Supplementary Material

Complete Genome of *Achalarus lyciades*, The First Representative of the Eudaminae Subfamily of Skippers

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Supplementary Table S1. Quality and composition of Lepidoptera genomes, related to Table 1.

This file contains multiple sheets and each sheet corresponds to one supplement table.

S1A Supplementary Table S1A. Information about other published Lepidoptera genomes.

S1B Supplementary Table S1B. Comparison of CEGMA gene coverage by a single scaffold in Lepidoptera genome drafts.

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Table S1A. Information about other published Lepidoptera genomes

Species	Genome assembly version	Official gene set version	Genome assembly link	Official gene set link
Bombyx mori	SilkDB V2.0	SilkDB V2.0 consensus gene set by GLEAN	ftp://silkdb.org/pub/current/Genome/silkworm_genome_v2.0.fa.tar.gz	ftp://silkdb.org/pub/current/Gene/Glean_genes/silkworm_glean_cds.fa.tar.gz
Calycopis cecrop	Calycopis cecrops V1.1	Calycopis cecrops V1.1	http://prodata.swmed.edu/LepDB/cce/calycopis_assembly_V1.1.fa.gz	http://prodata.swmed.edu/LepDB/cce/annotation_V1.1.tar.gz
Danaus plexippus	MonarchBase V3.0	MonarchBase V2.0	http://monarchbase.umassmed.edu/download/Dp_genome_v3.fasta.gz	http://monarchbase.umassmed.edu/download/Dp_geneset_OGS2_pep.fasta.gz
Heliconius melpomene	Heliconius Genome Project V1.1	Heliconius Genome Project V1.1	http://butterflygenome.org/sites/default/files/Hmel1-1_Release_20120601.tgz	http://butterflygenome.org/sites/default/files/Hmel1-1_Release_20120601.tgz
Lerema accius	Lerema accius V1.1	Lerema accius V1.1	http://prodata.swmed.edu/LepDB/lac/accius_assembly_V1.1.fa.gz	http://prodata.swmed.edu/LepDB/lac/annotation_V1.1.tar.gz
Manduca sexta	Manduca Base 20140407	Manduca Base 20140407	ftp://ftp.bioinformatics.ksu.edu/pub/Manduca/OGS2/OGS2_20140407_scaffolds.fa	ftp://ftp.bioinformatics.ksu.edu/pub/Manduca/OGS2/OGS2_20140407_proteins.fa

Species	Genome assembly version	Official gene set version	Genome assembly link	Official gene set link
Melitaea cinxia	MelCinx1.0	MelCinx1.0	ftp://ftp.ensemblgenomes.org/pub/metazoa/release-26/fasta/melitaea_cinxia/dna/Melitaea_cinxia.MelCinx1.0.26.dna.genome.fa.gz	ftp://ftp.ensemblgenomes.org/pub/metazoa/release-26/fasta/melitaea_cinxia/pep/Melitaea_cinxia.MelCinx1.0.26.pep.all.fa.gz
Papilio glaucus	Papilio glaucus V1.1	Papilio glaucus V1.1	http://prodata.swmed.edu/LepDB/pgl/glaucus_assembly_V1.1.fa.gz	http://prodata.swmed.edu/LepDB/pgl/annotation_V1.1.tar.gz
Papilio polytes	Papilio Base 20141023	Papilio Base 20141023	http://papilio.bio.titech.ac.jp/genome-browser//download/pp/scaffold.fasta.gz	http://papilio.bio.titech.ac.jp/genome-browser//download/pp/Ppolytes.v1.0.0.pep.faa.gz
Papilio xuthus	Papilio Base 20141023	Papilio Base 20141023	http://papilio.bio.titech.ac.jp/genome-browser//download/px/scaffold.fasta.gz	http://papilio.bio.titech.ac.jp/genome-browser//download/px/Pxuthus.v1.0.0.pep.faa.gz
Phoebis sennae	Phoebis sennae V1.1	Phoebis sennae V1.1	http://prodata.swmed.edu/LepDB/pse/sennae_assembly_V1.1.fa.gz	http://prodata.swmed.edu/LepDB/pse/annotation_V1.1.tar.gz
Pieris rapae	Pieris rapae v2	Pieris rapae v2		
Plutella xylostella	DBM-DB V2	DBM-DB V1.0	ftp://iae.fafu.edu.cn/pub/DBM-DB.v1.0/Scaffold/P.xylostella.scaffolds.fasta.tar.gz	ftp://iae.fafu.edu.cn/pub/DBM-DB.v1.0/Gene/P.xylostella.gene.fasta.tar.gz

Table S1B. Comparison of CEGMA gene coverage by a single scaffold in Lepidoptera genome drafts

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG10130-PA___KOG3457	0.485	0.683	0.683	0.683	0.683	0.683	0.485	0.485	0.485	0.683	0.000	0.485	0.683	0.485
CG10149-PB___KOG1463	1.000	1.000	0.913	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG10174-PA___KOG2104	0.656	1.000	0.992	0.992	0.992	0.969	1.000	1.000	1.000	1.000	0.977	0.992	1.000	1.000
CG10206-PA___KOG2572	0.814	0.834	0.813	0.816	0.844	0.836	0.832	0.834	0.854	0.746	0.814	0.754	0.814	0.820
CG10212-PA___KOG0933	0.574	0.486	0.157	0.597	0.664	0.317	0.123	0.192	0.525	0.515	0.187	0.460	0.431	0.665
CG10222-PA___KOG1533	0.961	0.971	0.906	0.935	0.906	0.929	0.906	0.925	0.977	0.935	0.906	0.932	0.922	0.903
CG10230-PA___KOG2908	0.666	0.580	0.836	0.773	0.666	0.731	0.569	0.679	0.721	0.700	0.710	0.715	0.407	0.849
CG10279-PF___KOG0331	0.748	0.760	0.743	0.760	0.748	0.750	0.748	0.715	0.705	0.748	0.748	0.751	0.713	0.755
CG10354-PA___KOG2044	0.754	0.747	0.740	0.725	0.802	0.739	0.536	0.780	0.734	0.765	0.734	0.756	0.770	0.765

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG10418-PA___KOG3448	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG10423-PA___KOG1779	0.871	0.965	0.906	0.894	0.812	0.871	0.871	0.871	0.871	0.894	0.871	0.871	0.965	0.871
CG10424-PA___KOG3974	0.947	0.924	0.924	0.907	0.934	0.924	0.967	0.920	0.930	0.934	0.917	0.940	0.953	0.940
CG10506-PA___KOG1148	0.906	0.941	0.949	0.929	0.959	0.923	0.656	0.841	0.845	0.901	0.913	0.908	0.891	0.927
CG10602-PB___KOG1047	0.798	0.759	0.824	0.762	0.909	0.765	0.827	0.827	0.668	0.671	0.829	0.824	0.762	0.827
CG10627-PA___KOG2537	0.833	0.887	0.784	0.913	0.929	0.931	0.809	0.871	0.893	0.933	0.136	0.896	0.740	0.851
CG10635-PA___KOG1760	0.871	0.871	0.871	0.928	0.871	0.871	0.871	0.871	0.827	0.871	0.914	0.906	0.878	0.820
CG10648-PA___KOG3064	0.328	0.326	0.328	0.465	0.483	0.000	0.448	0.448	0.265	0.445	0.448	0.465	0.358	0.500
CG10652-PA___KOG2988	0.938	0.938	0.938	0.938	0.938	0.938	0.982	0.598	0.938	0.938	0.938	0.938	0.938	0.938
CG1065-PA___KOG1255	0.939	0.976	0.927	0.979	0.988	0.979	0.964	0.939	1.000	0.964	0.964	0.982	0.933	0.964

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CG10688-PA___KOG3189	0.984	0.996	0.996	0.996	0.988	0.984	0.988	0.992	0.988	0.976	0.988	0.969	0.969	0.973
CG10724-PA___KOG0318	0.867	0.851	0.844	0.888	0.603	0.915	0.734	0.734	0.885	0.860	0.438	0.813	0.296	0.980
CG10753-PA___KOG3428	0.648	0.648	0.648	0.648	0.648	0.648	0.648	0.648	0.648	0.648	0.648	0.648	0.648	0.648
CG1088-PB___KOG1664	0.881	0.881	0.881	0.877	0.881	0.881	0.859	0.881	0.885	0.881	0.885	0.885	0.881	0.885
CG10903-PA___KOG1541	0.924	0.953	0.957	0.881	0.975	1.000	0.650	0.841	0.895	1.000	0.957	0.949	0.729	1.000
CG10932-PA___KOG1390	0.922	0.893	0.888	0.893	0.915	0.925	0.827	0.942	0.827	0.908	0.925	0.922	0.922	0.920
CG10938-PA___KOG0176	0.992	1.000	0.992	0.992	0.992	0.992	0.776	0.992	0.992	0.992	1.000	0.992	0.984	0.992
CG10944-PA___KOG1646	0.835	0.849	0.830	0.830	0.849	0.830	0.596	0.835	0.835	0.849	0.849	0.830	0.830	0.835
CG11001-PA___KOG0544	0.890	0.890	0.890	0.890	0.890	0.890	0.890	0.890	0.890	0.890	0.881	0.890	0.697	1.000
CG1100-PA___KOG1498	0.676	0.692	0.694	0.769	0.644	0.698	0.692	0.678	0.678	0.678	0.740	0.698	0.656	0.686

