tubulin at 56D	7.93E-04	72	9	12.5%
GO:0000226 microtubule cytoskeleton organization and biogenesis	CG9476	FBgn0003886	alpha-Tubulin at 85E	7.93E-04	72	9	12.5%
GO:0035295 tube development	CG11949	FBgn0010434	coracle	7.93E-04	72	9	12.5%
GO:0035295 tube development	CG12210	FBgn0003660	Synaptobrevin	7.93E-04	72	9	12.5%
GO:0035295 tube development	CG12369	FBgn0010238	Lachesin	7.93E-04	72	9	12.5%
GO:0035295 tube development	CG14779	FBgn0013720	pickel	7.93E-04	72	9	12.5%
GO:0035295 tube development	CG15792	FBgn0005634	zipper	7.93E-04	72	9	12.5%
GO:0035295 tube development	CG5670	FBgn0002921	Na pump alpha subunit	7.93E-04	72	9	12.5%
GO:0035295 tube development	CG6827	FBgn0013997	Neurexin IV	7.93E-04	72	9	12.5%
GO:0035295 tube development	CG8416	FBgn0014020		7.93E-04	72	9	12.5%
GO:0035295 tube development	CG9261	FBgn0015777	nervana 2	7.93E-04	72	9	12.5%
GO:0006457 protein folding	CG10635	FBgn0035603		8.17E-04	119	12	10.1%
GO:0006457 protein folding	CG11001	FBgn0013954	FK506-binding protein 2	8.17E-04	119	12	10.1%
GO:0006457 protein folding	CG14894	FBgn0038428		8.17E-04	119	12	10.1%

GO:0006457 protein folding	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	8.17E-04	119	12	10.1%
GO:0006457 protein folding	CG3381	FBgn0051961		8.17E-04	119	12	10.1%
GO:0006457 protein folding	CG4535	FBgn0029174	FK506-binding protein FKBP59	8.17E-04	119	12	10.1%
GO:0006457 protein folding	CG4599	FBgn0032586	Tetratricopeptide repeat protein 2	8.17E-04	119	12	10.1%
GO:0006457 protein folding	CG5525	FBgn0032444		8.17E-04	119	12	10.1%
GO:0006457 protein folding	CG7033	FBgn0030086		8.17E-04	119	12	10.1%
GO:0006457 protein folding	CG8231	FBgn0027329		8.17E-04	119	12	10.1%
GO:0006457 protein folding	CG8258	FBgn0033342		8.17E-04	119	12	10.1%
GO:0006457 protein folding	CG8351	FBgn0037632		8.17E-04	119	12	10.1%
GO:0006461 protein complex assembly	CG11949	FBgn0010434	coracle	1.05E-03	90	10	11.1%
GO:0006461 protein complex assembly	CG7902	FBgn0004862	bagpipe	1.05E-03	90	10	11.1%
GO:0006461 protein complex assembly	CG14894	FBgn0038428		1.05E-03	90	10	11.1%
GO:0006461 protein complex assembly	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	1.05E-03	90	10	11.1%
GO:0006461 protein complex assembly	CG4254	FBgn0011726	twinstar	1.05E-03	90	10	11.1%
GO:0006461 protein complex assembly	CG4599	FBgn0032586	Tetratricopeptide repeat protein 2	1.05E-03	90	10	11.1%
GO:0006461 protein complex assembly	CG5670	FBgn0002921	Na pump alpha subunit	1.05E-03	90	10	11.1%
GO:0006461 protein complex assembly	CG6383	FBgn0000368	crumbs	1.05E-03	90	10	11.1%
GO:0006461 protein complex assembly	CG6827	FBgn0013997	Neurexin IV	1.05E-03	90	10	11.1%
GO:0006461 protein complex assembly	CG9261	FBgn0015777	nervana 2	1.05E-03	90	10	11.1%
GO:0016477 cell migration	CG11081	FBgn0025741	plexin A	1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG12530	FBgn0010341	Cdc42	1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG15792	FBgn0005634	zipper	1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG3171	FBgn0046687	trapped in endoderm-1	1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG3401	FBgn0003888	beta-Tubulin at 60D	1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG3595	FBgn0003514	spaghetti squash	1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG3637	FBgn0025865	Cortactin	1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG4254	FBgn0011726	twinstar	1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG5803	FBgn0000636	Fascin 3	1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG7555	FBgn0036736		1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG8076	NA	NA	1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG8416	FBgn0014020		1.06E-03	157	14	8.9%
GO:0016477 cell migration	CG9755	FBgn0003165	pumilio	1.06E-03	157	14	8.9%
GO:0009792 embryonic development (sensu Metazoa)	CG11949	FBgn0010434	coracle	1.19E-03	159	14	8.8%

GO:0009792 embryonic development (sensu Metazoa)	CG12530	FBgn0010341	Cdc42	1.19E-03	159	14	8.8%
GO:0009792 embryonic development (sensu Metazoa)	CG7902	FBgn0004862	bagpipe	1.19E-03	159	14	8.8%
GO:0009792 embryonic development (sensu Metazoa)	CG15792	FBgn0005634	zipper	1.19E-03	159	14	8.8%
GO:0009792 embryonic development (sensu Metazoa)	CG1768	FBgn0011202	diaphanous	1.19E-03	159	14	8.8%
GO:0009792 embryonic development (sensu Metazoa)	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	1.19E-03	159	14	8.8%
GO:0009792 embryonic development (sensu Metazoa)	CG2275	FBgn0001291	Jun-related antigen	1.19E-03	159	14	8.8%
GO:0009792 embryonic development (sensu Metazoa)	CG1956	FBgn0004636	Roughened	1.19E-03	159	14	8.8%
GO:0009792 embryonic development (sensu Metazoa)	CG5562	FBgn0024234	glass bottom boat	1.19E-03	159	14	8.8%
GO:0009792 embryonic development (sensu Metazoa)	CG5771	FBgn0015790	Rab-protein 11	1.19E-03	159	14	8.8%
GO:0009792 embryonic development (sensu Metazoa)	CG6827	FBgn0013997	Neurexin IV	1.19E-03	159	14	8.8%
GO:0009792 embryonic development (sensu Metazoa)	CG8416	FBgn0014020		1.19E-03	159	14	8.8%
GO:0009792 embryonic development (sensu Metazoa)	CG9553	FBgn0000308	chickadee	1.19E-03	159	14	8.8%
GO:0009792 embryonic development (sensu Metazoa)	CG9755	FBgn0003165	pumilio	1.19E-03	159	14	8.8%
GO:0001738 morphogenesis of a polarized epithelium	CG15792	FBgn0005634	zipper	1.21E-03	48	7	14.6%
GO:0001738 morphogenesis of a polarized epithelium	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	1.21E-03	48	7	14.6%
GO:0001738 morphogenesis of a polarized epithelium	CG2275	FBgn0001291	Jun-related antigen	1.21E-03	48	7	14.6%
GO:0001738 morphogenesis of a polarized epithelium	CG3595	FBgn0003514	spaghetti squash	1.21E-03	48	7	14.6%
GO:0001738 morphogenesis of a polarized epithelium	CG6383	FBgn0000368	crumbs	1.21E-03	48	7	14.6%
GO:0001738 morphogenesis of a polarized epithelium	CG8056	FBgn0052177		1.21E-03	48	7	14.6%
GO:0001738 morphogenesis of a polarized epithelium	CG8416	FBgn0014020		1.21E-03	48	7	14.6%
GO:0001700 embryonic development (sensu Insecta)	CG11949	FBgn0010434	coracle	1.23E-03	108	11	10.2%

GO:0001700 embryonic development (sensu Insecta)	CG12530	FBgn0010341	Cdc42	1.23E-03	108	11	10.2%
GO:0001700 embryonic development (sensu Insecta)	CG15792	FBgn0005634	zipper	1.23E-03	108	11	10.2%
GO:0001700 embryonic development (sensu Insecta)	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	1.23E-03	108	11	10.2%
GO:0001700 embryonic development (sensu Insecta)	CG2275	FBgn0001291	Jun-related antigen	1.23E-03	108	11	10.2%
GO:0001700 embryonic development (sensu Insecta)	CG1956	FBgn0004636	Roughened	1.23E-03	108	11	10.2%
GO:0001700 embryonic development (sensu Insecta)	CG5562	FBgn0024234	glass bottom boat	1.23E-03	108	11	10.2%
GO:0001700 embryonic development (sensu Insecta)	CG6827	FBgn0013997	Neurexin IV	1.23E-03	108	11	10.2%
GO:0001700 embryonic development (sensu Insecta)	CG8416	FBgn0014020		1.23E-03	108	11	10.2%
GO:0001700 embryonic development (sensu Insecta)	CG9553	FBgn0000308	chickadee	1.23E-03	108	11	10.2%
GO:0001700 embryonic development (sensu Insecta)	CG9755	FBgn0003165	pumilio	1.23E-03	108	11	10.2%
GO:0051169 nuclear transport	CG10174	FBgn0032680	Nuclear transport factor-2 related	1.39E-03	63	8	12.7%
GO:0051169 nuclear transport	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	1.39E-03	63	8	12.7%
GO:0051169 nuclear transport	CG1740	FBgn0031145	Nuclear transport factor-2	1.39E-03	63	8	12.7%
GO:0051169 nuclear transport	CG2048	FBgn0002413	discs overgrown	1.39E-03	63	8	12.7%
GO:0051169 nuclear transport	CG4006	FBgn0010379		1.39E-03	63	8	12.7%
GO:0051169 nuclear transport	CG4057	FBgn0041582		1.39E-03	63	8	12.7%
GO:0051169 nuclear transport	CG5848	FBgn0000250	cactus	1.39E-03	63	8	12.7%
GO:0051169 nuclear transport	CG9426	FBgn0032485		1.39E-03	63	8	12.7%
GO:0051301 cell division	CG10060	FBgn0001104	G protein alpha1 subunit 65A	1.55E-03	111	11	9.9%
GO:0051301 cell division	CG15792	FBgn0005634	zipper	1.55E-03	111	11	9.9%
GO:0051301 cell division	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	1.55E-03	111	11	9.9%
GO:0051301 cell division	CG1768	FBgn0011202	diaphanous	1.55E-03	111	11	9.9%
GO:0051301 cell division	CG3595	FBgn0003514	spaghetti squash	1.55E-03	111	11	9.9%
GO:0051301 cell division	CG4173	FBgn0014029	Septin-2	1.55E-03	111	11	9.9%
GO:0051301 cell division	CG4254	FBgn0011726	twinstar	1.55E-03	111	11	9.9%
GO:0051301 cell division	CG1956	FBgn0004636	Roughened	1.55E-03	111	11	9.9%
GO:0051301 cell division	CG8416	FBgn0014020		1.55E-03	111	11	9.9%

Age-specific age-related GO terms in Cluster 1

GO:0051301 cell division	CG9553	FBgn0000308	chickadee	1.55E-03	111	11	9.9%
GO:0051301 cell division	CG9755	FBgn0003165	pumilio	1.55E-03	111	11	9.9%
GO:0031175 neurite morphogenesis	CG11081	FBgn0025741	plexin A	2.06E-03	115	11	9.6%
GO:0031175 neurite morphogenesis	CG12369	FBgn0010238	Lachesin	2.06E-03	115	11	9.6%
GO:0031175 neurite morphogenesis	CG12530	FBgn0010341	Cdc42	2.06E-03	115	11	9.6%
GO:0031175 neurite morphogenesis	CG18319	FBgn0000173	bendless	2.06E-03	115	11	9.6%
GO:0031175 neurite morphogenesis	CG3359	FBgn0024211	midline fasciclin	2.06E-03	115	11	9.6%
GO:0031175 neurite morphogenesis	CG3401	FBgn0003888	beta-Tubulin at 60D	2.06E-03	115	11	9.6%
GO:0031175 neurite morphogenesis	CG5803	FBgn0000636	Fasciclin 3	2.06E-03	115	11	9.6%
GO:0031175 neurite morphogenesis	CG7555	FBgn0036736		2.06E-03	115	11	9.6%
GO:0031175 neurite morphogenesis	CG8416	FBgn0014020		2.06E-03	115	11	9.6%
GO:0031175 neurite morphogenesis	CG8440	FBgn0015754	Lissencephaly-1	2.06E-03	115	11	9.6%
GO:0031175 neurite morphogenesis	CG9755	FBgn0003165	pumilio	2.06E-03	115	11	9.6%
GO:0006913 nucleocytoplasmic transport	CG10174	FBgn0032680	Nuclear transport factor-2 related	2.29E-03	68	8	11.8%
GO:0006913 nucleocytoplasmic transport	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	2.29E-03	68	8	11.8%
GO:0006913 nucleocytoplasmic transport	CG1740	FBgn0031145	Nuclear transport factor-2	2.29E-03	68	8	11.8%
GO:0006913 nucleocytoplasmic transport	CG2048	FBgn0002413	discs overgrown	2.29E-03	68	8	11.8%
GO:0006913 nucleocytoplasmic transport	CG4006	FBgn0010379		2.29E-03	68	8	11.8%
GO:0006913 nucleocytoplasmic transport	CG4057	FBgn0041582		2.29E-03	68	8	11.8%
GO:0006913 nucleocytoplasmic transport	CG5848	FBgn0000250	cactus	2.29E-03	68	8	11.8%
GO:0006913 nucleocytoplasmic transport	CG9426	FBgn0032485		2.29E-03	68	8	11.8%
GO:0001736 establishment of planar polarity	CG15792	FBgn0005634	zipper	2.34E-03	40	6	15.0%
GO:0001736 establishment of planar polarity	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	2.34E-03	40	6	15.0%
GO:0001736 establishment of planar polarity	CG2275	FBgn0001291	Jun-related antigen	2.34E-03	40	6	15.0%
GO:0001736 establishment of planar polarity	CG3595	FBgn0003514	spaghetti squash	2.34E-03	40	6	15.0%
GO:0001736 establishment of planar polarity	CG8056	FBgn0052177		2.34E-03	40	6	15.0%
GO:0001736 establishment of planar polarity	CG8416	FBgn0014020		2.34E-03	40	6	15.0%
GO:0007164 establishment of tissue polarity	CG15792	FBgn0005634	zipper	2.34E-03	40	6	15.0%
GO:0007164 establishment of tissue polarity	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	2.34E-03	40	6	15.0%
GO:0007164 establishment of tissue polarity	CG2275	FBgn0001291	Jun-related antigen	2.34E-03	40	6	15.0%
GO:0007164 establishment of tissue polarity	CG3595	FBgn0003514	spaghetti squash	2.34E-03	40	6	15.0%
GO:0007164 establishment of tissue polarity	CG8056	FBgn0052177		2.34E-03	40	6	15.0%
GO:0007164 establishment of tissue polarity	CG8416	FBgn0014020		2.34E-03	40	6	15.0%
GO:0045197 establishment and or maintenance of epithelial cell polarity	CG10701	FBgn0011661	Moesin	2.36E-03	17	4	23.5%
GO:0045197 establishment and or maintenance of epithelial cell polarity	CG1084	FBgn0037240	Contactin	2.36E-03	17	4	23.5%