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CG11089-PA___KOG2555	0.986	0.985	0.985	0.988	0.976	0.985	0.438	0.985	0.988	0.980	0.988	0.983	0.990	0.986
CG11110-PA___KOG1568	0.948	0.948	0.948	0.948	0.948	0.948	0.994	0.948	0.971	0.948	0.930	0.942	0.936	0.953
CG11115-PA___KOG2807	0.718	0.781	0.834	0.825	0.989	0.777	0.629	0.893	0.809	0.670	0.813	0.813	0.813	0.868
CG11137-PA___KOG3318	0.892	0.874	0.868	0.874	0.904	1.000	0.904	0.892	0.946	0.850	1.000	1.000	0.868	0.892
CG11154-PA___KOG1350	0.901	0.901	0.901	0.901	0.901	0.901	0.901	0.901	0.901	0.901	0.897	0.897	0.901	0.901
CG11208-PA___KOG1185	0.837	0.900	0.944	0.928	0.919	0.921	0.768	0.921	0.910	0.923	0.910	0.921	0.909	0.931
CG11246-PA___KOG3400	1.000	1.000	1.000	1.000	1.000	1.000	0.913	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG11255-PA___KOG2854	0.925	0.951	0.939	0.942	0.850	0.945	0.931	0.928	0.934	0.390	0.465	0.942	0.939	0.936
CG11267-PA___KOG1641	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.981	0.990	1.000	0.990
CG11271-PA___KOG3406	0.886	0.736	0.886	0.886	0.886	0.886	0.886	0.886	0.871	0.886	0.843	0.886	0.600	0.857

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CG1129-PB___KOG1322	1.000	1.000	1.000	1.000	0.970	1.000	1.000	0.968	1.000	1.000	1.000	1.000	1.000	1.000
CG11334-PB___KOG1468	0.932	0.890	0.945	0.948	0.948	0.981	0.951	0.915	0.951	0.948	0.948	0.923	0.948	0.953
CG11397-PA___KOG0996	0.419	0.408	0.414	0.402	0.477	0.411	0.216	0.459	0.485	0.368	0.421	0.367	0.406	0.391
CG11471-PC___KOG0434	0.989	0.950	0.990	0.990	0.990	0.990	0.991	0.989	0.991	0.990	0.640	0.989	0.989	0.989
CG11482-PA___KOG1979	0.826	0.765	0.862	0.771	0.197	0.896	0.752	0.839	0.771	0.898	0.845	0.773	0.809	0.782
CG11567-PA___KOG1158	0.906	0.897	0.899	0.899	0.899	0.904	0.906	0.835	0.890	0.890	0.865	0.900	0.200	0.899
CG11611-PA___KOG1733	0.806	0.817	0.817	0.817	0.806	0.817	0.806	0.806	0.839	0.839	0.817	0.839	0.860	0.806
CG1163-PA___KOG3405	0.742	0.636	0.636	0.636	0.742	0.742	0.742	0.742	0.636	0.636	0.636	0.742	0.795	0.742
CG11654-PA___KOG1370	0.982	0.988	0.984	0.984	0.984	0.984	0.995	0.982	0.834	0.982	0.982	0.988	0.984	0.982
CG11660-PB___KOG2270	0.645	0.647	0.666	0.647	0.645	0.645	0.625	0.645	0.645	0.645	0.643	0.647	0.469	0.645

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CG11661-PC___KOG0450	0.950	0.843	0.966	0.963	0.947	0.940	0.532	0.939	0.945	0.367	0.954	0.942	0.921	0.949
CG11738-PA___KOG3273	1.000	1.000	1.000	1.000	0.726	1.000	1.000	0.780	0.705	1.000	1.000	1.000	1.000	1.000
CG11785-PA___KOG1691	0.976	0.836	0.850	0.952	0.942	0.966	0.942	0.957	0.860	0.971	0.870	0.966	0.841	0.797
CG11793-PA___KOG0441	0.922	0.877	0.864	0.916	0.877	0.864	0.721	0.961	0.981	0.877	0.909	0.883	0.935	0.922
CG11837-PA___KOG0820	0.801	0.993	0.993	0.993	0.993	0.990	0.993	0.993	0.599	0.993	0.993	0.990	0.599	0.993
CG11857-PA___KOG1688	0.627	0.681	0.637	0.637	0.789	0.466	0.686	0.799	0.779	0.804	0.721	0.804	0.637	0.814
CG11876-PA___KOG0524	0.907	0.776	0.896	0.907	0.915	0.907	0.574	0.861	0.910	0.921	0.918	0.915	0.921	0.904
CG11920-PA___KOG2781	0.846	0.960	0.950	0.950	0.950	0.950	0.475	0.950	0.970	0.950	0.953	0.950	0.843	0.970
CG11958-PB___KOG0675	0.677	0.682	0.691	0.690	0.680	0.686	0.277	0.388	0.675	0.616	0.660	0.690	0.677	0.693
CG11979-PA___KOG3218	0.995	0.995	0.886	0.995	0.995	0.995	0.995	1.000	0.995	0.995	0.995	0.995	1.000	0.995

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CG11980-PB___KOG2948	0.942	0.897	0.916	0.916	0.889	0.914	0.908	0.908	0.925	0.928	0.919	0.914	0.919	0.903
CG11981-PA___KOG0180	0.995	0.990	0.995	0.995	0.515	0.981	0.913	0.995	0.995	0.995	0.995	0.995	0.995	0.995
CG12000-PB___KOG0185	0.844	0.888	0.803	0.803	0.517	0.855	0.874	0.840	0.851	0.874	0.792	0.874	0.836	0.888
CG12018-PA___KOG2732	0.870	0.826	0.803	0.824	0.951	0.845	0.907	0.889	0.914	0.685	0.692	0.762	0.694	0.836
CG12140-PA___KOG2415	0.783	0.907	0.866	0.904	0.911	0.874	0.792	0.969	0.911	0.795	0.836	0.891	0.815	0.904
CG12141-PB___KOG1885	0.814	0.821	0.814	0.839	0.839	0.814	0.814	0.814	0.839	0.814	0.817	0.822	0.821	0.821
CG12170-PA___KOG1394	0.966	0.970	0.970	0.970	0.970	0.975	0.943	0.979	0.993	0.975	0.968	0.961	0.640	0.961
CG12217-PA___KOG0373	0.993	0.993	1.000	1.000	0.664	0.993	0.993	1.000	1.000	1.000	0.993	1.000	0.990	0.993
CG12233-PB___KOG0785	0.915	0.913	0.828	0.886	0.897	0.767	0.603	0.913	0.770	0.926	0.910	0.915	0.913	0.915
CG12264-PA___KOG1549	0.864	0.814	0.862	0.870	0.862	0.862	0.844	0.864	0.510	0.862	0.866	0.864	0.860	0.862

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CG12276-PA___KOG2014	0.959	0.959	0.959	0.959	0.959	0.524	0.959	0.959	0.959	0.959	0.941	0.959	0.959	0.959
CG12323-PB___KOG0175	0.675	0.675	0.675	0.675	0.675	0.675	0.675	0.929	0.675	0.350	0.675	0.675	0.675	0.834
CG12325-PA___KOG0291	0.765	0.740	0.687	0.797	0.763	0.765	0.636	0.813	0.752	0.748	0.280	0.735	0.415	0.834
CG12334-PA___KOG1654	0.959	0.975	0.959	0.959	0.959	0.959	0.959	0.959	0.975	0.959	0.975	0.975	0.975	0.975
CG12390-PA___KOG1800	0.989	0.927	0.916	0.916	0.976	0.929	0.914	0.914	0.839	0.942	0.925	0.944	0.914	0.925
CG12413-PA___KOG1145	0.752	0.595	0.535	0.852	0.661	0.727	0.291	0.551	0.647	0.641	0.679	0.647	0.735	0.716
CG1242-PA___KOG0019	0.905	0.905	0.905	0.905	0.904	0.901	0.904	0.905	0.904	0.905	0.905	0.904	0.904	0.904
CG1249-PA___KOG3459	0.967	0.867	0.867	0.867	0.867	0.867	0.892	0.867	0.892	0.867	0.892	0.867	0.867	0.867
CG1250-PA___KOG1986	1.000	1.000	1.000	0.990	0.942	0.999	0.867	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG12529-PA___KOG0563	0.924	0.922	0.922	0.922	0.924	0.924	0.924	0.924	0.928	0.916	0.924	0.924	0.924	0.924