Age-specific age-related GO terms in Cluster 1

GO:0045197 establishment and or maintenance of epithelial cell polarity	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	2.36E-03	17	4	23.5%
GO:0045197 establishment and or maintenance of epithelial cell polarity	CG6383	FBgn0000368	crumbs	2.36E-03	17	4	23.5%
GO:0046843 dorsal appendage formation	CG12530	FBgn0010341	Cdc42	2.36E-03	17	4	23.5%
GO:0046843 dorsal appendage formation	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	2.36E-03	17	4	23.5%
GO:0046843 dorsal appendage formation	CG2275	FBgn0001291	Jun-related antigen	2.36E-03	17	4	23.5%
GO:0046843 dorsal appendage formation	CG5848	FBgn0000250	cactus	2.36E-03	17	4	23.5%
GO:0019725 cell homeostasis	CG10620	FBgn0036299	Transferrin 2	2.51E-03	69	8	11.6%
GO:0019725 cell homeostasis	CG7902	FBgn0004862	bagpipe	2.51E-03	69	8	11.6%
GO:0019725 cell homeostasis	CG1469	FBgn0015221	Ferritin 2 light chain homologue	2.51E-03	69	8	11.6%
GO:0019725 cell homeostasis	CG1633	FBgn0040309	thioredoxin peroxidase 1	2.51E-03	69	8	11.6%
GO:0019725 cell homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	2.51E-03	69	8	11.6%
GO:0019725 cell homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	2.51E-03	69	8	11.6%
GO:0019725 cell homeostasis	CG10939	FBgn0010620	SRY interacting protein 1	2.51E-03	69	8	11.6%
GO:0019725 cell homeostasis	CG9023	FBgn0015872	Drip	2.51E-03	69	8	11.6%
GO:0007300 nurse cell to oocyte transport (sensu Insecta)	CG5248	FBgn0020278	locomotion defects	2.90E-03	29	5	17.2%
GO:0007300 nurse cell to oocyte transport (sensu Insecta)	CG1977	FBgn0003470	alpha Spectrin	2.90E-03	29	5	17.2%
GO:0007300 nurse cell to oocyte transport (sensu Insecta)	CG3595	FBgn0003514	spaghetti squash	2.90E-03	29	5	17.2%
GO:0007300 nurse cell to oocyte transport (sensu Insecta)	CG3637	FBgn0025865	Cortactin	2.90E-03	29	5	17.2%
GO:0007300 nurse cell to oocyte transport (sensu Insecta)	CG9553	FBgn0000308	chickadee	2.90E-03	29	5	17.2%
GO:0030005 di- tri-valent inorganic cation homeostasis	CG10620	FBgn0036299	Transferrin 2	2.95E-03	18	4	22.2%
GO:0030005 di- tri-valent inorganic cation homeostasis	CG1469	FBgn0015221	Ferritin 2 light chain homologue	2.95E-03	18	4	22.2%
GO:0030005 di- tri-valent inorganic cation homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	2.95E-03	18	4	22.2%
GO:0030005 di- tri-valent inorganic cation homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	2.95E-03	18	4	22.2%
GO:0035088 establishment and or maintenance of apical basal cell polarity	CG10701	FBgn0011661	Moesin	2.95E-03	18	4	22.2%
GO:0035088 establishment and or maintenance of apical basal cell polarity	CG1084	FBgn0037240	Contactin	2.95E-03	18	4	22.2%

Age-specific age-related GO terms in Cluster 1

GO:0035088 establishment and or maintenance of apical basal cell polarity	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	2.95E-03	18	4	22.2%
GO:0035088 establishment and or maintenance of apical basal cell polarity	CG6383	FBgn0000368	crumbs	2.95E-03	18	4	22.2%
GO:0007297 follicle cell migration (sensu Insecta)	CG15792	FBgn0005634	zipper	3.38E-03	30	5	16.7%
GO:0007297 follicle cell migration (sensu Insecta)	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	3.38E-03	30	5	16.7%
GO:0007297 follicle cell migration (sensu Insecta)	CG3595	FBgn0003514	spaghetti squash	3.38E-03	30	5	16.7%
GO:0007297 follicle cell migration (sensu Insecta)	CG3637	FBgn0025865	Cortactin	3.38E-03	30	5	16.7%
GO:0007297 follicle cell migration (sensu Insecta)	CG4254	FBgn0011726	twinstar	3.38E-03	30	5	16.7%
GO:0007243 protein kinase cascade	CG11804	FBgn0029092		3.50E-03	123	11	8.9%
GO:0007243 protein kinase cascade	CG12530	FBgn0010341	Cdc42	3.50E-03	123	11	8.9%
GO:0007243 protein kinase cascade	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	3.50E-03	123	11	8.9%
GO:0007243 protein kinase cascade	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	3.50E-03	123	11	8.9%
GO:0007243 protein kinase cascade	CG2275	FBgn0001291	Jun-related antigen	3.50E-03	123	11	8.9%
GO:0007243 protein kinase cascade	CG1956	FBgn0004636	Roughened	3.50E-03	123	11	8.9%
GO:0007243 protein kinase cascade	CG5848	FBgn0000250	cactus	3.50E-03	123	11	8.9%
GO:0007243 protein kinase cascade	CG7511	NA	NA	3.50E-03	123	11	8.9%
GO:0007243 protein kinase cascade	CG8056	FBgn0052177		3.50E-03	123	11	8.9%
GO:0007243 protein kinase cascade	CG8416	FBgn0014020		3.50E-03	123	11	8.9%
GO:0007243 protein kinase cascade	CG9031	FBgn0028546	Ras suppressor-1	3.50E-03	123	11	8.9%
GO:0007308 oocyte construction	CG10701	FBgn0011661	Moesin	3.59E-03	73	8	11.0%
GO:0007308 oocyte construction	CG11254	FBgn0016034	maelstrom	3.59E-03	73	8	11.0%
GO:0007308 oocyte construction	CG17870	FBgn0004907		3.59E-03	73	8	11.0%
GO:0007308 oocyte construction	CG1977	FBgn0003470	alpha Spectrin	3.59E-03	73	8	11.0%
GO:0007308 oocyte construction	CG5061	FBgn0028388	capulet	3.59E-03	73	8	11.0%
GO:0007308 oocyte construction	CG5771	FBgn0015790	Rab-protein 11	3.59E-03	73	8	11.0%
GO:0007308 oocyte construction	CG8440	FBgn0015754	Lissencephaly-1	3.59E-03	73	8	11.0%
GO:0007308 oocyte construction	CG9553	FBgn0000308	chickadee	3.59E-03	73	8	11.0%
GO:0042592 homeostasis	CG10620	FBgn0036299	Transferrin 2	3.59E-03	73	8	11.0%
GO:0042592 homeostasis	CG7902	FBgn0004862	bagpipe	3.59E-03	73	8	11.0%
GO:0042592 homeostasis	CG1469	FBgn0015221	Ferritin 2 light chain homologue	3.59E-03	73	8	11.0%
GO:0042592 homeostasis	CG1633	FBgn0040309	thioredoxin peroxidase 1	3.59E-03	73	8	11.0%

Age-specific age-related GO terms in Cluster 1

GO:0042592 homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	3.59E-03	73	8	11.0%
GO:0042592 homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	3.59E-03	73	8	11.0%
GO:0042592 homeostasis	CG10939	FBgn0010620	SRY interacting protein 1	3.59E-03	73	8	11.0%
GO:0042592 homeostasis	CG9023	FBgn0015872	Drip	3.59E-03	73	8	11.0%
GO:0016325 oocyte microtubule cytoskeleton organization	CG11254	FBgn0016034	maelstrom	3.63E-03	19	4	21.1%
GO:0016325 oocyte microtubule cytoskeleton organization	CG17870	FBgn0004907		3.63E-03	19	4	21.1%
GO:0016325 oocyte microtubule cytoskeleton organization	CG5061	FBgn0028388	capulet	3.63E-03	19	4	21.1%
GO:0016325 oocyte microtubule cytoskeleton organization	CG5771	FBgn0015790	Rab-protein 11	3.63E-03	19	4	21.1%
GO:0030951 establishment and or maintenance of microtubule cytoskeleton polarity	CG11254	FBgn0016034	maelstrom	3.63E-03	19	4	21.1%
GO:0030951 establishment and or maintenance of microtubule cytoskeleton polarity	CG17870	FBgn0004907		3.63E-03	19	4	21.1%
GO:0030951 establishment and or maintenance of microtubule cytoskeleton polarity	CG5061	FBgn0028388	capulet	3.63E-03	19	4	21.1%
GO:0030951 establishment and or maintenance of microtubule cytoskeleton polarity	CG5771	FBgn0015790	Rab-protein 11	3.63E-03	19	4	21.1%
GO:0030952 establishment and or maintenance of cytoskeleton polarity	CG11254	FBgn0016034	maelstrom	3.63E-03	19	4	21.1%
GO:0030952 establishment and or maintenance of cytoskeleton polarity	CG17870	FBgn0004907		3.63E-03	19	4	21.1%
GO:0030952 establishment and or maintenance of cytoskeleton polarity	CG5061	FBgn0028388	capulet	3.63E-03	19	4	21.1%
GO:0030952 establishment and or maintenance of cytoskeleton polarity	CG5771	FBgn0015790	Rab-protein 11	3.63E-03	19	4	21.1%
GO:0051261 protein depolymerization	CG10724	FBgn0036357		4.13E-03	10	3	30.0%
GO:0051261 protein depolymerization	CG17158	FBgn0011570	capping protein beta	4.13E-03	10	3	30.0%
GO:0051261 protein depolymerization	CG4254	FBgn0011726	twinstar	4.13E-03	10	3	30.0%
GO:0006875 metal ion homeostasis	CG10620	FBgn0036299	Transferrin 2	4.42E-03	20	4	20.0%
GO:0006875 metal ion homeostasis	CG1469	FBgn0015221	Ferritin 2 light chain homologue	4.42E-03	20	4	20.0%
GO:0006875 metal ion homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	4.42E-03	20	4	20.0%
GO:0006875 metal ion homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	4.42E-03	20	4	20.0%
GO:0006605 protein targeting	CG10174	FBgn0032680	Nuclear transport factor-2 related	4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG10225	FBgn0039110		4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG11949	FBgn0010434	coracle	4.54E-03	223	16	7.2%

GO:0006605 protein targeting	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG1740	FBgn0031145	Nuclear transport factor-2	4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG2048	FBgn0002413	discs overgrown	4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG2093	FBgn0033194		4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG4006	FBgn0010379		4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG4057	FBgn0041582		4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG4663	FBgn0033812		4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG5081	FBgn0033583	Syntaxin 7	4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG5662	FBgn0030620		4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG5848	FBgn0000250	cactus	4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG7654	FBgn0036928	Translocase of outer membrane 20	4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG9426	FBgn0032485		4.54E-03	223	16	7.2%
GO:0006605 protein targeting	CG9556	FBgn0013746	alien	4.54E-03	223	16	7.2%
GO:0048110 oocyte construction (sensu Insecta)	CG10701	FBgn0011661	Moesin	5.35E-03	47	6	12.8%
GO:0048110 oocyte construction (sensu Insecta)	CG11254	FBgn0016034	maelstrom	5.35E-03	47	6	12.8%
GO:0048110 oocyte construction (sensu Insecta)	CG17870	FBgn0004907		5.35E-03	47	6	12.8%
GO:0048110 oocyte construction (sensu Insecta)	CG5771	FBgn0015790	Rab-protein 11	5.35E-03	47	6	12.8%
GO:0048110 oocyte construction (sensu Insecta)	CG8440	FBgn0015754	Lissencephaly-1	5.35E-03	47	6	12.8%
GO:0048110 oocyte construction (sensu Insecta)	CG9553	FBgn0000308	chickadee	5.35E-03	47	6	12.8%
GO:0048111 oocyte axis determination (sensu Insecta)	CG10701	FBgn0011661	Moesin	5.35E-03	47	6	12.8%
GO:0048111 oocyte axis determination (sensu Insecta)	CG11254	FBgn0016034	maelstrom	5.35E-03	47	6	12.8%
GO:0048111 oocyte axis determination (sensu Insecta)	CG17870	FBgn0004907		5.35E-03	47	6	12.8%
GO:0048111 oocyte axis determination (sensu Insecta)	CG5771	FBgn0015790	Rab-protein 11	5.35E-03	47	6	12.8%
GO:0048111 oocyte axis determination (sensu Insecta)	CG8440	FBgn0015754	Lissencephaly-1	5.35E-03	47	6	12.8%
GO:0048111 oocyte axis determination (sensu Insecta)	CG9553	FBgn0000308	chickadee	5.35E-03	47	6	12.8%
GO:0007409 axonogenesis	CG11081	FBgn0025741	plexin A	5.49E-03	95	9	9.5%
GO:0007409 axonogenesis	CG12369	FBgn0010238	Lachesin	5.49E-03	95	9	9.5%
GO:0007409 axonogenesis	CG12530	FBgn0010341	Cdc42	5.49E-03	95	9	9.5%
GO:0007409 axonogenesis	CG18319	FBgn0000173	bendless	5.49E-03	95	9	9.5%
GO:0007409 axonogenesis	CG3359	FBgn0024211	midline fasciclin	5.49E-03	95	9	9.5%
GO:0007409 axonogenesis	CG3401	FBgn0003888	beta-Tubulin at 60D	5.49E-03	95	9	9.5%
GO:0007409 axonogenesis	CG5803	FBgn0000636	Fasciclin 3	5.49E-03	95	9	9.5%
GO:0007409 axonogenesis	CG7555	FBgn0036736		5.49E-03	95	9	9.5%
GO:0007409 axonogenesis	CG8416	FBgn0014020		5.49E-03	95	9	9.5%
GO:0030855 epithelial cell differentiation	CG15792	FBgn0005634	zipper	5.54E-03	11	3	27.3%