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG12602-PA___KOG2189	0.910	0.791	0.883	0.906	0.902	0.917	0.908	0.901	0.924	0.923	0.920	0.915	0.842	0.918
CG1263-PA___KOG2309	0.934	0.934	0.934	0.934	0.934	0.934	0.860	0.934	0.934	0.934	0.934	0.934	0.934	0.934
CG12770-PA___KOG3284	0.962	0.882	0.962	0.962	0.962	0.976	0.773	0.972	0.815	0.986	0.962	0.986	0.962	0.986
CG12792-PA___KOG0302	0.895	0.880	0.950	0.864	0.891	0.805	0.912	0.950	0.906	0.888	0.847	0.897	0.875	0.978
CG1291-PA___KOG0853	0.960	0.960	0.960	0.948	0.944	0.988	0.927	0.960	1.000	1.000	0.960	0.998	0.988	0.960
CG12975-PA___KOG1088	0.992	0.992	0.992	0.992	0.992	0.992	0.992	0.992	0.992	0.992	0.992	0.992	0.544	0.992
CG13090-PA___KOG2017	0.522	0.683	0.839	0.848	0.531	0.674	0.641	0.782	0.606	0.729	0.548	0.841	0.822	0.813
CG13277-PA___KOG1781	0.928	0.928	0.928	0.928	0.928	0.928	0.901	0.937	0.901	0.901	0.928	0.928	0.937	0.928
CG13281-PA___KOG1992	0.768	0.845	0.731	0.889	0.890	0.882	0.465	0.737	0.767	0.756	0.519	0.886	0.797	0.939
CG13348-PA___KOG2783	0.921	0.923	0.923	0.925	0.923	0.907	0.923	0.923	0.923	0.923	0.923	0.923	0.925	0.923

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG13369-PA___KOG2855	0.895	0.882	0.951	0.931	0.567	0.921	0.931	0.725	0.928	0.921	0.918	0.793	0.895	0.748
CG13389-PA___KOG0400	0.947	0.947	0.947	0.947	0.947	0.947	0.947	0.947	0.947	0.947	0.947	0.947	0.947	0.947
CG13391-PB___KOG0188	0.997	0.995	0.997	0.995	0.997	0.996	0.990	0.997	0.997	0.995	0.997	0.990	0.996	0.996
CG13393-PA___KOG1746	1.000	1.000	1.000	0.947	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG1341-PA___KOG0729	0.922	0.965	0.935	0.947	1.000	0.965	0.866	0.965	0.965	0.965	0.965	0.961	0.965	0.963
CG1345-PA___KOG1268	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG1354-PA___KOG1491	0.874	0.960	0.965	0.960	0.960	0.967	0.967	0.967	0.965	0.960	0.962	0.970	0.960	0.960
CG13628-PA___KOG3497	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG13667-PA___KOG1159	0.866	0.822	0.971	0.993	0.839	0.995	0.914	0.892	0.985	0.971	0.993	0.967	0.901	0.967
CG1406-PA___KOG1644	0.733	0.733	0.726	0.733	0.729	0.891	0.729	0.729	0.218	0.733	0.729	0.808	0.624	0.827

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG14214-PA___KOG3498	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG14231-PA___KOG2707	0.871	0.880	0.939	0.885	0.893	0.885	0.890	0.893	0.932	0.898	0.927	0.876	0.932	0.890
CG14512-PA___KOG3349	0.953	0.953	0.948	0.948	0.948	0.965	0.948	0.849	0.855	0.930	0.936	0.959	0.953	0.983
CG14618-PA___KOG2967	0.713	0.541	0.613	0.800	0.609	0.653	0.413	0.613	0.484	0.622	0.613	0.556	0.628	0.566
CG1475-PB___KOG3204	0.956	0.947	0.956	0.956	0.903	0.951	0.951	0.850	0.981	0.956	0.830	0.956	0.913	0.956
CG14999-PA___KOG0991	0.870	0.904	0.813	0.985	0.904	0.940	0.756	0.937	0.937	0.979	0.922	0.985	0.979	0.910
CG15081-PC___KOG3090	0.934	0.934	0.984	0.984	0.934	0.934	0.934	0.934	0.934	0.934	0.934	0.934	0.934	0.984
CG1515-PA___KOG0861	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990
CG1518-PA___KOG2292	0.868	0.874	0.901	0.873	0.889	0.723	0.804	0.877	0.878	0.916	0.854	0.874	0.839	0.863
CG1519-PA___KOG0184	0.953	0.949	0.953	0.953	0.953	0.949	0.953	0.953	0.949	0.976	0.598	0.740	0.953	0.953

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG1524-PB___KOG0407	0.921	0.895	0.921	0.921	0.921	0.921	0.520	0.921	0.921	0.908	0.921	0.921	0.921	0.921
CG1528-PA___KOG1078	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.994	1.000	0.998	0.994	1.000	1.000
CG15433-PA___KOG2535	0.987	0.982	0.987	0.987	0.980	0.987	0.577	0.664	0.993	0.987	0.993	0.966	0.987	0.986
CG15442-PA___KOG1742	0.773	0.873	0.767	0.767	0.767	0.767	0.480	0.767	0.767	0.767	0.773	0.767	0.767	0.767
CG15481-PA___KOG1068	0.870	0.794	0.866	0.862	0.838	0.874	0.433	0.777	0.781	0.802	0.874	0.923	0.838	0.785
CG15527-PA___KOG3502	0.769	0.769	0.769	0.769	0.769	0.769	0.769	0.769	0.769	0.769	0.769	0.769	0.769	0.769
CG15811-PA___KOG1300	0.931	0.920	0.903	0.903	0.933	0.920	0.903	0.930	0.920	0.814	0.798	0.990	0.906	0.955
CG1598-PA___KOG2825	0.899	0.914	0.950	0.935	0.976	0.905	0.798	0.908	0.935	0.840	0.938	0.899	0.938	0.914
CG1618-PA___KOG0741	0.941	0.961	0.973	0.956	0.946	0.952	0.563	0.948	0.771	0.882	0.950	0.946	0.918	0.946
CG1633-PB___KOG0852	0.903	0.969	0.897	0.974	0.969	0.969	0.908	1.000	0.969	0.928	0.969	0.969	0.897	0.974

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG1639-PA___KOG3404	1.000	1.000	0.786	1.000	1.000	1.000	1.000	0.959	1.000	1.000	0.993	1.000	1.000	1.000
CG1640-PB___KOG0258	0.786	0.786	0.193	0.835	0.852	0.720	0.352	0.813	0.811	0.781	0.760	0.809	0.793	0.802
CG1660-PA___KOG3479	0.792	0.760	0.760	0.760	0.760	0.760	0.760	0.760	0.760	0.760	0.823	0.760	0.760	0.927
CG1666-PA___KOG0346	0.706	0.847	0.881	0.873	0.843	0.884	0.852	0.907	0.840	0.791	0.695	0.841	0.829	0.859
CG16792-PA___KOG3482	0.843	0.843	0.843	0.843	0.843	0.843	0.843	0.843	0.843	0.843	0.843	0.843	0.843	0.843
CG16912-PA___KOG2623	0.961	0.961	0.951	0.931	0.938	0.940	0.963	0.957	0.888	0.961	0.987	0.961	0.935	0.951
CG16935-PA___KOG0025	0.947	0.972	0.944	0.944	0.944	0.972	0.980	0.947	0.941	0.947	0.994	0.989	0.939	0.958
CG16982-PA___KOG2930	0.963	0.963	1.000	0.963	0.963	0.972	0.963	0.972	0.991	0.862	0.963	0.963	0.963	0.908
CG17146-PA___KOG3079	0.807	0.812	0.802	0.812	0.559	0.797	0.827	0.807	0.802	0.817	0.817	0.807	0.545	0.807
CG17158-PA___KOG3174	0.968	0.975	0.975	0.975	0.968	0.975	0.845	0.975	0.978	0.394	0.971	0.968	0.968	0.964

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG17209-PA___KOG0261	0.867	0.948	0.897	0.926	0.821	0.896	0.786	0.720	0.910	0.908	0.640	0.933	0.748	0.930
CG17273-PA___KOG1355	0.955	0.833	0.908	0.911	0.984	0.842	0.632	0.958	0.558	0.955	0.922	0.757	0.924	0.866
CG1728-PA___KOG3489	0.955	0.955	0.652	0.955	0.955	0.955	0.955	0.955	0.933	0.944	0.629	0.955	0.955	0.955
CG17331-PA___KOG0177	0.960	0.975	0.985	0.985	0.960	0.955	0.965	0.975	0.985	0.970	0.975	0.985	0.985	0.980
CG17333-PA___KOG3147	0.480	0.492	0.410	0.414	0.463	0.410	0.520	0.520	0.480	0.500	0.520	0.463	0.525	0.525
CG17337-PA___KOG2276	0.956	0.749	0.891	0.950	0.950	0.950	0.522	0.967	0.948	0.962	0.950	0.962	0.566	0.852
CG17369-PA___KOG1351	0.910	0.984	1.000	0.998	1.000	1.000	0.609	1.000	0.992	0.949	0.912	0.996	1.000	1.000
CG17420-RA___KOG1678	0.932	0.937	0.937	0.937	0.937	0.937	0.000	0.937	0.937	0.932	0.937	0.932	0.937	0.937
CG1743-PC___KOG0683	0.997	0.997	0.997	0.997	0.997	0.992	1.000	0.981	1.000	1.000	0.997	1.000	1.000	0.997
CG17498-PA___KOG3285	0.976	0.962	0.962	0.976	0.981	0.966	0.971	0.981	0.971	0.976	0.981	0.957	0.966	0.966