Age-specific age-related GO terms in Cluster 1

GO:0030855 epithelial cell differentiation	CG6383	FBgn0000368	crumbs	5.54E-03	11	3	27.3%
GO:0030855 epithelial cell differentiation	CG8416	FBgn0014020		5.54E-03	11	3	27.3%
GO:0000912 cytokinesis formation of actomyosin apparatus	CG1768	FBgn0011202	diaphanous	7.20E-03	12	3	25.0%
GO:0000912 cytokinesis formation of actomyosin apparatus	CG4254	FBgn0011726	twinstar	7.20E-03	12	3	25.0%
GO:0000912 cytokinesis formation of actomyosin apparatus	CG9553	FBgn0000308	chickadee	7.20E-03	12	3	25.0%
GO:0000915 cytokinesis contractile ring formation	CG1768	FBgn0011202	diaphanous	7.20E-03	12	3	25.0%
GO:0000915 cytokinesis contractile ring formation	CG4254	FBgn0011726	twinstar	7.20E-03	12	3	25.0%
GO:0000915 cytokinesis contractile ring formation	CG9553	FBgn0000308	chickadee	7.20E-03	12	3	25.0%
GO:0007392 initiation of dorsal closure	CG15792	FBgn0005634	zipper	7.20E-03	12	3	25.0%
GO:0007392 initiation of dorsal closure	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	7.20E-03	12	3	25.0%
GO:0007392 initiation of dorsal closure	CG8416	FBgn0014020		7.20E-03	12	3	25.0%
GO:0031032 actomyosin structure organization and biogenesis	CG1768	FBgn0011202	diaphanous	7.20E-03	12	3	25.0%
GO:0031032 actomyosin structure organization and biogenesis	CG4254	FBgn0011726	twinstar	7.20E-03	12	3	25.0%
GO:0031032 actomyosin structure organization and biogenesis	CG9553	FBgn0000308	chickadee	7.20E-03	12	3	25.0%
GO:0000165 MAPKKK cascade	CG11804	FBgn0029092		7.66E-03	100	9	9.0%
GO:0000165 MAPKKK cascade	CG12530	FBgn0010341	Cdc42	7.66E-03	100	9	9.0%
GO:0000165 MAPKKK cascade	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	7.66E-03	100	9	9.0%
GO:0000165 MAPKKK cascade	CG2275	FBgn0001291	Jun-related antigen	7.66E-03	100	9	9.0%
GO:0000165 MAPKKK cascade	CG1956	FBgn0004636	Roughened	7.66E-03	100	9	9.0%
GO:0000165 MAPKKK cascade	CG7511	NA	NA	7.66E-03	100	9	9.0%
GO:0000165 MAPKKK cascade	CG8056	FBgn0052177		7.66E-03	100	9	9.0%
GO:0000165 MAPKKK cascade	CG8416	FBgn0014020		7.66E-03	100	9	9.0%
GO:0000165 MAPKKK cascade	CG9031	FBgn0028546	Ras suppressor-1	7.66E-03	100	9	9.0%
GO:0008103 oocyte microtubule cytoskeleton polarization	CG17870	FBgn0004907		9.12E-03	13	3	23.1%
GO:0008103 oocyte microtubule cytoskeleton polarization	CG5061	FBgn0028388	capulet	9.12E-03	13	3	23.1%
GO:0008103 oocyte microtubule cytoskeleton polarization	CG5771	FBgn0015790	Rab-protein 11	9.12E-03	13	3	23.1%
GO:0007017 microtubule-based process	CG10838	FBgn0028570		1.00E-02	181	13	7.2%
GO:0007017 microtubule-based process	CG10846	FBgn0040228	dynactin-subunit-p25	1.00E-02	181	13	7.2%
GO:0007017 microtubule-based process	CG11254	FBgn0016034	maelstrom	1.00E-02	181	13	7.2%
GO:0007017 microtubule-based process	CG14779	FBgn0013720	pickel	1.00E-02	181	13	7.2%
GO:0007017 microtubule-based process	CG17870	FBgn0004907		1.00E-02	181	13	7.2%

Age-specific age-related GO terms in Cluster 1

GO:0007017 microtubule-based process	CG3381	FBgn0051961		1.00E-02	181	13	7.2%
GO:0007017 microtubule-based process	CG3401	FBgn0003888	beta-Tubulin at 60D	1.00E-02	181	13	7.2%
GO:0007017 microtubule-based process	CG4869	FBgn0003890	beta-Tubulin at 97EF	1.00E-02	181	13	7.2%
GO:0007017 microtubule-based process	CG5061	FBgn0028388	capulet	1.00E-02	181	13	7.2%
GO:0007017 microtubule-based process	CG5771	FBgn0015790	Rab-protein 11	1.00E-02	181	13	7.2%
GO:0007017 microtubule-based process	CG8440	FBgn0015754	Lissencephaly-1	1.00E-02	181	13	7.2%
GO:0007017 microtubule-based process	CG9277	FBgn0003887	beta-Tubulin at 56D	1.00E-02	181	13	7.2%
GO:0007017 microtubule-based process	CG9476	FBgn0003886	alpha-Tubulin at 85E	1.00E-02	181	13	7.2%
GO:0006873 cell ion homeostasis	CG10620	FBgn0036299	Transferrin 2	1.01E-02	25	4	16.0%
GO:0006873 cell ion homeostasis	CG1469	FBgn0015221	Ferritin 2 light chain homologue	1.01E-02	25	4	16.0%
GO:0006873 cell ion homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	1.01E-02	25	4	16.0%
GO:0006873 cell ion homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	1.01E-02	25	4	16.0%
GO:0030003 cation homeostasis	CG10620	FBgn0036299	Transferrin 2	1.01E-02	25	4	16.0%
GO:0030003 cation homeostasis	CG1469	FBgn0015221	Ferritin 2 light chain homologue	1.01E-02	25	4	16.0%
GO:0030003 cation homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	1.01E-02	25	4	16.0%
GO:0030003 cation homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	1.01E-02	25	4	16.0%
GO:0050801 ion homeostasis	CG10620	FBgn0036299	Transferrin 2	1.01E-02	25	4	16.0%
GO:0050801 ion homeostasis	CG1469	FBgn0015221	Ferritin 2 light chain homologue	1.01E-02	25	4	16.0%
GO:0050801 ion homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	1.01E-02	25	4	16.0%
GO:0050801 ion homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	1.01E-02	25	4	16.0%
GO:0007309 oocyte axis determination	CG10701	FBgn0011661	Moesin	1.12E-02	71	7	9.9%
GO:0007309 oocyte axis determination	CG11254	FBgn0016034	maelstrom	1.12E-02	71	7	9.9%
GO:0007309 oocyte axis determination	CG17870	FBgn0004907		1.12E-02	71	7	9.9%
GO:0007309 oocyte axis determination	CG5061	FBgn0028388	capulet	1.12E-02	71	7	9.9%
GO:0007309 oocyte axis determination	CG5771	FBgn0015790	Rab-protein 11	1.12E-02	71	7	9.9%
GO:0007309 oocyte axis determination	CG8440	FBgn0015754	Lissencephaly-1	1.12E-02	71	7	9.9%
GO:0007309 oocyte axis determination	CG9553	FBgn0000308	chickadee	1.12E-02	71	7	9.9%
GO:0051049 regulation of transport	CG2048	FBgn0002413	discs overgrown	1.15E-02	55	6	10.9%
GO:0051049 regulation of transport	CG4006	FBgn0010379		1.15E-02	55	6	10.9%
GO:0051049 regulation of transport	CG4057	FBgn0041582		1.15E-02	55	6	10.9%
GO:0051049 regulation of transport	CG1956	FBgn0004636	Roughened	1.15E-02	55	6	10.9%
GO:0051049 regulation of transport	CG5848	FBgn0000250	cactus	1.15E-02	55	6	10.9%
GO:0051049 regulation of transport	CG9426	FBgn0032485		1.15E-02	55	6	10.9%
GO:0007298 border cell migration (sensu Insecta)	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	1.32E-02	27	4	14.8%
GO:0007298 border cell migration (sensu Insecta)	CG3595	FBgn0003514	spaghetti squash	1.32E-02	27	4	14.8%
GO:0007298 border cell migration (sensu Insecta)	CG3637	FBgn0025865	Cortactin	1.32E-02	27	4	14.8%

Age-specific age-related GO terms in Cluster 1

GO:0007298 border cell migration (sensu Insecta)	CG4254	FBgn0011726	twinstar	1.32E-02	27	4	14.8%
GO:0016203 muscle attachment	CG15792	FBgn0005634	zipper	1.38E-02	15	3	20.0%
GO:0016203 muscle attachment	CG8416	FBgn0014020		1.38E-02	15	3	20.0%
GO:0016203 muscle attachment	CG9277	FBgn0003887	beta-Tubulin at 56D	1.38E-02	15	3	20.0%
GO:0009611 response to wounding	CG12530	FBgn0010341	Cdc42	1.50E-02	28	4	14.3%
GO:0009611 response to wounding	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	1.50E-02	28	4	14.3%
GO:0009611 response to wounding	CG5848	FBgn0000250	cactus	1.50E-02	28	4	14.3%
GO:0009611 response to wounding	CG8416	FBgn0014020		1.50E-02	28	4	14.3%
GO:0007254 JNK cascade	CG12530	FBgn0010341	Cdc42	1.90E-02	45	5	11.1%
GO:0007254 JNK cascade	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	1.90E-02	45	5	11.1%
GO:0007254 JNK cascade	CG2275	FBgn0001291	Jun-related antigen	1.90E-02	45	5	11.1%
GO:0007254 JNK cascade	CG1956	FBgn0004636	Roughened	1.90E-02	45	5	11.1%
GO:0007254 JNK cascade	CG8416	FBgn0014020		1.90E-02	45	5	11.1%
GO:0031098 stress-activated protein kinase signaling pathway	CG12530	FBgn0010341	Cdc42	1.90E-02	45	5	11.1%
GO:0031098 stress-activated protein kinase signaling pathway	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	1.90E-02	45	5	11.1%
GO:0031098 stress-activated protein kinase signaling pathway	CG2275	FBgn0001291	Jun-related antigen	1.90E-02	45	5	11.1%
GO:0031098 stress-activated protein kinase signaling pathway	CG1956	FBgn0004636	Roughened	1.90E-02	45	5	11.1%
GO:0031098 stress-activated protein kinase signaling pathway	CG8416	FBgn0014020		1.90E-02	45	5	11.1%
GO:0008354 germ cell migration	CG3171	FBgn0046687	trapped in endoderm-1	1.91E-02	30	4	13.3%
GO:0008354 germ cell migration	CG8076	NA	NA	1.91E-02	30	4	13.3%
GO:0008354 germ cell migration	CG8416	FBgn0014020		1.91E-02	30	4	13.3%
GO:0008354 germ cell migration	CG9755	FBgn0003165	pumilio	1.91E-02	30	4	13.3%
GO:0006800 oxygen and reactive oxygen species metabolism	CG1633	FBgn0040309	thioredoxin peroxidase 1	1.99E-02	62	6	9.7%
GO:0006800 oxygen and reactive oxygen species metabolism	CG17530	FBgn0063494	Glutathione S transferase E6	1.99E-02	62	6	9.7%
GO:0006800 oxygen and reactive oxygen species metabolism	CG18522	FBgn0038347		1.99E-02	62	6	9.7%
GO:0006800 oxygen and reactive oxygen species metabolism	CG4199	FBgn0025628		1.99E-02	62	6	9.7%
GO:0006800 oxygen and reactive oxygen species metabolism	CG5164	FBgn0034335	Glutathione S transferase E1	1.99E-02	62	6	9.7%
GO:0006800 oxygen and reactive oxygen species metabolism	CG6776	FBgn0035904		1.99E-02	62	6	9.7%
GO:0007067 mitosis	CG15792	FBgn0005634	zipper	2.05E-02	220	14	6.4%

Age-specific age-related GO terms in Cluster 1

GO:0007067 mitosis	CG16983	FBgn0025637		2.05E-02	220	14	6.4%
GO:0007067 mitosis	CG17498	FBgn0035640		2.05E-02	220	14	6.4%
GO:0007067 mitosis	CG1768	FBgn0011202	diaphanous	2.05E-02	220	14	6.4%
GO:0007067 mitosis	CG3401	FBgn0003888	beta-Tubulin at 60D	2.05E-02	220	14	6.4%
GO:0007067 mitosis	CG4173	FBgn0014029	Septin-2	2.05E-02	220	14	6.4%
GO:0007067 mitosis	CG4254	FBgn0011726	twinstar	2.05E-02	220	14	6.4%
GO:0007067 mitosis	CG1956	FBgn0004636	Roughened	2.05E-02	220	14	6.4%
GO:0007067 mitosis	CG4869	FBgn0003890	beta-Tubulin at 97EF	2.05E-02	220	14	6.4%
GO:0007067 mitosis	CG7112	FBgn0035879		2.05E-02	220	14	6.4%
GO:0007067 mitosis	CG8440	FBgn0015754	Lissencephaly-1	2.05E-02	220	14	6.4%
GO:0007067 mitosis	CG9277	FBgn0003887	beta-Tubulin at 56D	2.05E-02	220	14	6.4%
GO:0007067 mitosis	CG9476	FBgn0003886	alpha-Tubulin at 85E	2.05E-02	220	14	6.4%
GO:0007067 mitosis	CG9755	FBgn0003165	pumilio	2.05E-02	220	14	6.4%
GO:0007028 cytoplasm organization and biogenesis	CG11949	FBgn0010434	coracle	2.08E-02	46	5	10.9%
GO:0007028 cytoplasm organization and biogenesis	CG5670	FBgn0002921	Na pump alpha subunit	2.08E-02	46	5	10.9%
GO:0007028 cytoplasm organization and biogenesis	CG6383	FBgn0000368	crumbs	2.08E-02	46	5	10.9%
GO:0007028 cytoplasm organization and biogenesis	CG6827	FBgn0013997	Neurexin IV	2.08E-02	46	5	10.9%
GO:0007028 cytoplasm organization and biogenesis	CG9261	FBgn0015777	nervana 2	2.08E-02	46	5	10.9%
GO:0000087 M phase of mitotic cell cycle	CG15792	FBgn0005634	zipper	2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG16983	FBgn0025637		2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG17498	FBgn0035640		2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG1768	FBgn0011202	diaphanous	2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG3401	FBgn0003888	beta-Tubulin at 60D	2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG4173	FBgn0014029	Septin-2	2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG4254	FBgn0011726	twinstar	2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG1956	FBgn0004636	Roughened	2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG4869	FBgn0003890	beta-Tubulin at 97EF	2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG7112	FBgn0035879		2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG8440	FBgn0015754	Lissencephaly-1	2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG9277	FBgn0003887	beta-Tubulin at 56D	2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG9476	FBgn0003886	alpha-Tubulin at 85E	2.13E-02	221	14	6.3%
GO:0000087 M phase of mitotic cell cycle	CG9755	FBgn0003165	pumilio	2.13E-02	221	14	6.3%
GO:0007018 microtubule-based movement	CG10838	FBgn0028570		2.24E-02	100	8	8.0%
GO:0007018 microtubule-based movement	CG10846	FBgn0040228	dynactin-subunit-p25	2.24E-02	100	8	8.0%
GO:0007018 microtubule-based movement	CG14779	FBgn0013720	pickel	2.24E-02	100	8	8.0%
GO:0007018 microtubule-based movement	CG3401	FBgn0003888	beta-Tubulin at 60D	2.24E-02	100	8	8.0%
GO:0007018 microtubule-based movement	CG4869	FBgn0003890	beta-Tubulin at 97EF	2.24E-02	100	8	8.0%
GO:0007018 microtubule-based movement	CG8440	FBgn0015754	Lissencephaly-1	2.24E-02	100	8	8.0%
GO:0007018 microtubule-based movement	CG9277	FBgn0003887	beta-Tubulin at 56D	2.24E-02	100	8	8.0%
GO:0007018 microtubule-based movement	CG9476	FBgn0003886	alpha-Tubulin at 85E	2.24E-02	100	8	8.0%

Age-specific age-related GO terms in Cluster 1

GO:0000278 mitotic cell cycle	CG15792	FBgn0005634	zipper	2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG16983	FBgn0025637		2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG17498	FBgn0035640		2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG1768	FBgn0011202	diaphanous	2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG17870	FBgn0004907		2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG3401	FBgn0003888	beta-Tubulin at 60D	2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG4173	FBgn0014029	Septin-2	2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG4254	FBgn0011726	twinstar	2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG1956	FBgn0004636	Roughened	2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG4869	FBgn0003890	beta-Tubulin at 97EF	2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG7112	FBgn0035879		2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG8440	FBgn0015754	Lissencephaly-1	2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG9277	FBgn0003887	beta-Tubulin at 56D	2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG9476	FBgn0003886	alpha-Tubulin at 85E	2.30E-02	245	15	6.1%
GO:0000278 mitotic cell cycle	CG9755	FBgn0003165	pumilio	2.30E-02	245	15	6.1%
GO:0030705 cytoskeleton-dependent intracellular transport	CG10838	FBgn0028570		2.36E-02	101	8	7.9%
GO:0030705 cytoskeleton-dependent intracellular transport	CG10846	FBgn0040228	dynactin-subunit-p25	2.36E-02	101	8	7.9%
GO:0030705 cytoskeleton-dependent intracellular transport	CG14779	FBgn0013720	pickel	2.36E-02	101	8	7.9%
GO:0030705 cytoskeleton-dependent intracellular transport	CG3401	FBgn0003888	beta-Tubulin at 60D	2.36E-02	101	8	7.9%
GO:0030705 cytoskeleton-dependent intracellular transport	CG4869	FBgn0003890	beta-Tubulin at 97EF	2.36E-02	101	8	7.9%
GO:0030705 cytoskeleton-dependent intracellular transport	CG8440	FBgn0015754	Lissencephaly-1	2.36E-02	101	8	7.9%
GO:0030705 cytoskeleton-dependent intracellular transport	CG9277	FBgn0003887	beta-Tubulin at 56D	2.36E-02	101	8	7.9%
GO:0030705 cytoskeleton-dependent intracellular transport	CG9476	FBgn0003886	alpha-Tubulin at 85E	2.36E-02	101	8	7.9%
GO:0042067 establishment of ommatidial polarity (sensu Endopterygota)	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	2.37E-02	32	4	12.5%
GO:0042067 establishment of ommatidial polarity (sensu Endopterygota)	CG2275	FBgn0001291	Jun-related antigen	2.37E-02	32	4	12.5%
GO:0042067 establishment of ommatidial polarity (sensu Endopterygota)	CG8056	FBgn0052177		2.37E-02	32	4	12.5%
GO:0042067 establishment of ommatidial polarity (sensu Endopterygota)	CG8416	FBgn0014020		2.37E-02	32	4	12.5%
GO:0016337 cell-cell adhesion	CG1084	FBgn0037240	Contactin	2.56E-02	122	9	7.4%
GO:0016337 cell-cell adhesion	CG12369	FBgn0010238	Lachesin	2.56E-02	122	9	7.4%
GO:0016337 cell-cell adhesion	CG1977	FBgn0003470	alpha Spectrin	2.56E-02	122	9	7.4%
GO:0016337 cell-cell adhesion	CG3359	FBgn0024211	midline fasciclin	2.56E-02	122	9	7.4%
GO:0016337 cell-cell adhesion	CG3622	FBgn0034778		2.56E-02	122	9	7.4%

Age-specific age-related GO terms in Cluster 1

GO:0016337 cell-cell adhesion	CG5803	FBgn0000636	Fasciclin 3	2.56E-02	122	9	7.4%
GO:0016337 cell-cell adhesion	CG6383	FBgn0000368	crumbs	2.56E-02	122	9	7.4%
GO:0016337 cell-cell adhesion	CG6827	FBgn0013997	Neurexin IV	2.56E-02	122	9	7.4%
GO:0016337 cell-cell adhesion	CG7123	FBgn0002527	Laminin B1	2.56E-02	122	9	7.4%
GO:0046530 photoreceptor cell differentiation	CG10701	FBgn0011661	Moesin	2.76E-02	85	7	8.2%
GO:0046530 photoreceptor cell differentiation	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	2.76E-02	85	7	8.2%
GO:0046530 photoreceptor cell differentiation	CG17870	FBgn0004907		2.76E-02	85	7	8.2%
GO:0046530 photoreceptor cell differentiation	CG18319	FBgn0000173	bendless	2.76E-02	85	7	8.2%
GO:0046530 photoreceptor cell differentiation	CG2275	FBgn0001291	Jun-related antigen	2.76E-02	85	7	8.2%
GO:0046530 photoreceptor cell differentiation	CG1956	FBgn0004636	Roughened	2.76E-02	85	7	8.2%
GO:0046530 photoreceptor cell differentiation	CG6383	FBgn0000368	crumbs	2.76E-02	85	7	8.2%
GO:0016358 dendrite morphogenesis	CG12530	FBgn0010341	Cdc42	2.90E-02	34	4	11.8%
GO:0016358 dendrite morphogenesis	CG8416	FBgn0014020		2.90E-02	34	4	11.8%
GO:0016358 dendrite morphogenesis	CG8440	FBgn0015754	Lissencephaly-1	2.90E-02	34	4	11.8%
GO:0016358 dendrite morphogenesis	CG9755	FBgn0003165	pumilio	2.90E-02	34	4	11.8%
GO:0016318 ommatidial rotation	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	3.04E-02	20	3	15.0%
GO:0016318 ommatidial rotation	CG8056	FBgn0052177		3.04E-02	20	3	15.0%
GO:0016318 ommatidial rotation	CG8416	FBgn0014020		3.04E-02	20	3	15.0%
GO:0007411 axon guidance	CG11081	FBgn0025741	plexin A	3.39E-02	70	6	8.6%
GO:0007411 axon guidance	CG12530	FBgn0010341	Cdc42	3.39E-02	70	6	8.6%
GO:0007411 axon guidance	CG3401	FBgn0003888	beta-Tubulin at 60D	3.39E-02	70	6	8.6%
GO:0007411 axon guidance	CG5803	FBgn0000636	Fasciclin 3	3.39E-02	70	6	8.6%
GO:0007411 axon guidance	CG7555	FBgn0036736		3.39E-02	70	6	8.6%
GO:0007411 axon guidance	CG8416	FBgn0014020		3.39E-02	70	6	8.6%
GO:0016081 synaptic vesicle docking during exocytosis	CG12210	FBgn0003660	Synaptobrevin	3.46E-02	21	3	14.3%
GO:0016081 synaptic vesicle docking during exocytosis	CG5081	FBgn0033583	Syntaxin 7	3.46E-02	21	3	14.3%
GO:0016081 synaptic vesicle docking during exocytosis	CG6827	FBgn0013997	Neurexin IV	3.46E-02	21	3	14.3%
GO:0007293 egg chamber formation (sensu Insecta)	CG17870	FBgn0004907		3.81E-02	37	4	10.8%
GO:0007293 egg chamber formation (sensu Insecta)	CG1977	FBgn0003470	alpha Spectrin	3.81E-02	37	4	10.8%
GO:0007293 egg chamber formation (sensu Insecta)	CG3637	FBgn0025865	Cortactin	3.81E-02	37	4	10.8%
GO:0007293 egg chamber formation (sensu Insecta)	CG8440	FBgn0015754	Lissencephaly-1	3.81E-02	37	4	10.8%
GO:0007059 chromosome segregation	CG16983	FBgn0025637		3.86E-02	111	8	7.2%
GO:0007059 chromosome segregation	CG17498	FBgn0035640		3.86E-02	111	8	7.2%
GO:0007059 chromosome segregation	CG17870	FBgn0004907		3.86E-02	111	8	7.2%
GO:0007059 chromosome segregation	CG3401	FBgn0003888	beta-Tubulin at 60D	3.86E-02	111	8	7.2%
GO:0007059 chromosome segregation	CG4869	FBgn0003890	beta-Tubulin at 97EF	3.86E-02	111	8	7.2%

Age-specific age-related GO terms in Cluster 1

GO:0007059 chromosome segregation	CG7112	FBgn0035879		3.86E-02	111	8	7.2%
GO:0007059 chromosome segregation	CG9277	FBgn0003887	beta-Tubulin at 56D	3.86E-02	111	8	7.2%
GO:0007059 chromosome segregation	CG9476	FBgn0003886	alpha-Tubulin at 85E	3.86E-02	111	8	7.2%
GO:0009798 axis specification	CG10701	FBgn0011661	Moesin	3.97E-02	153	10	6.5%
GO:0009798 axis specification	CG11254	FBgn0016034	maelstrom	3.97E-02	153	10	6.5%
GO:0009798 axis specification	CG5248	FBgn0020278	locomotion defects	3.97E-02	153	10	6.5%
GO:0009798 axis specification	CG17870	FBgn0004907		3.97E-02	153	10	6.5%
GO:0009798 axis specification	CG5061	FBgn0028388	capulet	3.97E-02	153	10	6.5%
GO:0009798 axis specification	CG5771	FBgn0015790	Rab-protein 11	3.97E-02	153	10	6.5%
GO:0009798 axis specification	CG5848	FBgn0000250	cactus	3.97E-02	153	10	6.5%
GO:0009798 axis specification	CG8440	FBgn0015754	Lissencephaly-1	3.97E-02	153	10	6.5%
GO:0009798 axis specification	CG9553	FBgn0000308	chickadee	3.97E-02	153	10	6.5%
GO:0009798 axis specification	CG9755	FBgn0003165	pumilio	3.97E-02	153	10	6.5%
GO:0000041 transition metal ion transport	CG10620	FBgn0036299	Transferrin 2	4.49E-02	10	2	20.0%
GO:0000041 transition metal ion transport	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	4.49E-02	10	2	20.0%
GO:0008062 eclosion rhythm	CG2048	FBgn0002413	discs overgrown	4.49E-02	10	2	20.0%
GO:0008062 eclosion rhythm	CG7391	FBgn0023076	Clock	4.49E-02	10	2	20.0%
GO:0008362 embryonic cuticle biosynthesis (sensu Insecta)	CG11949	FBgn0010434	coracle	4.49E-02	10	2	20.0%
GO:0008362 embryonic cuticle biosynthesis (sensu Insecta)	CG4006	FBgn0010379		4.49E-02	10	2	20.0%
GO:0030010 establishment of cell polarity	CG15792	FBgn0005634	zipper	4.49E-02	10	2	20.0%
GO:0030010 establishment of cell polarity	CG6383	FBgn0000368	crumbs	4.49E-02	10	2	20.0%
GO:0030725 ring canal formation	CG1977	FBgn0003470	alpha Spectrin	4.49E-02	10	2	20.0%
GO:0030725 ring canal formation	CG3637	FBgn0025865	Cortactin	4.49E-02	10	2	20.0%
GO:0043063 intercellular bridge organization and biogenesis	CG1977	FBgn0003470	alpha Spectrin	4.49E-02	10	2	20.0%
GO:0043063 intercellular bridge organization and biogenesis	CG3637	FBgn0025865	Cortactin	4.49E-02	10	2	20.0%
GO:0002164 larval development	CG10701	FBgn0011661	Moesin	4.50E-02	39	4	10.3%
GO:0002164 larval development	CG2720	FBgn0024352	Hsp70/Hsp90 organizing protein homolog	4.50E-02	39	4	10.3%
GO:0002164 larval development	CG1977	FBgn0003470	alpha Spectrin	4.50E-02	39	4	10.3%
GO:0002164 larval development	CG4859	FBgn0035049	Matrix metalloproteinase 1	4.50E-02	39	4	10.3%
GO:0007306 insect chorion formation	CG12530	FBgn0010341	Cdc42	4.50E-02	39	4	10.3%
GO:0007306 insect chorion formation	CG18247	FBgn0015295	Src homology 2, ankyrin repeat, tyrosine kinase	4.50E-02	39	4	10.3%
GO:0007306 insect chorion formation	CG2275	FBgn0001291	Jun-related antigen	4.50E-02	39	4	10.3%
GO:0007306 insect chorion formation	CG5848	FBgn0000250	cactus	4.50E-02	39	4	10.3%
GO:0048113 pole plasm assembly (sensu Insecta)	CG10701	FBgn0011661	Moesin	4.50E-02	39	4	10.3%
GO:0048113 pole plasm assembly (sensu Insecta)	CG11254	FBgn0016034	maelstrom	4.50E-02	39	4	10.3%