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG17521-PA___KOG0857	0.959	0.744	0.959	0.959	0.954	0.959	0.954	0.621	0.950	0.954	0.959	0.959	0.954	0.959
CG17565-PA___KOG0365	0.869	0.871	0.881	0.948	0.869	0.876	0.783	0.864	0.876	0.876	0.864	0.912	0.864	0.857
CG17611-PA___KOG3185	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG17652-PA___KOG3164	0.616	0.616	0.616	0.616	0.616	0.616	0.616	0.616	0.735	0.751	0.751	0.608	0.616	0.747
CG17654-PA___KOG2670	0.995	0.995	0.938	0.995	0.991	0.995	0.995	0.995	0.995	0.995	0.995	0.995	0.859	0.995
CG17737-PA___KOG1770	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.928	1.000	0.991	1.000	1.000	1.000
CG1789-PA___KOG3237	0.676	0.689	0.626	0.622	0.681	0.718	0.689	0.672	0.685	0.731	0.685	0.000	0.685	0.689
CG17903-PA___KOG3453	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG1796-PA___KOG0285	0.828	0.737	0.749	0.749	0.749	0.749	0.135	0.667	0.749	0.749	0.592	0.828	0.826	0.749
CG18001-PA___KOG3499	0.873	0.915	0.873	0.887	0.873	0.000	0.887	0.873	0.887	0.873	0.901	0.986	0.873	0.873

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG18174-PA___KOG1555	1.000	1.000	1.000	1.000	1.000	1.000	0.362	1.000	0.964	1.000	1.000	0.997	0.511	1.000
CG18315-PA___KOG1712	0.945	0.956	0.760	0.765	0.967	0.956	0.951	0.945	0.951	0.945	0.825	0.951	0.847	0.951
CG18495-PA___KOG0182	1.000	0.682	0.922	1.000	0.996	1.000	0.890	1.000	0.922	1.000	0.886	0.914	0.833	0.922
CG18591-PA___KOG1774	0.958	0.958	0.958	0.958	0.958	0.958	0.958	0.958	0.968	0.958	0.958	0.958	0.958	0.968
CG18627-PA___KOG0366	0.914	0.914	0.914	0.914	0.914	0.914	0.914	0.914	0.914	0.914	0.914	0.914	0.894	0.908
CG1883-PA___KOG3320	0.703	0.908	0.985	0.985	0.974	0.985	0.779	0.974	0.944	0.851	0.974	0.974	0.985	0.985
CG1983-PA___KOG3157	0.847	0.835	0.835	0.918	0.875	0.843	0.847	0.961	0.839	0.776	0.847	0.851	0.455	0.765
CG1994-PA___KOG2036	0.830	0.829	0.745	0.811	0.166	0.831	0.674	0.783	0.792	0.834	0.748	0.806	0.787	0.802
CG2013-PA___KOG0419	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG2021-PA___KOG1784	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.979	0.990	0.990	0.990

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG2033-PE___KOG1754	1.000	0.962	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.969	1.000
CG2128-PA___KOG1342	0.952	0.927	0.945	0.995	0.879	0.954	0.843	0.945	0.868	0.968	0.932	0.936	0.945	0.945
CG2171-PC___KOG1643	0.976	0.992	1.000	0.996	1.000	1.000	1.000	0.992	0.851	1.000	0.980	1.000	1.000	0.988
CG2210-PA___KOG0888	0.890	0.925	0.896	0.896	0.908	0.896	0.890	0.908	0.890	0.925	0.890	0.931	0.919	0.902
CG2238-PB___KOG0469	0.986	0.975	0.851	0.986	0.819	0.986	0.797	0.884	0.986	0.986	0.987	0.987	0.557	0.987
CG2241-PA___KOG0728	0.983	0.983	0.983	0.983	0.973	0.958	0.973	0.983	0.973	0.958	0.983	0.973	0.968	0.983
CG2245-PA___KOG0567	0.987	0.822	0.987	0.987	0.980	0.000	0.934	0.993	0.970	0.987	0.983	0.983	0.970	0.983
CG2260-PA___KOG1272	0.764	0.708	0.728	0.710	0.770	0.702	0.703	0.752	0.690	0.703	0.695	0.700	0.708	0.761
CG2263-PA___KOG2784	0.840	0.922	0.956	0.952	0.920	0.373	0.956	0.926	0.449	0.918	0.922	0.924	0.926	0.956
CG2453-PA___KOG1540	0.791	0.785	0.894	0.887	0.861	0.950	0.712	0.798	0.798	0.838	0.891	0.570	0.795	0.798

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG2637-PA___KOG1241	0.955	0.971	0.972	0.972	0.972	0.964	0.862	0.962	0.960	0.968	0.325	0.958	0.971	0.962
CG2656-PA___KOG1534	0.944	0.986	0.982	0.965	0.982	0.958	0.989	0.986	0.975	0.989	0.986	0.989	0.989	0.993
CG2674-PE___KOG1506	0.892	0.941	0.782	0.946	0.941	0.941	0.831	0.941	0.941	0.946	0.941	0.946	0.922	0.941
CG2827-PA___KOG2772	0.946	0.955	0.931	0.982	0.931	0.988	0.798	0.934	0.934	0.934	0.916	0.982	0.982	0.967
CG2852-PA___KOG0880	0.772	0.782	0.670	0.777	0.767	0.772	0.772	0.772	0.796	0.786	0.786	0.786	0.772	0.772
CG2862-PA___KOG3275	0.834	0.742	0.848	0.848	0.715	0.821	0.808	0.834	0.821	0.954	0.795	0.841	0.907	0.848
CG2863-PA___KOG0271	0.971	0.951	0.961	0.957	0.957	0.982	0.945	0.957	0.961	0.963	0.957	0.975	0.975	0.955
CG2885-PA___KOG0084	0.673	0.643	0.439	0.658	0.832	0.673	0.842	0.872	0.862	0.617	0.842	0.888	0.842	0.888
CG2925-PA___KOG2636	0.528	0.897	0.855	0.893	0.859	0.891	0.766	0.891	0.897	0.897	0.909	0.919	0.859	0.702
CG2934-PA___KOG2957	0.989	0.989	0.989	0.989	0.983	0.991	0.994	0.989	0.991	0.989	0.989	0.989	0.989	0.989

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG2960-PA___KOG0003	0.992	0.992	0.992	0.992	0.992	0.992	0.597	0.992	0.953	0.992	1.000	0.992	0.992	0.992
CG2968-PA___KOG1758	0.703	0.595	0.639	0.639	0.430	0.614	0.639	0.639	0.690	0.747	0.589	0.633	0.639	0.639
CG2976-PA___KOG0530	0.916	0.958	0.964	0.958	0.970	0.997	0.970	0.961	0.970	0.955	0.997	0.979	0.976	0.985
CG3011-PA___KOG2467	0.862	0.881	0.881	0.881	0.896	0.862	0.866	0.866	0.857	0.874	0.855	0.872	0.846	0.861
CG3018-PA___KOG0424	0.994	0.994	1.000	0.994	1.000	1.000	0.994	1.000	0.856	0.963	1.000	1.000	1.000	1.000
CG3127-PA___KOG1367	0.976	0.964	0.969	0.964	0.966	0.966	0.935	0.971	0.962	0.969	0.959	0.976	0.966	0.964
CG31305-PG___KOG0756	0.893	0.893	0.893	0.893	0.893	0.896	0.893	0.921	0.893	0.660	0.799	0.893	0.893	0.893
CG3157-PA___KOG1374	0.918	0.950	0.950	0.950	0.950	0.943	0.771	0.939	0.950	0.937	0.947	0.939	0.947	0.939
CG31692-PA___KOG1458	0.949	0.952	0.955	0.955	0.958	0.000	0.737	0.928	0.949	0.958	0.955	0.955	0.958	0.958
CG3186-PA___KOG3271	0.975	0.975	0.975	0.975	0.975	0.975	0.975	0.975	0.975	0.894	0.975	0.975	0.975	0.975