Age-specific age-related GO terms in Cluster 1

GO:0048113 pole plasm assembly (sensu Insecta)	CG5771	FBgn0015790	Rab-protein 11	4.50E-02	39	4	10.3%
GO:0048113 pole plasm assembly (sensu Insecta)	CG9553	FBgn0000308	chickadee	4.50E-02	39	4	10.3%
GO:0006997 nuclear organization and biogenesis	CG11254	FBgn0016034	maelstrom	4.88E-02	24	3	12.5%
GO:0006997 nuclear organization and biogenesis	CG8076	NA	NA	4.88E-02	24	3	12.5%
GO:0006997 nuclear organization and biogenesis	CG8440	FBgn0015754	Lissencephaly-1	4.88E-02	24	3	12.5%

Acp-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:0006963 antibacterial polypeptide induction	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	3.48E-06	15	5	33.3%
GO:0006963 antibacterial polypeptide induction	CG11992	FBgn0014018	Relish	3.48E-06	15	5	33.3%
GO:0006963 antibacterial polypeptide induction	CG16910	FBgn0041205	kenny	3.48E-06	15	5	33.3%
GO:0006963 antibacterial polypeptide induction	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	3.48E-06	15	5	33.3%
GO:0006963 antibacterial polypeptide induction	CG5490	FBgn0003717	Toll	3.48E-06	15	5	33.3%
GO:0008298 intracellular mRNA localization	CG18621	NA	NA	9.03E-05	44	6	13.6%
GO:0008298 intracellular mRNA localization	CG8201	FBgn0026193		9.03E-05	44	6	13.6%
GO:0008298 intracellular mRNA localization	CG5448	NA	NA	9.03E-05	44	6	13.6%
GO:0008298 intracellular mRNA localization	CG5753	FBgn0003520	staufen	9.03E-05	44	6	13.6%
GO:0008298 intracellular mRNA localization	CG7507	FBgn0010349	Dynein heavy chain 64C	9.03E-05	44	6	13.6%
GO:0008298 intracellular mRNA localization	CG8556	FBgn0014011		9.03E-05	44	6	13.6%
GO:0045451 pole plasm oskar mRNA localization	CG18621	NA	NA	1.35E-04	30	5	16.7%
GO:0045451 pole plasm oskar mRNA localization	CG8201	FBgn0026193		1.35E-04	30	5	16.7%
GO:0045451 pole plasm oskar mRNA localization	CG5448	NA	NA	1.35E-04	30	5	16.7%
GO:0045451 pole plasm oskar mRNA localization	CG5753	FBgn0003520	staufen	1.35E-04	30	5	16.7%
GO:0045451 pole plasm oskar mRNA localization	CG8556	FBgn0014011		1.35E-04	30	5	16.7%
GO:0030029 actin filament-based process	CG18621	NA	NA	1.60E-04	92	8	8.7%
GO:0030029 actin filament-based process	CG11341	FBgn0035533		1.60E-04	92	8	8.7%
GO:0030029 actin filament-based process	CG8201	FBgn0026193		1.60E-04	92	8	8.7%
GO:0030029 actin filament-based process	CG1404	FBgn0020255		1.60E-04	92	8	8.7%
GO:0030029 actin filament-based process	CG14622	FBgn0025641		1.60E-04	92	8	8.7%
GO:0030029 actin filament-based process	CG7850	FBgn0004210	puckered	1.60E-04	92	8	8.7%
GO:0030029 actin filament-based process	CG8261	FBgn0004921	G protein gamma 1	1.60E-04	92	8	8.7%
GO:0030029 actin filament-based process	CG8978	FBgn0001961	Suppressor of profilin 2	1.60E-04	92	8	8.7%
GO:0030036 actin cytoskeleton organization and biogenesis	CG18621	NA	NA	1.60E-04	92	8	8.7%
GO:0030036 actin cytoskeleton organization and biogenesis	CG11341	FBgn0035533		1.60E-04	92	8	8.7%
GO:0030036 actin cytoskeleton organization and biogenesis	CG8201	FBgn0026193		1.60E-04	92	8	8.7%
GO:0030036 actin cytoskeleton organization and biogenesis	CG1404	FBgn0020255		1.60E-04	92	8	8.7%
GO:0030036 actin cytoskeleton organization and biogenesis	CG14622	FBgn0025641		1.60E-04	92	8	8.7%

GO:0030036 actin cytoskeleton organization and biogenesis	CG7850	FBgn0004210	puckered	1.60E-04	92	8	8.7%
GO:0030036 actin cytoskeleton organization and biogenesis	CG8261	FBgn0004921	G protein gamma 1	1.60E-04	92	8	8.7%
GO:0030036 actin cytoskeleton organization and biogenesis	CG8978	FBgn0001961	Suppressor of profilin 2	1.60E-04	92	8	8.7%
GO:0019094 pole plasm mRNA localization	CG18621	NA	NA	1.85E-04	32	5	15.6%
GO:0019094 pole plasm mRNA localization	CG8201	FBgn0026193		1.85E-04	32	5	15.6%
GO:0019094 pole plasm mRNA localization	CG5448	NA	NA	1.85E-04	32	5	15.6%
GO:0019094 pole plasm mRNA localization	CG5753	FBgn0003520	staufer	1.85E-04	32	5	15.6%
GO:0019094 pole plasm mRNA localization	CG8556	FBgn0014011		1.85E-04	32	5	15.6%
GO:0007316 pole plasm RNA localization	CG18621	NA	NA	2.15E-04	33	5	15.2%
GO:0007316 pole plasm RNA localization	CG8201	FBgn0026193		2.15E-04	33	5	15.2%
GO:0007316 pole plasm RNA localization	CG5448	NA	NA	2.15E-04	33	5	15.2%
GO:0007316 pole plasm RNA localization	CG5753	FBgn0003520	staufer	2.15E-04	33	5	15.2%
GO:0007316 pole plasm RNA localization	CG8556	FBgn0014011		2.15E-04	33	5	15.2%
GO:0016311 dephosphorylation	CG10975	FBgn0014007	Protein tyrosine phosphatase 69D	2.66E-04	99	8	8.1%
GO:0016311 dephosphorylation	CG11438	FBgn0037164		2.66E-04	99	8	8.1%
GO:0016311 dephosphorylation	CG17746	FBgn0035425		2.66E-04	99	8	8.1%
GO:0016311 dephosphorylation	CG18093	NA	NA	2.66E-04	99	8	8.1%
GO:0016311 dephosphorylation	CG4993	FBgn0024734		2.66E-04	99	8	8.1%
GO:0016311 dephosphorylation	CG7850	FBgn0004210	puckered	2.66E-04	99	8	8.1%
GO:0016311 dephosphorylation	CG9181	FBgn0003138	Protein tyrosine phosphatase 61F	2.66E-04	99	8	8.1%
GO:0016311 dephosphorylation	CG9493	FBgn0031799		2.66E-04	99	8	8.1%
GO:0006470 protein amino acid dephosphorylation	CG10975	FBgn0014007	Protein tyrosine phosphatase 69D	3.42E-04	78	7	9.0%
GO:0006470 protein amino acid dephosphorylation	CG17746	FBgn0035425		3.42E-04	78	7	9.0%
GO:0006470 protein amino acid dephosphorylation	CG18093	NA	NA	3.42E-04	78	7	9.0%
GO:0006470 protein amino acid dephosphorylation	CG4993	FBgn0024734		3.42E-04	78	7	9.0%
GO:0006470 protein amino acid dephosphorylation	CG7850	FBgn0004210	puckered	3.42E-04	78	7	9.0%
GO:0006470 protein amino acid dephosphorylation	CG9181	FBgn0003138	Protein tyrosine phosphatase 61F	3.42E-04	78	7	9.0%
GO:0006470 protein amino acid dephosphorylation	CG9493	FBgn0031799		3.42E-04	78	7	9.0%
GO:0019731 antibacterial humoral response	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	3.74E-04	37	5	13.5%
GO:0019731 antibacterial humoral response	CG11992	FBgn0014018	Relish	3.74E-04	37	5	13.5%
GO:0019731 antibacterial humoral response	CG16910	FBgn0041205	kenny	3.74E-04	37	5	13.5%

GO:0019731 antibacterial humoral response	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	3.74E-04	37	5	13.5%
GO:0019731 antibacterial humoral response	CG5490	FBgn0003717	Toll	3.74E-04	37	5	13.5%
GO:0019730 antimicrobial humoral response	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	4.68E-04	59	6	10.2%
GO:0019730 antimicrobial humoral response	CG11992	FBgn0014018	Relish	4.68E-04	59	6	10.2%
GO:0019730 antimicrobial humoral response	CG16910	FBgn0041205	kenny	4.68E-04	59	6	10.2%
GO:0019730 antimicrobial humoral response	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	4.68E-04	59	6	10.2%
GO:0019730 antimicrobial humoral response	CG5490	FBgn0003717	Toll	4.68E-04	59	6	10.2%
GO:0019730 antimicrobial humoral response	CG6819	FBgn0026207	members only	4.68E-04	59	6	10.2%
GO:0048113 pole plasm assembly (sensu Insecta)	CG18621	NA	NA	4.81E-04	39	5	12.8%
GO:0048113 pole plasm assembly (sensu Insecta)	CG8201	FBgn0026193		4.81E-04	39	5	12.8%
GO:0048113 pole plasm assembly (sensu Insecta)	CG5448	NA	NA	4.81E-04	39	5	12.8%
GO:0048113 pole plasm assembly (sensu Insecta)	CG5753	FBgn0003520	stauen	4.81E-04	39	5	12.8%
GO:0048113 pole plasm assembly (sensu Insecta)	CG8556	FBgn0014011		4.81E-04	39	5	12.8%
GO:0007315 pole plasm assembly	CG18621	NA	NA	6.09E-04	41	5	12.2%
GO:0007315 pole plasm assembly	CG8201	FBgn0026193		6.09E-04	41	5	12.2%
GO:0007315 pole plasm assembly	CG5448	NA	NA	6.09E-04	41	5	12.2%
GO:0007315 pole plasm assembly	CG5753	FBgn0003520	stauen	6.09E-04	41	5	12.2%
GO:0007315 pole plasm assembly	CG8556	FBgn0014011		6.09E-04	41	5	12.2%
GO:0006403 RNA localization	CG18621	NA	NA	6.22E-04	86	7	8.1%
GO:0006403 RNA localization	CG8201	FBgn0026193		6.22E-04	86	7	8.1%
GO:0006403 RNA localization	CG1404	FBgn0020255		6.22E-04	86	7	8.1%
GO:0006403 RNA localization	CG5448	NA	NA	6.22E-04	86	7	8.1%
GO:0006403 RNA localization	CG5753	FBgn0003520	stauen	6.22E-04	86	7	8.1%
GO:0006403 RNA localization	CG7507	FBgn0010349	Dynein heavy chain 64C	6.22E-04	86	7	8.1%
GO:0006403 RNA localization	CG8556	FBgn0014011		6.22E-04	86	7	8.1%
GO:0048112 oocyte anterior posterior axis determination (sensu Insecta)	CG18621	NA	NA	6.82E-04	42	5	11.9%
GO:0048112 oocyte anterior posterior axis determination (sensu Insecta)	CG8201	FBgn0026193		6.82E-04	42	5	11.9%
GO:0048112 oocyte anterior posterior axis determination (sensu Insecta)	CG5448	NA	NA	6.82E-04	42	5	11.9%
GO:0048112 oocyte anterior posterior axis determination (sensu Insecta)	CG5753	FBgn0003520	stauen	6.82E-04	42	5	11.9%
GO:0048112 oocyte anterior posterior axis determination (sensu Insecta)	CG8556	FBgn0014011		6.82E-04	42	5	11.9%
GO:0045087 innate immune response	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	7.23E-04	11	3	27.3%

Acg-specific age-related GO terms in Cluster 2

GO:0045087 innate immune response	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	7.23E-04	11	3	27.3%
GO:0045087 innate immune response	CG5490	FBgn0003717	Toll	7.23E-04	11	3	27.3%
GO:0006959 humoral immune response	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	9.28E-04	67	6	9.0%
GO:0006959 humoral immune response	CG11992	FBgn0014018	Relish	9.28E-04	67	6	9.0%
GO:0006959 humoral immune response	CG16910	FBgn0041205	kenny	9.28E-04	67	6	9.0%
GO:0006959 humoral immune response	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	9.28E-04	67	6	9.0%
GO:0006959 humoral immune response	CG5490	FBgn0003717	Toll	9.28E-04	67	6	9.0%
GO:0006959 humoral immune response	CG6819	FBgn0026207	members only	9.28E-04	67	6	9.0%
GO:0000270 peptidoglycan metabolism	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	9.52E-04	12	3	25.0%
GO:0000270 peptidoglycan metabolism	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	9.52E-04	12	3	25.0%
GO:0000270 peptidoglycan metabolism	CG8995	FBgn0030695	Peptidoglycan recognition protein LE	9.52E-04	12	3	25.0%
GO:0009253 peptidoglycan catabolism	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	9.52E-04	12	3	25.0%
GO:0009253 peptidoglycan catabolism	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	9.52E-04	12	3	25.0%
GO:0009253 peptidoglycan catabolism	CG8995	FBgn0030695	Peptidoglycan recognition protein LE	9.52E-04	12	3	25.0%
GO:0048110 oocyte construction (sensu Insecta)	CG18621	NA	NA	1.15E-03	47	5	10.6%
GO:0048110 oocyte construction (sensu Insecta)	CG8201	FBgn0026193		1.15E-03	47	5	10.6%
GO:0048110 oocyte construction (sensu Insecta)	CG5448	NA	NA	1.15E-03	47	5	10.6%
GO:0048110 oocyte construction (sensu Insecta)	CG5753	FBgn0003520	staufer	1.15E-03	47	5	10.6%
GO:0048110 oocyte construction (sensu Insecta)	CG8556	FBgn0014011		1.15E-03	47	5	10.6%
GO:0048111 oocyte axis determination (sensu Insecta)	CG18621	NA	NA	1.15E-03	47	5	10.6%
GO:0048111 oocyte axis determination (sensu Insecta)	CG8201	FBgn0026193		1.15E-03	47	5	10.6%
GO:0048111 oocyte axis determination (sensu Insecta)	CG5448	NA	NA	1.15E-03	47	5	10.6%
GO:0048111 oocyte axis determination (sensu Insecta)	CG5753	FBgn0003520	staufer	1.15E-03	47	5	10.6%
GO:0048111 oocyte axis determination (sensu Insecta)	CG8556	FBgn0014011		1.15E-03	47	5	10.6%
GO:0008063 Toll signaling pathway	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	1.20E-03	28	4	14.3%
GO:0008063 Toll signaling pathway	CG11992	FBgn0014018	Relish	1.20E-03	28	4	14.3%
GO:0008063 Toll signaling pathway	CG16910	FBgn0041205	kenny	1.20E-03	28	4	14.3%
GO:0008063 Toll signaling pathway	CG5490	FBgn0003717	Toll	1.20E-03	28	4	14.3%
GO:0007309 oocyte axis determination	CG18621	NA	NA	1.26E-03	71	6	8.5%
GO:0007309 oocyte axis determination	CG8201	FBgn0026193		1.26E-03	71	6	8.5%

Acg-specific age-related GO terms in Cluster 2

GO:0007309 oocyte axis determination	CG5448	NA	NA	1.26E-03	71	6	8.5%
GO:0007309 oocyte axis determination	CG5753	FBgn0003520	staufen	1.26E-03	71	6	8.5%
GO:0007309 oocyte axis determination	CG7507	FBgn0010349	Dynein heavy chain 64C	1.26E-03	71	6	8.5%
GO:0007309 oocyte axis determination	CG8556	FBgn0014011		1.26E-03	71	6	8.5%
GO:0007308 oocyte construction	CG18621	NA	NA	1.46E-03	73	6	8.2%
GO:0007308 oocyte construction	CG8201	FBgn0026193		1.46E-03	73	6	8.2%
GO:0007308 oocyte construction	CG5448	NA	NA	1.46E-03	73	6	8.2%
GO:0007308 oocyte construction	CG5753	FBgn0003520	staufen	1.46E-03	73	6	8.2%
GO:0007308 oocyte construction	CG7507	FBgn0010349	Dynein heavy chain 64C	1.46E-03	73	6	8.2%
GO:0007308 oocyte construction	CG8556	FBgn0014011		1.46E-03	73	6	8.2%
GO:0007314 oocyte anterior posterior axis determination	CG18621	NA	NA	1.98E-03	53	5	9.4%
GO:0007314 oocyte anterior posterior axis determination	CG8201	FBgn0026193		1.98E-03	53	5	9.4%
GO:0007314 oocyte anterior posterior axis determination	CG5448	NA	NA	1.98E-03	53	5	9.4%
GO:0007314 oocyte anterior posterior axis determination	CG5753	FBgn0003520	staufen	1.98E-03	53	5	9.4%
GO:0007314 oocyte anterior posterior axis determination	CG8556	FBgn0014011		1.98E-03	53	5	9.4%
GO:0006955 immune response	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	2.13E-03	106	7	6.6%
GO:0006955 immune response	CG11992	FBgn0014018	Relish	2.13E-03	106	7	6.6%
GO:0006955 immune response	CG16910	FBgn0041205	kenny	2.13E-03	106	7	6.6%
GO:0006955 immune response	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	2.13E-03	106	7	6.6%
GO:0006955 immune response	CG5490	FBgn0003717	Toll	2.13E-03	106	7	6.6%
GO:0006955 immune response	CG6819	FBgn0026207	members only	2.13E-03	106	7	6.6%
GO:0006955 immune response	CG8995	FBgn0030695	Peptidoglycan recognition protein LE	2.13E-03	106	7	6.6%
GO:0007455 eye-antennal disc metamorphosis	CG12230	FBgn0000257	carnation	2.27E-03	137	8	5.8%
GO:0007455 eye-antennal disc metamorphosis	CG3629	FBgn0000157	Distal-less	2.27E-03	137	8	5.8%
GO:0007455 eye-antennal disc metamorphosis	CG3874	FBgn0042641	fringe connection	2.27E-03	137	8	5.8%
GO:0007455 eye-antennal disc metamorphosis	CG7850	FBgn0004210	puckered	2.27E-03	137	8	5.8%
GO:0007455 eye-antennal disc metamorphosis	CG8075	FBgn0015838	Van Gogh	2.27E-03	137	8	5.8%
GO:0007455 eye-antennal disc metamorphosis	CG8556	FBgn0014011		2.27E-03	137	8	5.8%
GO:0007455 eye-antennal disc metamorphosis	CG8978	FBgn0001961	Suppressor of profilin 2	2.27E-03	137	8	5.8%
GO:0007455 eye-antennal disc metamorphosis	CG9695	FBgn0000414	Disabled	2.27E-03	137	8	5.8%
GO:0035214 eye-antennal disc development	CG12230	FBgn0000257	carnation	2.37E-03	138	8	5.8%
GO:0035214 eye-antennal disc development	CG3629	FBgn0000157	Distal-less	2.37E-03	138	8	5.8%
GO:0035214 eye-antennal disc development	CG3874	FBgn0042641	fringe connection	2.37E-03	138	8	5.8%
GO:0035214 eye-antennal disc development	CG7850	FBgn0004210	puckered	2.37E-03	138	8	5.8%
GO:0035214 eye-antennal disc development	CG8075	FBgn0015838	Van Gogh	2.37E-03	138	8	5.8%
GO:0035214 eye-antennal disc development	CG8556	FBgn0014011		2.37E-03	138	8	5.8%
GO:0035214 eye-antennal disc development	CG8978	FBgn0001961	Suppressor of profilin 2	2.37E-03	138	8	5.8%

Acg-specific age-related GO terms in Cluster 2

GO:0035214 eye-antennal disc development	CG9695	FBgn0000414	Disabled	2.37E-03	138	8	5.8%
GO:0007015 actin filament organization	CG8201	FBgn0026193		2.96E-03	58	5	8.6%
GO:0007015 actin filament organization	CG1404	FBgn0020255		2.96E-03	58	5	8.6%
GO:0007015 actin filament organization	CG7850	FBgn0004210	puckered	2.96E-03	58	5	8.6%
GO:0007015 actin filament organization	CG8261	FBgn0004921	G protein gamma 1	2.96E-03	58	5	8.6%
GO:0007015 actin filament organization	CG8978	FBgn0001961	Suppressor of profilin 2	2.96E-03	58	5	8.6%
GO:0009613 response to pest pathogen or parasite	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	3.17E-03	85	6	7.1%
GO:0009613 response to pest pathogen or parasite	CG11992	FBgn0014018	Relish	3.17E-03	85	6	7.1%
GO:0009613 response to pest pathogen or parasite	CG16910	FBgn0041205	kenny	3.17E-03	85	6	7.1%
GO:0009613 response to pest pathogen or parasite	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	3.17E-03	85	6	7.1%
GO:0009613 response to pest pathogen or parasite	CG5490	FBgn0003717	Toll	3.17E-03	85	6	7.1%
GO:0009613 response to pest pathogen or parasite	CG6819	FBgn0026207	members only	3.17E-03	85	6	7.1%
GO:0007317 regulation of pole plasm oskar mRNA localization	CG8201	FBgn0026193		3.28E-03	18	3	16.7%
GO:0007317 regulation of pole plasm oskar mRNA localization	CG5448	NA	NA	3.28E-03	18	3	16.7%
GO:0007317 regulation of pole plasm oskar mRNA localization	CG5753	FBgn0003520	staufen	3.28E-03	18	3	16.7%
GO:0000902 cellular morphogenesis	CG11579	FBgn0000117	armadillo	3.56E-03	215	10	4.7%
GO:0000902 cellular morphogenesis	CG8201	FBgn0026193		3.56E-03	215	10	4.7%
GO:0000902 cellular morphogenesis	CG13809	FBgn0035317		3.56E-03	215	10	4.7%
GO:0000902 cellular morphogenesis	CG1404	FBgn0020255		3.56E-03	215	10	4.7%
GO:0000902 cellular morphogenesis	CG14637	FBgn0015331	abstrakt	3.56E-03	215	10	4.7%
GO:0000902 cellular morphogenesis	CG7850	FBgn0004210	puckered	3.56E-03	215	10	4.7%
GO:0000902 cellular morphogenesis	CG8075	FBgn0015838	Van Gogh	3.56E-03	215	10	4.7%
GO:0000902 cellular morphogenesis	CG8261	FBgn0004921	G protein gamma 1	3.56E-03	215	10	4.7%
GO:0000902 cellular morphogenesis	CG8556	FBgn0014011		3.56E-03	215	10	4.7%
GO:0000902 cellular morphogenesis	CG9695	FBgn0000414	Disabled	3.56E-03	215	10	4.7%
GO:0042742 defense response to bacteria	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	3.69E-03	61	5	8.2%
GO:0042742 defense response to bacteria	CG11992	FBgn0014018	Relish	3.69E-03	61	5	8.2%
GO:0042742 defense response to bacteria	CG16910	FBgn0041205	kenny	3.69E-03	61	5	8.2%
GO:0042742 defense response to bacteria	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	3.69E-03	61	5	8.2%
GO:0042742 defense response to bacteria	CG5490	FBgn0003717	Toll	3.69E-03	61	5	8.2%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG12230	FBgn0000257	carnation	3.90E-03	118	7	5.9%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG3874	FBgn0042641	fringe connection	3.90E-03	118	7	5.9%

Acg-specific age-related GO terms in Cluster 2

GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG7850	FBgn0004210	puckered	3.90E-03	118	7	5.9%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG8075	FBgn0015838	Van Gogh	3.90E-03	118	7	5.9%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG8556	FBgn0014011		3.90E-03	118	7	5.9%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG8978	FBgn0001961	Suppressor of profilin 2	3.90E-03	118	7	5.9%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG9695	FBgn0000414	Disabled	3.90E-03	118	7	5.9%
GO:0009617 response to bacteria	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	5.18E-03	66	5	7.6%
GO:0009617 response to bacteria	CG11992	FBgn0014018	Relish	5.18E-03	66	5	7.6%
GO:0009617 response to bacteria	CG16910	FBgn0041205	kenny	5.18E-03	66	5	7.6%
GO:0009617 response to bacteria	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	5.18E-03	66	5	7.6%
GO:0009617 response to bacteria	CG5490	FBgn0003717	Toll	5.18E-03	66	5	7.6%
GO:0007389 pattern specification	CG18621	NA	NA	7.67E-03	240	10	4.2%
GO:0007389 pattern specification	CG11579	FBgn0000117	armadillo	7.67E-03	240	10	4.2%
GO:0007389 pattern specification	CG8201	FBgn0026193		7.67E-03	240	10	4.2%
GO:0007389 pattern specification	CG3629	FBgn0000157	Distal-less	7.67E-03	240	10	4.2%
GO:0007389 pattern specification	CG3874	FBgn0042641	fringe connection	7.67E-03	240	10	4.2%
GO:0007389 pattern specification	CG5448	NA	NA	7.67E-03	240	10	4.2%
GO:0007389 pattern specification	CG5490	FBgn0003717	Toll	7.67E-03	240	10	4.2%
GO:0007389 pattern specification	CG5753	FBgn0003520	staufen	7.67E-03	240	10	4.2%
GO:0007389 pattern specification	CG7507	FBgn0010349	Dynein heavy chain 64C	7.67E-03	240	10	4.2%
GO:0007389 pattern specification	CG8556	FBgn0014011		7.67E-03	240	10	4.2%
GO:0007452 imaginal disc metamorphosis	CG12230	FBgn0000257	carnation	8.40E-03	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG3411	FBgn0004101	blistered	8.40E-03	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG3629	FBgn0000157	Distal-less	8.40E-03	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG3874	FBgn0042641	fringe connection	8.40E-03	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG7850	FBgn0004210	puckered	8.40E-03	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG8075	FBgn0015838	Van Gogh	8.40E-03	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG8556	FBgn0014011		8.40E-03	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG8978	FBgn0001961	Suppressor of profilin 2	8.40E-03	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG9695	FBgn0000414	Disabled	8.40E-03	206	9	4.4%
GO:0043207 response to external biotic stimulus	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	1.10E-02	110	6	5.5%
GO:0043207 response to external biotic stimulus	CG11992	FBgn0014018	Relish	1.10E-02	110	6	5.5%
GO:0043207 response to external biotic stimulus	CG16910	FBgn0041205	kenny	1.10E-02	110	6	5.5%
GO:0043207 response to external biotic stimulus	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	1.10E-02	110	6	5.5%
GO:0043207 response to external biotic stimulus	CG5490	FBgn0003717	Toll	1.10E-02	110	6	5.5%
GO:0043207 response to external biotic stimulus	CG6819	FBgn0026207	members only	1.10E-02	110	6	5.5%
GO:0009611 response to wounding	CG11992	FBgn0014018	Relish	1.16E-02	28	3	10.7%