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG3193-PA___KOG1915	0.933	0.930	0.937	0.937	0.937	0.923	0.936	0.927	0.855	0.927	0.925	0.937	0.936	0.927
CG32253-PA___KOG2971	0.728	0.728	0.728	0.728	0.625	0.759	0.717	0.728	0.728	0.717	0.728	0.717	0.773	0.773
CG3225-PA___KOG0922	0.926	0.937	0.944	0.934	0.944	0.938	0.934	0.926	0.888	0.798	0.987	0.938	0.928	0.938
CG32505-PA___KOG0372	1.000	1.000	1.000	1.000	1.000	1.000	0.763	1.000	1.000	0.760	0.984	1.000	1.000	1.000
CG32527-PB___KOG0462	0.826	0.815	0.815	0.845	0.815	0.597	0.481	0.835	0.846	0.816	0.867	0.818	0.859	0.799
CG3283-PA___KOG3049	0.846	0.846	0.846	0.846	0.846	0.846	0.846	0.846	0.916	0.815	0.916	0.916	0.916	0.916
CG33005-PA___KOG2906	1.000	1.000	1.000	1.000	1.000	0.991	1.000	1.000	0.991	0.991	1.000	1.000	1.000	1.000
CG3319-PA___KOG0659	0.966	0.938	0.960	0.952	0.853	0.958	0.808	0.949	0.983	0.941	0.986	0.932	0.938	0.929
CG33297-PC___KOG0211	0.980	0.980	0.959	0.980	0.980	0.980	0.980	0.980	0.980	0.980	0.980	0.980	0.980	0.980
CG3329-PA___KOG0173	0.780	0.832	0.791	0.791	0.839	0.927	0.967	0.817	0.810	0.799	0.971	0.813	0.784	0.941

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG3333-PA___KOG2529	0.825	0.817	0.790	0.817	0.780	0.788	0.813	0.784	0.809	0.344	0.825	0.825	0.823	0.800
CG3395-PD___KOG3301	0.934	0.918	0.934	0.934	0.934	0.934	0.934	0.934	0.934	0.934	0.934	0.934	0.934	0.934
CG3416-PA___KOG1556	0.850	0.858	0.858	0.858	0.850	0.858	0.858	0.847	0.850	0.850	0.855	0.858	0.850	0.858
CG3422-PA___KOG0183	0.876	0.900	0.904	0.900	0.924	0.924	0.924	0.876	0.924	0.924	0.768	0.920	0.924	0.924
CG3450-PA___KOG3493	1.000	0.986	1.000	1.000	1.000	1.000	0.986	0.986	0.743	0.986	0.986	0.986	0.946	0.986
CG3460-PA___KOG2613	0.875	0.874	0.875	0.875	0.883	0.883	0.864	0.875	0.874	0.870	0.860	0.843	0.843	0.875
CG3469-PA___KOG0367	0.768	0.838	0.856	0.856	0.793	0.816	0.364	0.793	0.790	0.813	0.674	0.788	0.753	0.811
CG3476-PA___KOG0758	0.970	0.970	0.960	0.960	0.977	0.977	0.977	0.983	0.960	0.977	0.983	0.973	0.967	0.987
CG3499-PB___KOG0734	0.615	0.468	0.630	0.639	0.578	0.649	0.600	0.536	0.654	0.634	0.688	0.638	0.627	0.661
CG3534-PA___KOG2531	0.495	0.881	0.868	0.817	0.870	0.864	0.727	0.741	0.770	0.830	0.000	0.857	0.801	0.875

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG3539-PD___KOG1301	0.856	0.880	0.926	0.933	0.748	0.944	0.757	0.815	0.894	0.895	0.843	0.933	0.860	0.929
CG3564-PA___KOG1692	0.890	0.900	0.900	0.900	0.895	0.900	0.900	1.000	0.900	0.904	0.904	0.895	0.904	0.900
CG3590-PA___KOG2700	0.992	0.793	0.992	0.996	0.992	0.992	0.992	0.902	0.983	0.992	0.905	0.902	0.992	0.992
CG3608-PA___KOG1235	0.811	0.846	0.854	0.850	0.721	0.844	0.857	0.852	0.855	0.850	0.838	0.836	0.636	0.832
CG3612-PA___KOG1353	0.984	0.991	0.991	0.991	0.975	0.995	0.758	0.555	0.973	0.973	0.539	0.993	0.953	0.976
CG3664-PA___KOG0092	0.800	0.791	0.800	0.791	0.782	0.464	0.855	0.805	0.791	0.791	0.805	0.777	0.836	0.759
CG3671-PA___KOG1291	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.811	0.000
CG3704-PA___KOG1532	0.590	0.582	0.582	0.590	0.601	0.582	0.598	0.491	0.324	0.593	0.611	0.590	0.585	0.619
CG3724-PA___KOG2653	0.967	0.876	0.963	0.965	0.967	0.965	0.971	0.942	0.969	0.969	0.965	0.965	0.965	0.948
CG3731-PA___KOG0960	0.994	0.955	0.955	0.955	0.994	0.955	0.994	0.994	0.994	0.994	0.994	0.994	0.994	0.949

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG3821-PA___KOG0556	0.902	0.902	0.774	0.900	0.898	0.898	0.278	0.660	0.776	0.827	0.833	0.902	0.594	0.897
CG3861-PA___KOG2617	0.963	0.991	0.963	0.970	0.963	0.953	0.963	0.972	0.963	0.963	0.434	0.970	0.963	0.963
CG3911-PA___KOG3330	1.000	0.642	0.927	1.000	0.927	0.927	0.916	1.000	0.927	0.927	0.609	1.000	1.000	0.927
CG3931-PA___KOG3013	0.679	0.957	0.702	0.896	0.943	0.913	0.528	0.936	0.903	0.709	0.920	0.936	0.936	0.936
CG3948-PA___KOG3343	0.960	0.960	0.960	0.874	0.960	0.960	0.960	0.960	0.960	0.880	0.960	0.960	0.886	0.960
CG3949-PA___KOG3387	0.938	0.969	0.969	0.969	0.930	0.969	0.969	0.992	0.969	0.969	0.969	0.969	0.969	0.969
CG3997-PA___KOG0002	0.981	0.981	0.981	0.981	0.981	0.981	0.981	0.981	0.981	0.981	0.654	0.981	1.000	0.981
CG4003-PA___KOG1942	0.921	0.996	0.996	0.996	0.996	0.996	0.884	0.972	0.993	0.952	0.643	0.993	0.921	0.993
CG4008-PA___KOG2775	0.791	0.826	0.826	0.826	0.826	0.822	0.699	0.826	0.826	0.826	0.826	0.826	0.826	0.826
CG4016-PB___KOG1358	0.716	0.861	0.748	0.874	0.870	0.776	0.763	0.842	0.821	0.859	0.859	0.825	0.823	0.823

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG4046-PA___KOG1753	0.872	0.872	0.872	0.872	0.879	0.879	0.872	0.893	0.872	0.879	0.886	0.872	0.879	0.872
CG4082-PA___KOG0481	0.996	0.922	0.996	0.999	0.951	0.997	0.715	0.886	0.981	0.996	1.000	0.996	1.000	0.995
CG4083-PA___KOG1566	0.921	0.932	0.932	0.924	0.932	0.926	0.929	0.988	0.771	0.932	0.918	0.932	0.932	0.976
CG4087-PA___KOG1762	0.593	0.593	0.991	0.965	0.965	0.982	0.593	0.593	0.965	0.593	0.593	0.593	0.982	0.982
CG4097-PA___KOG0179	0.975	0.966	0.966	0.966	0.975	0.975	0.975	0.975	0.975	0.966	0.966	0.975	0.975	0.975
CG4108-PA___KOG3232	0.961	0.985	0.961	0.961	0.980	0.961	0.995	0.961	0.961	0.961	0.348	0.990	0.985	0.966
CG4111-PB___KOG3436	0.984	0.766	0.984	0.984	0.984	0.984	0.621	0.984	0.984	0.984	0.984	0.984	0.984	0.984
CG4147-PC___KOG0100	0.904	0.959	0.921	0.959	0.907	0.938	0.921	0.904	0.938	0.944	0.938	0.907	0.909	0.938
CG4152-PA___KOG0948	0.901	0.902	0.902	0.902	0.903	0.897	0.766	0.898	0.995	0.902	0.888	0.797	0.903	0.899
CG4185-PA___KOG0871	0.728	0.734	0.734	0.734	0.734	0.734	0.734	0.717	0.734	0.734	0.734	0.734	0.734	0.734

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG4236-PA___KOG0264	0.972	0.831	0.970	0.970	0.979	0.972	0.833	0.856	0.789	0.972	0.411	0.970	0.972	0.977
CG4258-PA___KOG2874	0.902	0.815	0.873	0.876	0.902	0.855	0.789	0.890	0.855	0.861	0.896	0.884	0.890	0.884
CG4260-PA___KOG1077	1.000	1.000	0.984	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG4265-PA___KOG1415	0.982	0.982	0.982	0.982	0.978	0.978	0.982	0.969	0.978	0.978	0.965	0.974	0.961	0.974
CG4279-PA___KOG1782	0.877	0.978	0.855	0.978	0.978	0.971	0.978	0.949	0.978	0.978	0.000	0.978	0.978	0.971
CG4307-PA___KOG1662	0.895	0.895	0.895	0.895	0.890	0.890	0.886	0.895	0.895	0.871	0.895	0.890	0.895	0.876
CG4311-PA___KOG1393	0.970	0.966	0.966	0.966	0.966	0.966	0.966	0.970	0.966	0.966	0.966	0.979	0.966	0.966
CG4347-PA___KOG2638	0.969	0.969	0.969	0.969	0.969	0.969	0.969	0.975	0.969	0.969	0.988	0.969	0.969	0.967
CG4364-PA___KOG2481	0.702	0.702	0.702	0.701	0.697	0.702	0.701	0.702	0.462	0.701	0.702	0.701	0.576	0.697
CG4406-PA___KOG1349	0.817	0.817	0.860	0.817	0.831	0.817	0.812	0.817	0.817	0.817	0.817	0.817	0.885	0.789

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG4422-PA___KOG1439	1.000	1.000	1.000	1.000	0.980	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.995	1.000
CG4494-PA___KOG1769	0.901	0.901	0.901	0.901	0.901	0.901	0.901	0.901	0.901	0.901	0.912	0.901	0.901	0.868
CG4573-PA___KOG1149	0.936	0.947	0.936	0.936	0.936	0.975	0.760	0.971	0.947	0.930	0.939	0.936	0.939	0.957
CG4610-PA___KOG2311	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.943	0.000
CG4634-PA___KOG1626	0.643	0.608	0.342	0.581	0.581	0.614	0.605	0.581	0.708	0.581	0.602	0.581	0.569	0.932
CG4651-PA___KOG3295	0.836	0.817	0.836	0.799	0.836	0.849	0.443	0.831	0.836	0.817	0.858	0.580	0.817	0.836
CG4659-PA___KOG0780	0.951	0.953	0.953	0.953	0.951	0.951	0.951	0.953	0.953	0.951	0.953	0.951	0.949	0.951
CG4685-PB___KOG2451	0.992	0.943	0.943	0.943	0.941	0.980	0.943	0.943	0.943	0.943	0.943	0.943	0.971	0.943
CG4759-PA___KOG3418	0.831	0.875	0.831	0.831	0.831	0.831	0.831	0.831	0.831	0.831	0.831	1.000	0.831	0.831
CG4769-PA___KOG3052	0.779	0.779	0.773	0.773	0.711	0.776	0.640	0.769	0.779	0.727	0.779	0.584	0.503	0.782

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG4800-PA___KOG1727	0.954	0.988	0.954	0.948	0.954	0.948	0.942	0.948	0.919	0.948	0.954	0.954	0.942	0.514
CG4849-PA___KOG0468	0.995	0.994	0.539	0.996	0.990	0.996	0.699	0.868	0.996	0.995	0.848	0.995	0.967	0.968
CG4858-PA___KOG3022	0.828	0.839	0.843	0.870	0.851	0.989	0.835	0.824	0.828	0.847	0.862	0.847	0.839	0.854
CG4866-PA___KOG4655	0.956	0.978	0.962	0.956	0.956	0.956	0.709	0.962	0.962	0.962	0.956	0.956	0.956	0.962
CG4918-PB___KOG3449	0.509	0.570	0.509	0.509	0.509	0.509	0.000	0.518	0.544	0.509	0.509	0.509	0.570	0.509
CG4938-PA___KOG2509	0.794	0.813	0.806	0.806	0.789	0.792	0.789	0.801	0.813	0.811	0.794	0.402	0.574	0.792
CG5029-PA___KOG0788	0.790	0.612	0.624	0.767	0.750	0.727	0.376	0.787	0.790	0.784	0.701	0.796	0.756	0.851
CG5033-PA___KOG0650	0.748	0.624	0.000	0.741	0.814	0.814	0.069	0.813	0.702	0.810	0.772	0.754	0.811	0.818
CG5091-PA___KOG2575	0.987	0.987	0.983	0.983	0.983	0.983	0.983	0.987	0.926	0.960	0.983	0.987	0.987	0.987
CG5163-PA___KOG3463	0.963	0.963	0.963	0.963	0.963	0.963	0.963	0.963	0.963	0.963	0.963	0.963	0.991	0.963

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG5165-PA___KOG0625	0.993	0.966	0.556	0.984	0.759	0.973	0.982	0.993	0.986	0.127	0.988	0.995	0.856	0.995
CG5183-PA___KOG3106	0.808	0.986	0.944	0.944	0.944	0.000	1.000	0.944	0.991	0.944	0.944	0.944	0.826	0.944
CG5188-PA___KOG2738	0.619	0.884	0.830	0.818	0.623	0.846	0.626	0.786	0.626	0.619	0.821	0.852	0.846	0.846
CG5193-PA___KOG1597	0.940	0.943	0.940	0.940	0.940	0.940	0.934	0.940	0.940	0.823	0.940	0.940	0.940	0.940
CG5205-PA___KOG0952	0.804	0.810	0.788	0.789	0.733	0.801	0.741	0.733	0.776	0.596	0.680	0.573	0.752	0.786
CG5214-PA___KOG0559	0.695	0.693	0.693	0.693	0.691	0.693	0.633	0.301	0.695	0.693	0.633	0.469	0.693	0.693
CG5220-PA___KOG1099	0.828	0.828	0.898	0.967	0.828	0.828	0.828	0.828	0.861	0.828	0.828	0.828	0.828	0.828
CG5258-PA___KOG3167	0.963	1.000	1.000	1.000	1.000	1.000	1.000	0.950	1.000	1.000	0.950	1.000	0.988	1.000
CG5266-PA___KOG0181	0.970	0.945	0.945	0.936	0.945	0.962	0.753	0.949	0.970	0.940	0.949	0.949	0.945	0.966
CG5268-PA___KOG3442	0.845	0.894	0.894	0.894	0.915	0.915	0.796	0.915	0.796	0.866	0.824	0.796	0.908	0.859

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG5277-PA___KOG3163	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG5288-PA___KOG0631	0.929	0.929	0.929	0.929	0.931	0.925	0.929	0.931	0.929	0.935	0.957	0.931	0.929	0.931
CG5338-PB___KOG3411	0.853	0.840	0.904	0.878	0.904	0.000	0.385	0.833	0.872	0.853	0.801	0.821	0.513	0.846
CG5353-PB___KOG1637	0.959	0.961	0.967	0.977	0.973	0.667	0.786	0.962	0.971	0.533	0.544	0.686	0.967	0.971
CG5371-PA___KOG1112	0.978	0.978	0.978	0.978	0.989	0.979	0.979	0.984	0.978	0.978	0.978	0.978	0.979	0.986
CG5378-PA___KOG0687	0.733	0.851	0.731	0.815	0.874	0.810	0.733	0.787	0.736	0.731	0.731	0.759	0.718	0.713
CG5384-PA___KOG1872	0.777	0.878	0.899	0.952	0.811	0.662	0.254	0.817	0.836	0.773	0.735	0.800	0.695	0.847
CG5517-PA___KOG0959	0.479	0.571	0.530	0.599	0.746	0.775	0.000	0.691	0.694	0.519	0.632	0.590	0.656	0.804
CG5519-PA___KOG0289	0.909	0.812	0.907	0.899	0.895	0.915	0.237	0.715	0.937	0.919	0.931	0.913	0.905	0.905
CG5525-PA___KOG0358	0.979	0.856	0.751	0.994	0.981	0.989	0.816	0.878	0.985	0.994	0.581	0.869	0.858	0.957

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG5547-PB___KOG2803	0.868	0.721	0.881	0.820	0.820	0.881	0.881	0.934	0.881	0.942	0.959	0.561	0.876	0.845
CG5589-PA___KOG0344	0.672	0.553	0.545	0.677	0.439	0.582	0.650	0.548	0.590	0.593	0.662	0.487	0.553	0.691
CG5605-PC___KOG0688	0.902	0.884	0.943	0.934	0.900	0.934	0.528	0.934	0.934	0.966	0.590	0.934	0.918	0.567
CG5629-PB___KOG2728	0.885	0.901	0.277	0.908	0.898	0.892	0.796	0.892	0.863	0.914	0.589	0.908	0.892	0.796
CG5677-PA___KOG3372	1.000	0.972	0.972	0.972	0.972	0.972	0.983	0.972	0.944	1.000	1.000	1.000	0.994	0.972
CG5705-PA___KOG2726	0.891	0.888	0.913	0.913	0.913	0.896	0.888	0.875	0.883	0.888	0.913	0.888	0.880	0.590
CG5706-PA___KOG2472	0.997	0.990	0.947	0.998	0.971	0.997	0.656	0.993	0.997	0.995	0.239	0.998	0.995	0.961
CG5823-PA___KOG0894	0.613	0.563	0.574	0.574	0.606	0.479	0.606	0.606	0.472	0.574	0.472	0.574	0.609	0.574
CG5827-PA___KOG0402	0.753	0.968	0.957	0.957	0.957	0.957	0.957	0.774	0.957	0.957	0.957	0.957	0.957	0.957
CG5864-PA___KOG0934	0.994	0.994	0.994	0.994	0.994	0.994	0.994	0.994	0.994	0.994	0.994	0.994	0.994	0.994