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GO:0009611 response to wounding	CG6449	FBgn0036101	ninjurin A	1.16E-02	28	3	10.7%
GO:0009611 response to wounding	CG7850	FBgn0004210	puckered	1.16E-02	28	3	10.7%
GO:0031175 neurite morphogenesis	CG10975	FBgn0014007	Protein tyrosine phosphatase 69D	1.35E-02	115	6	5.2%
GO:0031175 neurite morphogenesis	CG18376	NA	NA	1.35E-02	115	6	5.2%
GO:0031175 neurite morphogenesis	CG6449	FBgn0036101	ninjurin A	1.35E-02	115	6	5.2%
GO:0031175 neurite morphogenesis	CG7507	FBgn0010349	Dynein heavy chain 64C	1.35E-02	115	6	5.2%
GO:0031175 neurite morphogenesis	CG8978	FBgn0001961	Suppressor of profilin 2	1.35E-02	115	6	5.2%
GO:0031175 neurite morphogenesis	CG9181	FBgn0003138	Protein tyrosine phosphatase 61F	1.35E-02	115	6	5.2%
GO:0006605 protein targeting	CG12192	FBgn0034827		1.37E-02	223	9	4.0%
GO:0006605 protein targeting	CG12230	FBgn0000257	carnation	1.37E-02	223	9	4.0%
GO:0006605 protein targeting	CG13892	FBgn0035141	Cyclophilin-like	1.37E-02	223	9	4.0%
GO:0006605 protein targeting	CG1404	FBgn0020255		1.37E-02	223	9	4.0%
GO:0006605 protein targeting	CG6313	NA	NA	1.37E-02	223	9	4.0%
GO:0006605 protein targeting	CG5300	FBgn0032243		1.37E-02	223	9	4.0%
GO:0006605 protein targeting	CG5448	NA	NA	1.37E-02	223	9	4.0%
GO:0006605 protein targeting	CG5808	FBgn0027617		1.37E-02	223	9	4.0%
GO:0006605 protein targeting	CG6819	FBgn0026207	members only	1.37E-02	223	9	4.0%
GO:0001763 branching morphogenesis	CG11579	FBgn0000117	armadillo	1.41E-02	30	3	10.0%
GO:0001763 branching morphogenesis	CG3411	FBgn0004101	blistered	1.41E-02	30	3	10.0%
GO:0001763 branching morphogenesis	CG6819	FBgn0026207	members only	1.41E-02	30	3	10.0%
GO:0051049 regulation of transport	CG5448	NA	NA	1.41E-02	55	4	7.3%
GO:0051049 regulation of transport	CG6819	FBgn0026207	members only	1.41E-02	55	4	7.3%
GO:0051049 regulation of transport	CG7980	FBgn0035255		1.41E-02	55	4	7.3%
GO:0051049 regulation of transport	CG8287	FBgn0015796	Rab-protein 8	1.41E-02	55	4	7.3%
GO:0035146 tube fusion	CG11579	FBgn0000117	armadillo	1.44E-02	11	2	18.2%
GO:0035146 tube fusion	CG6819	FBgn0026207	members only	1.44E-02	11	2	18.2%
GO:0035147 tracheal branch fusion	CG11579	FBgn0000117	armadillo	1.44E-02	11	2	18.2%
GO:0035147 tracheal branch fusion	CG6819	FBgn0026207	members only	1.44E-02	11	2	18.2%
GO:0046328 regulation of JNK cascade	CG11579	FBgn0000117	armadillo	1.44E-02	11	2	18.2%
GO:0046328 regulation of JNK cascade	CG7850	FBgn0004210	puckered	1.44E-02	11	2	18.2%
GO:0009798 axis specification	CG18621	NA	NA	1.54E-02	153	7	4.6%
GO:0009798 axis specification	CG8201	FBgn0026193		1.54E-02	153	7	4.6%
GO:0009798 axis specification	CG5448	NA	NA	1.54E-02	153	7	4.6%
GO:0009798 axis specification	CG5490	FBgn0003717	Toll	1.54E-02	153	7	4.6%
GO:0009798 axis specification	CG5753	FBgn0003520	staufen	1.54E-02	153	7	4.6%
GO:0009798 axis specification	CG7507	FBgn0010349	Dynein heavy chain 64C	1.54E-02	153	7	4.6%
GO:0009798 axis specification	CG8556	FBgn0014011		1.54E-02	153	7	4.6%
GO:0008360 regulation of cell shape	CG11579	FBgn0000117	armadillo	1.54E-02	86	5	5.8%
GO:0008360 regulation of cell shape	CG8201	FBgn0026193		1.54E-02	86	5	5.8%
GO:0008360 regulation of cell shape	CG1404	FBgn0020255		1.54E-02	86	5	5.8%
GO:0008360 regulation of cell shape	CG7850	FBgn0004210	puckered	1.54E-02	86	5	5.8%
GO:0008360 regulation of cell shape	CG8261	FBgn0004921	G protein gamma 1	1.54E-02	86	5	5.8%

GO:0050830 defense response to Gram-positive bacteria	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	1.70E-02	12	2	16.7%
GO:0050830 defense response to Gram-positive bacteria	CG5490	FBgn0003717	Toll	1.70E-02	12	2	16.7%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG12230	FBgn0000257	carnation	1.93E-02	160	7	4.4%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG3874	FBgn0042641	fringe connection	1.93E-02	160	7	4.4%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG7850	FBgn0004210	puckered	1.93E-02	160	7	4.4%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG8075	FBgn0015838	Van Gogh	1.93E-02	160	7	4.4%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG8556	FBgn0014011		1.93E-02	160	7	4.4%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG8978	FBgn0001961	Suppressor of profilin 2	1.93E-02	160	7	4.4%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG9695	FBgn0000414	Disabled	1.93E-02	160	7	4.4%
GO:0007318 pole plasm protein localization	CG8201	FBgn0026193		1.99E-02	13	2	15.4%
GO:0007318 pole plasm protein localization	CG5753	FBgn0003520	staufen	1.99E-02	13	2	15.4%
GO:0009966 regulation of signal transduction	CG11579	FBgn0000117	armadillo	2.01E-02	92	5	5.4%
GO:0009966 regulation of signal transduction	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	2.01E-02	92	5	5.4%
GO:0009966 regulation of signal transduction	CG8201	FBgn0026193		2.01E-02	92	5	5.4%
GO:0009966 regulation of signal transduction	CG6537	NA	NA	2.01E-02	92	5	5.4%
GO:0009966 regulation of signal transduction	CG7850	FBgn0004210	puckered	2.01E-02	92	5	5.4%
GO:0007409 axonogenesis	CG10975	FBgn0014007	Protein tyrosine phosphatase 69D	2.28E-02	95	5	5.3%
GO:0007409 axonogenesis	CG18376	NA	NA	2.28E-02	95	5	5.3%
GO:0007409 axonogenesis	CG6449	FBgn0036101	ninjurin A	2.28E-02	95	5	5.3%
GO:0007409 axonogenesis	CG8978	FBgn0001961	Suppressor of profilin 2	2.28E-02	95	5	5.3%
GO:0007409 axonogenesis	CG9181	FBgn0003138	Protein tyrosine phosphatase 61F	2.28E-02	95	5	5.3%
GO:0019732 antifungal humoral response	CG11992	FBgn0014018	Relish	2.30E-02	14	2	14.3%
GO:0019732 antifungal humoral response	CG5490	FBgn0003717	Toll	2.30E-02	14	2	14.3%
GO:0001654 eye morphogenesis	CG12230	FBgn0000257	carnation	2.37E-02	167	7	4.2%
GO:0001654 eye morphogenesis	CG3874	FBgn0042641	fringe connection	2.37E-02	167	7	4.2%
GO:0001654 eye morphogenesis	CG7850	FBgn0004210	puckered	2.37E-02	167	7	4.2%
GO:0001654 eye morphogenesis	CG8075	FBgn0015838	Van Gogh	2.37E-02	167	7	4.2%
GO:0001654 eye morphogenesis	CG8556	FBgn0014011		2.37E-02	167	7	4.2%
GO:0001654 eye morphogenesis	CG8978	FBgn0001961	Suppressor of profilin 2	2.37E-02	167	7	4.2%
GO:0001654 eye morphogenesis	CG9695	FBgn0000414	Disabled	2.37E-02	167	7	4.2%
GO:0007293 egg chamber formation (sensu Insecta)	CG11579	FBgn0000117	armadillo	2.47E-02	37	3	8.1%

GO:0007293 egg chamber formation (sensu Insecta)	CG8201	FBgn0026193		2.47E-02	37	3	8.1%
GO:0007293 egg chamber formation (sensu Insecta)	CG7507	FBgn0010349	Dynein heavy chain 64C	2.47E-02	37	3	8.1%
GO:0008105 asymmetric protein localization	CG8201	FBgn0026193		2.47E-02	37	3	8.1%
GO:0008105 asymmetric protein localization	CG6313	NA	NA	2.47E-02	37	3	8.1%
GO:0008105 asymmetric protein localization	CG5753	FBgn0003520	stauen	2.47E-02	37	3	8.1%
GO:0016052 carbohydrate catabolism	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	2.58E-02	66	4	6.1%
GO:0016052 carbohydrate catabolism	CG3724	FBgn0004654	Phosphogluconate dehydrogenase	2.58E-02	66	4	6.1%
GO:0016052 carbohydrate catabolism	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	2.58E-02	66	4	6.1%
GO:0016052 carbohydrate catabolism	CG8995	FBgn0030695	Peptidoglycan recognition protein LE	2.58E-02	66	4	6.1%
GO:0044275 cellular carbohydrate catabolism	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	2.58E-02	66	4	6.1%
GO:0044275 cellular carbohydrate catabolism	CG3724	FBgn0004654	Phosphogluconate dehydrogenase	2.58E-02	66	4	6.1%
GO:0044275 cellular carbohydrate catabolism	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	2.58E-02	66	4	6.1%
GO:0044275 cellular carbohydrate catabolism	CG8995	FBgn0030695	Peptidoglycan recognition protein LE	2.58E-02	66	4	6.1%
GO:0050829 defense response to Gram-negative bacteria	CG11992	FBgn0014018	Relish	2.62E-02	15	2	13.3%
GO:0050829 defense response to Gram-negative bacteria	CG4432	FBgn0035976	Peptidoglycan recognition protein LC	2.62E-02	15	2	13.3%
GO:0007163 establishment and or maintenance of cell polarity	CG11579	FBgn0000117	armadillo	2.98E-02	69	4	5.8%
GO:0007163 establishment and or maintenance of cell polarity	CG14637	FBgn0015331	abstrakt	2.98E-02	69	4	5.8%
GO:0007163 establishment and or maintenance of cell polarity	CG7850	FBgn0004210	puckered	2.98E-02	69	4	5.8%
GO:0007163 establishment and or maintenance of cell polarity	CG8075	FBgn0015838	Van Gogh	2.98E-02	69	4	5.8%
GO:0007411 axon guidance	CG10975	FBgn0014007	Protein tyrosine phosphatase 69D	3.12E-02	70	4	5.7%
GO:0007411 axon guidance	CG18376	NA	NA	3.12E-02	70	4	5.7%
GO:0007411 axon guidance	CG6449	FBgn0036101	ninjurin A	3.12E-02	70	4	5.7%
GO:0007411 axon guidance	CG9181	FBgn0003138	Protein tyrosine phosphatase 61F	3.12E-02	70	4	5.7%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG16910	FBgn0041205	kenny	3.23E-02	41	3	7.3%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG5490	FBgn0003717	Toll	3.23E-02	41	3	7.3%

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GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG6819	FBgn0026207	members only	3.23E-02	41	3	7.3%
GO:0017157 regulation of exocytosis	CG5448	NA	NA	3.23E-02	41	3	7.3%
GO:0017157 regulation of exocytosis	CG7980	FBgn0035255		3.23E-02	41	3	7.3%
GO:0017157 regulation of exocytosis	CG8287	FBgn0015796	Rab-protein 8	3.23E-02	41	3	7.3%
GO:0007016 cytoskeletal anchoring	CG11579	FBgn0000117	armadillo	3.32E-02	17	2	11.8%
GO:0007016 cytoskeletal anchoring	CG6313	NA	NA	3.32E-02	17	2	11.8%
GO:0007294 oocyte cell fate determination (sensu Insecta)	CG8201	FBgn0026193		3.32E-02	17	2	11.8%
GO:0007294 oocyte cell fate determination (sensu Insecta)	CG7507	FBgn0010349	Dynein heavy chain 64C	3.32E-02	17	2	11.8%
GO:0030706 oocyte differentiation (sensu Insecta)	CG8201	FBgn0026193		3.32E-02	17	2	11.8%
GO:0030706 oocyte differentiation (sensu Insecta)	CG7507	FBgn0010349	Dynein heavy chain 64C	3.32E-02	17	2	11.8%
GO:0007017 microtubule-based process	CG8201	FBgn0026193		3.47E-02	181	7	3.9%
GO:0007017 microtubule-based process	CG12192	FBgn0034827		3.47E-02	181	7	3.9%
GO:0007017 microtubule-based process	CG13809	FBgn0035317		3.47E-02	181	7	3.9%
GO:0007017 microtubule-based process	CG5300	FBgn0032243		3.47E-02	181	7	3.9%
GO:0007017 microtubule-based process	CG5753	FBgn0003520	staufer	3.47E-02	181	7	3.9%
GO:0007017 microtubule-based process	CG7507	FBgn0010349	Dynein heavy chain 64C	3.47E-02	181	7	3.9%
GO:0007017 microtubule-based process	CG8556	FBgn0014011		3.47E-02	181	7	3.9%
GO:0009994 oocyte differentiation	CG8201	FBgn0026193		3.70E-02	18	2	11.1%
GO:0009994 oocyte differentiation	CG7507	FBgn0010349	Dynein heavy chain 64C	3.70E-02	18	2	11.1%
GO:0050832 defense response to fungi	CG11992	FBgn0014018	Relish	3.70E-02	18	2	11.1%
GO:0050832 defense response to fungi	CG5490	FBgn0003717	Toll	3.70E-02	18	2	11.1%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG16910	FBgn0041205	kenny	3.86E-02	44	3	6.8%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG5490	FBgn0003717	Toll	3.86E-02	44	3	6.8%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG6819	FBgn0026207	members only	3.86E-02	44	3	6.8%
GO:0009620 response to fungi	CG11992	FBgn0014018	Relish	4.09E-02	19	2	10.5%
GO:0009620 response to fungi	CG5490	FBgn0003717	Toll	4.09E-02	19	2	10.5%
GO:0016325 oocyte microtubule cytoskeleton organization	CG8201	FBgn0026193		4.09E-02	19	2	10.5%
GO:0016325 oocyte microtubule cytoskeleton organization	CG8556	FBgn0014011		4.09E-02	19	2	10.5%
GO:0030716 oocyte cell fate determination	CG8201	FBgn0026193		4.09E-02	19	2	10.5%
GO:0030716 oocyte cell fate determination	CG7507	FBgn0010349	Dynein heavy chain 64C	4.09E-02	19	2	10.5%
GO:0030951 establishment and or maintenance of microtubule cytoskeleton polarity	CG8201	FBgn0026193		4.09E-02	19	2	10.5%
GO:0030951 establishment and or maintenance of microtubule cytoskeleton polarity	CG8556	FBgn0014011		4.09E-02	19	2	10.5%

GO:0030952 establishment and or maintenance of cytoskeleton polarity	CG8201	FBgn0026193		4.09E-02	19	2	10.5%
GO:0030952 establishment and or maintenance of cytoskeleton polarity	CG8556	FBgn0014011		4.09E-02	19	2	10.5%
GO:0007264 small GTPase mediated signal transduction	CG1404	FBgn0020255		4.35E-02	113	5	4.4%
GO:0007264 small GTPase mediated signal transduction	CG15069	FBgn0034357		4.35E-02	113	5	4.4%
GO:0007264 small GTPase mediated signal transduction	CG7980	FBgn0035255		4.35E-02	113	5	4.4%
GO:0007264 small GTPase mediated signal transduction	CG8287	FBgn0015796	Rab-protein 8	4.35E-02	113	5	4.4%
GO:0007264 small GTPase mediated signal transduction	CG8556	FBgn0014011		4.35E-02	113	5	4.4%
GO:0009948 anterior posterior axis specification	CG18621	NA	NA	4.35E-02	113	5	4.4%
GO:0009948 anterior posterior axis specification	CG8201	FBgn0026193		4.35E-02	113	5	4.4%
GO:0009948 anterior posterior axis specification	CG5448	NA	NA	4.35E-02	113	5	4.4%
GO:0009948 anterior posterior axis specification	CG5753	FBgn0003520	staußen	4.35E-02	113	5	4.4%
GO:0009948 anterior posterior axis specification	CG8556	FBgn0014011		4.35E-02	113	5	4.4%
GO:0016579 protein deubiquitination	CG7023	FBgn0039025		4.91E-02	21	2	9.5%
GO:0016579 protein deubiquitination	CG8830	FBgn0033738		4.91E-02	21	2	9.5%