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG5915-PA___KOG0394	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.947	1.000	0.784	1.000	1.000	1.000
CG5919-PA___KOG0142	0.840	0.813	0.821	0.821	0.821	0.805	0.642	0.825	0.844	0.837	0.829	0.813	0.615	0.829
CG5946-PA___KOG0534	0.933	0.866	0.927	0.927	0.863	0.863	0.876	0.933	0.863	0.857	0.933	0.857	0.933	0.920
CG5949-PA___KOG0969	0.987	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.959	1.000	1.000	1.000	1.000	1.000
CG5970-PA___KOG2749	0.762	0.995	0.991	0.988	0.995	0.993	0.557	0.988	0.993	0.986	0.974	0.988	0.986	0.986
CG6007-PA___KOG1211	0.980	0.986	0.980	0.986	0.980	0.980	0.976	0.980	0.984	0.766	0.980	0.969	0.980	0.984
CG6016-PA___KOG2877	0.708	0.828	0.610	0.744	0.830	0.763	0.835	0.821	0.804	0.933	0.804	0.926	0.931	0.739
CG6050-PA___KOG0460	0.839	0.837	0.839	0.837	0.863	0.835	0.837	0.837	0.837	0.839	0.839	0.859	0.771	0.888
CG6056-PA___KOG0935	0.993	0.993	0.993	0.993	0.993	0.993	0.979	0.993	0.993	0.993	0.993	0.993	0.993	0.762
CG6057-PA___KOG0018	0.774	0.825	0.501	0.877	0.819	0.798	0.618	0.810	0.807	0.538	0.827	0.533	0.747	0.844

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG6197-PA___KOG2047	0.991	0.971	0.971	0.971	0.973	0.898	0.967	0.973	0.799	0.898	0.977	0.973	0.898	0.898
CG6213-PA___KOG1772	0.593	0.568	0.593	0.653	0.958	0.610	0.475	0.653	0.508	0.593	0.458	0.508	0.000	0.636
CG6223-PA___KOG1058	0.676	0.622	0.197	0.678	0.611	0.782	0.255	0.228	0.696	0.652	0.655	0.676	0.694	0.676
CG6230-PA___KOG0209	0.785	0.893	0.916	0.917	0.967	0.914	0.914	0.889	0.922	0.933	0.926	0.895	0.915	0.921
CG6233-PA___KOG1816	0.757	0.584	0.984	0.748	0.789	0.950	0.757	0.763	0.757	0.763	0.972	0.811	0.767	0.770
CG6258-PA___KOG2035	1.000	1.000	1.000	1.000	0.978	1.000	0.759	1.000	0.978	1.000	1.000	0.978	1.000	0.978
CG6335-PA___KOG1936	0.954	0.948	0.950	0.950	0.962	0.958	0.950	0.954	0.837	0.950	0.992	0.948	0.952	0.956
CG6341-PA___KOG1668	0.859	0.809	0.855	0.855	0.855	0.714	0.439	0.882	0.851	0.855	0.855	0.870	0.855	0.882
CG6415-PA___KOG2770	0.938	0.948	0.948	0.948	0.948	0.951	0.924	0.943	0.921	0.951	0.892	0.948	0.919	0.926
CG6439-PA___KOG0784	0.765	0.906	0.720	0.833	0.884	0.871	0.488	0.830	0.860	0.755	0.881	0.822	0.879	0.833

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG6476-PB___KOG0466	0.901	0.933	0.935	0.954	0.933	0.901	0.828	0.901	0.941	0.926	0.920	0.901	0.901	0.655
CG6510-PA___KOG0829	0.955	0.955	0.955	0.955	0.955	0.955	0.663	0.955	0.955	0.955	0.955	0.955	0.955	0.955
CG6546-PA___KOG0679	0.815	0.838	0.986	1.000	0.972	0.892	0.725	0.840	0.969	0.930	0.915	0.972	0.725	0.986
CG6601-PA___KOG0094	0.995	0.995	0.990	0.995	0.995	0.995	0.756	0.990	0.785	0.995	0.770	0.995	0.545	0.885
CG6603-PA___KOG0103	0.827	0.780	0.549	0.766	0.760	0.815	0.812	0.678	0.778	0.799	0.807	0.771	0.857	0.795
CG6610-PA___KOG1775	0.946	0.946	0.880	0.880	0.946	0.946	0.946	0.946	0.957	0.880	0.957	0.946	0.946	0.913
CG6699-PA___KOG0276	0.852	0.768	0.251	0.792	0.857	0.824	0.852	0.785	0.857	0.813	0.861	0.886	0.855	0.824
CG6719-PA___KOG3313	0.867	0.805	0.872	0.805	0.846	0.841	0.800	0.867	0.662	0.867	0.769	0.800	0.790	0.800
CG6724-PA___KOG0313	0.922	0.891	0.898	0.945	0.743	0.876	0.753	0.886	0.948	0.895	0.905	0.886	0.941	0.910
CG6750-PA___KOG3188	0.831	0.867	0.867	0.879	0.879	0.867	0.867	0.879	0.879	0.879	0.867	0.867	0.560	0.867

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG6764-PA___KOG1723	0.703	0.703	0.703	0.703	0.703	0.703	0.703	0.703	0.703	0.703	0.703	0.703	0.734	0.703
CG6767-PB___KOG1448	0.889	0.889	0.918	0.889	0.879	0.879	0.946	0.889	0.915	0.889	0.961	0.920	0.720	0.884
CG6769-PA___KOG2785	0.724	0.741	0.720	0.712	0.739	0.763	0.685	0.659	0.759	0.771	0.734	0.722	0.637	0.732
CG6840-PA___KOG4392	0.898	0.898	0.924	0.898	0.898	0.898	0.780	0.898	0.898	0.941	0.898	0.898	0.898	0.898
CG6841-PA___KOG0495	0.944	0.943	0.948	0.962	0.962	0.962	0.430	0.959	0.942	0.944	0.959	0.961	0.961	0.961
CG6854-PC___KOG2387	0.900	0.879	0.892	0.865	0.887	0.850	0.879	0.896	0.896	0.898	0.879	0.884	0.674	0.889
CG6871-PA___KOG0047	0.943	0.929	0.939	0.943	0.943	0.963	0.943	0.943	0.943	0.943	0.925	0.941	0.943	0.941
CG6876-PA___KOG2574	0.821	0.813	0.851	0.819	0.843	0.592	0.777	0.849	0.849	0.821	0.815	0.851	0.817	0.847
CG6877-PA___KOG2981	0.625	0.613	0.634	0.634	0.737	0.634	0.517	0.707	0.538	0.634	0.728	0.628	0.556	0.628
CG6988-PA___KOG0190	0.851	0.785	0.841	0.851	0.835	0.811	0.670	0.811	0.847	0.835	0.843	0.813	0.827	0.831

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG6998-PB___KOG3430	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.911	1.000	1.000	1.000
CG7007-PA___KOG0233	0.939	0.986	0.986	0.986	0.977	0.977	0.977	0.977	0.977	0.977	0.977	0.981	0.981	0.977
CG7024-PA___KOG0225	0.719	0.752	0.744	0.740	0.738	0.604	0.598	0.619	0.727	0.719	0.000	0.719	0.721	0.719
CG7033-PC___KOG0363	0.976	0.976	0.968	0.976	0.976	0.996	0.624	0.852	0.974	0.978	0.976	0.974	0.560	0.976
CG7048-PA___KOG3048	0.870	0.645	0.870	0.645	0.680	0.675	0.675	0.680	0.462	0.840	0.846	0.686	0.680	0.870
CG7057-PA___KOG0938	1.000	0.868	1.000	0.993	1.000	0.995	0.900	1.000	0.993	1.000	1.000	1.000	1.000	1.000
CG7073-PA___KOG0077	1.000	0.928	0.727	1.000	1.000	1.000	0.675	0.794	0.928	1.000	0.814	1.000	1.000	1.000
CG7108-PA___KOG2851	0.585	0.588	0.679	0.740	0.727	0.907	0.740	0.827	0.727	0.893	0.911	0.909	0.740	0.583
CG7109-PA___KOG0371	1.000	0.997	1.000	1.000	1.000	1.000	0.974	1.000	1.000	0.894	0.716	1.000	0.677	1.000
CG7111-PA___KOG0279	1.000	1.000	1.000	1.000	1.000	1.000	0.674	1.000	1.000	1.000	1.000	1.000	1.000	0.978