Acp-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:0006614 SRP-dependent cotranslational protein-membrane targeting	CG10130	FBgn0010638		3.57E-07	17	6	35.3%
GO:0006614 SRP-dependent cotranslational protein-membrane targeting	CG11642	FBgn0040340		3.57E-07	17	6	35.3%
GO:0006614 SRP-dependent cotranslational protein-membrane targeting	CG2522	FBgn0010391	GTP-binding protein	3.57E-07	17	6	35.3%
GO:0006614 SRP-dependent cotranslational protein-membrane targeting	CG4659	FBgn0010747	Signal recognition particle protein 54k	3.57E-07	17	6	35.3%
GO:0006614 SRP-dependent cotranslational protein-membrane targeting	CG5417	FBgn0038808		3.57E-07	17	6	35.3%
GO:0006614 SRP-dependent cotranslational protein-membrane targeting	CG9539	FBgn0026571		3.57E-07	17	6	35.3%
GO:0006613 cotranslational protein-membrane targeting	CG10130	FBgn0010638		5.28E-07	18	6	33.3%
GO:0006613 cotranslational protein-membrane targeting	CG11642	FBgn0040340		5.28E-07	18	6	33.3%
GO:0006613 cotranslational protein-membrane targeting	CG2522	FBgn0010391	GTP-binding protein	5.28E-07	18	6	33.3%
GO:0006613 cotranslational protein-membrane targeting	CG4659	FBgn0010747	Signal recognition particle protein 54k	5.28E-07	18	6	33.3%
GO:0006613 cotranslational protein-membrane targeting	CG5417	FBgn0038808		5.28E-07	18	6	33.3%
GO:0006613 cotranslational protein-membrane targeting	CG9539	FBgn0026571		5.28E-07	18	6	33.3%
GO:0045047 protein-ER targeting	CG10130	FBgn0010638		5.28E-07	18	6	33.3%
GO:0045047 protein-ER targeting	CG11642	FBgn0040340		5.28E-07	18	6	33.3%
GO:0045047 protein-ER targeting	CG2522	FBgn0010391	GTP-binding protein	5.28E-07	18	6	33.3%
GO:0045047 protein-ER targeting	CG4659	FBgn0010747	Signal recognition particle protein 54k	5.28E-07	18	6	33.3%
GO:0045047 protein-ER targeting	CG5417	FBgn0038808		5.28E-07	18	6	33.3%
GO:0045047 protein-ER targeting	CG9539	FBgn0026571		5.28E-07	18	6	33.3%
GO:0006612 protein-membrane targeting	CG10130	FBgn0010638		1.07E-06	20	6	30.0%
GO:0006612 protein-membrane targeting	CG11642	FBgn0040340		1.07E-06	20	6	30.0%
GO:0006612 protein-membrane targeting	CG2522	FBgn0010391	GTP-binding protein	1.07E-06	20	6	30.0%
GO:0006612 protein-membrane targeting	CG4659	FBgn0010747	Signal recognition particle protein 54k	1.07E-06	20	6	30.0%
GO:0006612 protein-membrane targeting	CG5417	FBgn0038808		1.07E-06	20	6	30.0%
GO:0006612 protein-membrane targeting	CG9539	FBgn0026571		1.07E-06	20	6	30.0%
GO:0051235 maintenance of localization	CG5474	FBgn0011016	Signal sequence receptor beta	2.84E-03	16	3	18.8%
GO:0051235 maintenance of localization	CG9035	FBgn0021795	Translocon-associated protein delta	2.84E-03	16	3	18.8%

Acp-specific age-related GO terms in Cluster 3

GO:0051235 maintenance of localization	CG9401	FBgn0002736	mago nashi	2.84E-03	16	3	18.8%
GO:0045045 secretory pathway	CG10130	FBgn0010638		5.10E-03	210	10	4.8%
GO:0045045 secretory pathway	CG11642	FBgn0040340		5.10E-03	210	10	4.8%
GO:0045045 secretory pathway	CG11958	FBgn0015622	Calnexin 99A	5.10E-03	210	10	4.8%
GO:0045045 secretory pathway	CG14813	FBgn0028969	delta-coatomer protein	5.10E-03	210	10	4.8%
GO:0045045 secretory pathway	CG1528	FBgn0028968	gamma-coatomer protein	5.10E-03	210	10	4.8%
GO:0045045 secretory pathway	CG2522	FBgn0010391	GTP-binding protein	5.10E-03	210	10	4.8%
GO:0045045 secretory pathway	CG3139	FBgn0004242	synaptotagmin	5.10E-03	210	10	4.8%
GO:0045045 secretory pathway	CG4659	FBgn0010747	Signal recognition particle protein 54k	5.10E-03	210	10	4.8%
GO:0045045 secretory pathway	CG5417	FBgn0038808		5.10E-03	210	10	4.8%
GO:0045045 secretory pathway	CG9539	FBgn0026571		5.10E-03	210	10	4.8%
GO:0046903 secretion	CG10130	FBgn0010638		7.71E-03	223	10	4.5%
GO:0046903 secretion	CG11642	FBgn0040340		7.71E-03	223	10	4.5%
GO:0046903 secretion	CG11958	FBgn0015622	Calnexin 99A	7.71E-03	223	10	4.5%
GO:0046903 secretion	CG14813	FBgn0028969	delta-coatomer protein	7.71E-03	223	10	4.5%
GO:0046903 secretion	CG1528	FBgn0028968	gamma-coatomer protein	7.71E-03	223	10	4.5%
GO:0046903 secretion	CG2522	FBgn0010391	GTP-binding protein	7.71E-03	223	10	4.5%
GO:0046903 secretion	CG3139	FBgn0004242	synaptotagmin	7.71E-03	223	10	4.5%
GO:0046903 secretion	CG4659	FBgn0010747	Signal recognition particle protein 54k	7.71E-03	223	10	4.5%
GO:0046903 secretion	CG5417	FBgn0038808		7.71E-03	223	10	4.5%
GO:0046903 secretion	CG9539	FBgn0026571		7.71E-03	223	10	4.5%
GO:0006486 protein amino acid glycosylation	CG13431	FBgn0034521	UDP-GlcNAc:a-3-D-mannoside-beta-1,2-N-acetylglucosaminyltransferase I	1.26E-02	76	5	6.6%
GO:0006486 protein amino acid glycosylation	CG2675	FBgn0024994		1.26E-02	76	5	6.6%
GO:0006486 protein amino acid glycosylation	CG2507	FBgn0002306	stranded at second	1.26E-02	76	5	6.6%
GO:0006486 protein amino acid glycosylation	CG7748	FBgn0011336	Oligosaccharyl transferase 3	1.26E-02	76	5	6.6%
GO:0006486 protein amino acid glycosylation	CG7870	FBgn0032012		1.26E-02	76	5	6.6%
GO:0009101 glycoprotein biosynthesis	CG13431	FBgn0034521	UDP-GlcNAc:a-3-D-mannoside-beta-1,2-N-acetylglucosaminyltransferase I	1.40E-02	78	5	6.4%
GO:0009101 glycoprotein biosynthesis	CG2675	FBgn0024994		1.40E-02	78	5	6.4%
GO:0009101 glycoprotein biosynthesis	CG2507	FBgn0002306	stranded at second	1.40E-02	78	5	6.4%
GO:0009101 glycoprotein biosynthesis	CG7748	FBgn0011336	Oligosaccharyl transferase 3	1.40E-02	78	5	6.4%
GO:0009101 glycoprotein biosynthesis	CG7870	FBgn0032012		1.40E-02	78	5	6.4%

GO:0009100 glycoprotein metabolism	CG13431	FBgn0034521	UDP-GlcNAc:a-3-D-mannoside-beta-1,2-N-acetylglucosaminyltransferase I	1.63E-02	81	5	6.2%
GO:0009100 glycoprotein metabolism	CG2675	FBgn0024994		1.63E-02	81	5	6.2%
GO:0009100 glycoprotein metabolism	CG2507	FBgn0002306	stranded at second	1.63E-02	81	5	6.2%
GO:0009100 glycoprotein metabolism	CG7748	FBgn0011336	Oligosaccharyl transferase 3	1.63E-02	81	5	6.2%
GO:0009100 glycoprotein metabolism	CG7870	FBgn0032012		1.63E-02	81	5	6.2%
GO:0008543 fibroblast growth factor receptor signaling pathway	CG1921	FBgn0014388	sprouty	1.65E-02	11	2	18.2%
GO:0008543 fibroblast growth factor receptor signaling pathway	CG7223	FBgn0010389	heartless	1.65E-02	11	2	18.2%
GO:0009996 negative regulation of cell fate specification	CG10291	NA	NA	1.65E-02	11	2	18.2%
GO:0009996 negative regulation of cell fate specification	CG1921	FBgn0014388	sprouty	1.65E-02	11	2	18.2%
GO:0008354 germ cell migration	CG10291	NA	NA	1.71E-02	30	3	10.0%
GO:0008354 germ cell migration	CG7223	FBgn0010389	heartless	1.71E-02	30	3	10.0%
GO:0008354 germ cell migration	CG8076	NA	NA	1.71E-02	30	3	10.0%
GO:0008347 glia cell migration	CG1464	FBgn0005558	eyeless	1.96E-02	12	2	16.7%
GO:0008347 glia cell migration	CG7223	FBgn0010389	heartless	1.96E-02	12	2	16.7%
GO:0008103 oocyte microtubule cytoskeleton polarization	CG3263	FBgn0000275	cAMP-dependent protein kinase R1	2.29E-02	13	2	15.4%
GO:0008103 oocyte microtubule cytoskeleton polarization	CG9401	FBgn0002736	mago nashi	2.29E-02	13	2	15.4%
GO:0045297 post-mating behavior	CG12212	FBgn0003053	pebbled	2.64E-02	14	2	14.3%
GO:0045297 post-mating behavior	CG4986	FBgn0011670	Male-specific RNA 57Dc	2.64E-02	14	2	14.3%
GO:0051336 regulation of hydrolase activity	CG4237	FBgn0020655	GTPase-activating protein 69C	2.64E-02	14	2	14.3%
GO:0051336 regulation of hydrolase activity	CG6838	FBgn0037182		2.64E-02	14	2	14.3%
GO:0007280 pole cell migration	CG10291	NA	NA	3.01E-02	15	2	13.3%
GO:0007280 pole cell migration	CG7223	FBgn0010389	heartless	3.01E-02	15	2	13.3%
GO:0045596 negative regulation of cell differentiation	CG10291	NA	NA	3.01E-02	15	2	13.3%
GO:0045596 negative regulation of cell differentiation	CG1921	FBgn0014388	sprouty	3.01E-02	15	2	13.3%
GO:0007492 endoderm development	CG1464	FBgn0005558	eyeless	3.39E-02	16	2	12.5%
GO:0007492 endoderm development	CG7223	FBgn0010389	heartless	3.39E-02	16	2	12.5%
GO:0042659 regulation of cell fate specification	CG10291	NA	NA	3.39E-02	16	2	12.5%
GO:0042659 regulation of cell fate specification	CG1921	FBgn0014388	sprouty	3.39E-02	16	2	12.5%
GO:0007424 tracheal system development (sensu Insecta)	CG10291	NA	NA	3.64E-02	100	5	5.0%
GO:0007424 tracheal system development (sensu Insecta)	CG1395	FBgn0003525	string	3.64E-02	100	5	5.0%

Acg-specific age-related GO terms in Cluster 3

GO:0007424 tracheal system development (sensu Insecta)	CG1921	FBgn0014388	sprouty	3.64E-02	100	5	5.0%
GO:0007424 tracheal system development (sensu Insecta)	CG12212	FBgn0003053	pebbled	3.64E-02	100	5	5.0%
GO:0007424 tracheal system development (sensu Insecta)	CG8996	FBgn0010516	walrus	3.64E-02	100	5	5.0%
GO:0007317 regulation of pole plasm oskar mRNA localization	CG3139	FBgn0004242	synaptotagmin	4.23E-02	18	2	11.1%
GO:0007317 regulation of pole plasm oskar mRNA localization	CG9401	FBgn0002736	mago nashi	4.23E-02	18	2	11.1%
GO:0044272 sulfur compound biosynthesis	CG1753	FBgn0031148		4.23E-02	18	2	11.1%
GO:0044272 sulfur compound biosynthesis	CG8433	NA	NA	4.23E-02	18	2	11.1%
GO:0007530 sex determination	CG12743	FBgn0003023	ovarian tumor	4.64E-02	44	3	6.8%
GO:0007530 sex determination	CG8076	NA	NA	4.64E-02	44	3	6.8%
GO:0007530 sex determination	CG9401	FBgn0002736	mago nashi	4.64E-02	44	3	6.8%
GO:0008258 head involution	CG12212	FBgn0003053	pebbled	4.67E-02	19	2	10.5%
GO:0008258 head involution	CG8996	FBgn0010516	walrus	4.67E-02	19	2	10.5%
GO:0016325 oocyte microtubule cytoskeleton organization	CG3263	FBgn0000275	cAMP-dependent protein kinase R1	4.67E-02	19	2	10.5%
GO:0016325 oocyte microtubule cytoskeleton organization	CG9401	FBgn0002736	mago nashi	4.67E-02	19	2	10.5%
GO:0030951 establishment and or maintenance of microtubule cytoskeleton polarity	CG3263	FBgn0000275	cAMP-dependent protein kinase R1	4.67E-02	19	2	10.5%
GO:0030951 establishment and or maintenance of microtubule cytoskeleton polarity	CG9401	FBgn0002736	mago nashi	4.67E-02	19	2	10.5%
GO:0030952 establishment and or maintenance of cytoskeleton polarity	CG3263	FBgn0000275	cAMP-dependent protein kinase R1	4.67E-02	19	2	10.5%
GO:0030952 establishment and or maintenance of cytoskeleton polarity	CG9401	FBgn0002736	mago nashi	4.67E-02	19	2	10.5%