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG7176-PC___KOG1526	0.868	0.828	0.881	0.911	0.879	0.868	0.866	0.866	0.868	0.868	0.883	0.868	0.868	0.868
CG7269-PB___KOG0329	0.948	0.948	0.948	0.948	0.948	0.948	0.948	0.948	0.941	0.948	0.946	0.948	0.939	0.948
CG7277-PA___KOG3855	0.831	0.682	0.803	0.785	0.713	0.441	0.812	0.705	0.822	0.789	0.805	0.797	0.831	0.824
CG7338-PA___KOG1980	0.907	0.929	0.926	0.929	0.962	0.924	0.961	0.962	0.942	0.948	0.849	0.928	0.933	0.930
CG7339-PA___KOG3297	0.880	0.880	0.880	0.880	0.880	0.880	0.730	0.880	0.622	0.880	0.880	0.880	0.880	0.880
CG7359-PA___KOG0862	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.981	1.000	1.000	1.000	1.000	1.000	1.000
CG7375-PA___KOG0420	0.984	0.984	0.984	0.984	0.984	0.984	0.984	0.984	0.984	0.984	0.984	0.984	0.984	0.984
CG7424-PA___KOG3464	1.000	0.962	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.924
CG7430-PA___KOG1335	0.943	0.943	0.937	0.943	0.943	0.949	0.863	0.901	0.941	0.943	0.933	0.943	0.929	0.943
CG7435-PA___KOG0073	1.000	1.000	1.000	1.000	0.773	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG7483-PA___KOG0328	0.983	0.983	0.983	0.983	0.983	0.983	0.983	0.983	0.998	0.983	0.983	0.980	0.983	0.983
CG7490-PA___KOG0815	0.792	0.792	0.619	0.792	0.849	0.808	0.827	0.824	0.849	0.792	0.808	0.827	0.808	1.000
CG7516-PA___KOG2321	0.821	0.720	0.816	0.716	0.781	0.805	0.673	0.715	0.972	0.698	0.963	0.711	0.699	0.702
CG7538-PA___KOG0477	0.949	0.975	0.980	0.981	0.928	0.861	0.939	0.775	0.886	0.922	0.923	0.821	0.948	0.973
CG7581-PA___KOG1036	0.982	0.823	0.972	0.985	0.972	0.972	0.792	0.982	0.988	0.982	0.988	0.976	0.988	0.988
CG7610-PC___KOG1531	0.862	0.872	0.872	0.883	0.933	0.856	0.862	0.883	0.906	0.862	0.896	0.893	0.862	0.883
CG7637-PA___KOG3503	0.846	0.908	0.923	0.769	0.908	0.892	1.000	1.000	0.908	0.569	0.662	0.769	1.000	0.969
CG7698-PA___KOG1137	0.882	0.866	0.581	0.879	0.836	0.892	0.353	0.863	0.800	0.866	0.726	0.705	0.629	0.863
CG7724-PA___KOG1430	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CG7726-PA___KOG0397	0.935	0.876	0.946	0.946	0.681	0.946	0.708	0.935	0.935	0.919	0.924	0.935	0.935	0.973

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG7808-PC___KOG3283	0.981	0.947	0.981	0.981	0.923	0.981	0.981	0.990	0.971	0.971	0.971	0.971	0.981	0.971
CG7823-PA___KOG3205	0.896	0.896	0.896	0.896	0.896	0.896	0.896	0.886	0.891	0.896	0.891	0.896	0.688	0.896
CG7834-PB___KOG3180	0.949	0.949	0.949	0.949	0.949	0.949	0.949	0.949	0.949	0.949	1.000	0.949	0.949	0.949
CG7857-PA___KOG2606	0.687	0.955	0.939	0.534	0.677	0.521	0.521	0.923	0.696	0.495	0.709	0.939	0.527	0.942
CG7883-PA___KOG1466	0.919	0.795	0.954	0.928	0.919	0.577	0.964	0.954	0.945	0.948	0.964	0.935	0.919	0.951
CG7925-PB___KOG1750	0.787	0.787	0.809	0.809	0.787	0.780	0.801	0.972	0.787	0.688	0.780	0.787	0.809	0.787
CG7939-PA___KOG0878	1.000	0.793	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.556	1.000	1.000	1.000	1.000
CG7948-PA___KOG1433	0.917	0.917	0.917	0.890	0.917	0.917	0.920	0.917	0.917	0.368	0.917	0.917	0.858	0.923
CG7961-PA___KOG0292	0.802	0.835	0.866	0.879	0.751	0.869	0.879	0.802	0.868	0.883	0.886	0.886	0.791	0.878
CG7993-PA___KOG3031	0.885	0.894	0.894	0.888	0.885	0.891	0.894	0.910	0.866	0.891	0.894	0.891	0.903	0.875

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG7998-PA___KOG1494	0.923	0.914	0.929	0.932	0.932	0.923	0.923	0.929	0.929	0.926	0.920	0.929	0.926	0.929
CG8019-PA___KOG1123	0.814	0.747	0.358	0.844	0.822	0.865	0.401	0.746	0.753	0.836	0.877	0.814	0.806	0.837
CG8036-PB___KOG0523	0.909	0.923	0.300	0.946	0.949	0.957	0.233	0.944	0.593	0.976	0.943	0.960	0.625	0.947
CG8048-PC___KOG2909	0.849	0.849	0.898	0.849	0.844	0.844	0.749	0.849	0.858	0.896	0.844	0.851	0.786	0.847
CG8142-PA___KOG0989	0.862	0.989	0.915	0.955	0.983	0.881	0.873	0.992	0.856	0.904	0.941	0.859	0.788	0.983
CG8186-PA___KOG1647	0.935	0.915	0.907	1.000	0.818	0.895	0.575	0.935	0.935	0.935	0.931	0.818	0.818	0.935
CG8210-PA___KOG3432	0.912	0.912	0.912	0.912	0.944	0.944	0.912	0.936	0.912	0.912	0.912	0.936	0.912	0.912
CG8228-PA___KOG1299	0.950	0.908	0.930	0.927	0.977	0.925	0.628	0.828	0.692	0.932	0.932	0.974	0.930	0.929
CG8231-PA___KOG0359	0.996	1.000	0.993	0.993	1.000	1.000	0.740	0.996	0.996	0.998	0.996	1.000	1.000	1.000
CG8239-PA___KOG2833	0.979	0.995	0.995	0.967	0.987	0.977	0.972	0.987	0.987	0.887	0.987	0.985	0.985	0.992

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG8251-PA___KOG2446	0.979	0.912	0.989	0.995	0.911	0.977	0.655	0.821	0.980	0.987	0.921	0.989	0.685	0.989
CG8258-PA___KOG0362	1.000	0.991	0.532	1.000	1.000	0.995	0.996	1.000	0.987	1.000	1.000	0.989	0.991	1.000
CG8284-PA___KOG0418	1.000	1.000	1.000	1.000	0.985	1.000	1.000	0.975	1.000	1.000	0.555	0.985	1.000	0.995
CG8327-PA___KOG1562	0.979	0.986	0.986	0.983	0.983	0.983	0.986	0.979	0.976	0.979	0.990	0.990	0.983	0.979
CG8332-PA___KOG0898	0.973	0.819	0.973	0.980	0.980	0.785	0.980	0.980	0.980	0.980	0.785	0.980	0.980	0.980
CG8340-PA___KOG1487	0.753	0.935	0.932	0.989	0.973	0.973	0.759	0.932	0.932	0.940	0.921	0.938	0.973	0.935
CG8351-PA___KOG0361	0.916	0.954	0.613	0.917	0.916	0.945	0.626	0.837	0.923	0.916	0.903	0.855	0.916	0.914
CG8392-PA___KOG0174	0.893	0.880	0.684	0.871	0.916	0.916	0.898	0.916	0.902	0.902	0.916	0.898	0.916	0.916
CG8402-PA___KOG0376	0.820	0.825	0.827	0.881	0.877	0.789	0.866	0.869	0.862	0.835	0.868	0.676	0.921	0.894
CG8417-PA___KOG2757	0.642	0.668	0.647	0.652	0.652	0.652	0.705	0.693	0.635	0.705	0.673	0.700	0.652	0.688

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG8439-PA___KOG0357	0.517	0.963	0.971	0.959	0.963	0.961	0.558	0.923	0.963	0.961	0.961	0.963	0.451	0.963
CG8495-PA___KOG3506	0.930	0.947	0.947	0.947	0.965	0.930	0.965	0.965	0.965	1.000	0.947	0.947	0.947	0.982
CG8542-PA___KOG0102	0.856	0.742	0.889	0.892	0.886	0.840	0.777	0.881	0.729	0.822	0.879	0.886	0.902	0.891
CG8627-PA___KOG0817	0.966	1.000	0.966	0.966	0.989	0.966	1.000	1.000	0.966	0.920	1.000	1.000	0.966	1.000
CG8636-PA___KOG0122	0.900	0.893	0.885	0.885	0.907	0.907	0.507	0.915	0.922	0.922	0.915	0.922	0.674	0.922
CG8648-PA___KOG2519	0.842	0.826	0.845	0.834	0.834	0.839	0.712	0.837	0.834	0.832	0.847	0.839	0.834	0.842
CG8721-PA___KOG0622	0.777	0.673	0.858	0.856	0.846	0.775	0.575	0.324	0.906	0.716	0.575	0.856	0.911	0.858
CG8728-PA___KOG2067	0.819	0.813	0.813	0.813	0.851	0.815	0.817	0.824	0.795	0.811	0.815	0.811	0.637	0.820
CG8732-PE___KOG1180	0.986	0.828	0.123	0.927	0.740	0.983	0.242	0.818	0.986	0.987	0.979	0.892	0.920	0.983
CG8798-PA___KOG2004	0.731	0.759	0.803	0.838	0.806	0.775	0.690	0.736	0.793	0.786	0.685	0.774	0.762	0.740

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG8808-PA___KOG0787	0.826	0.906	0.906	0.913	0.925	0.925	0.118	0.510	0.930	0.901	0.891	0.913	0.850	0.899
CG8857-PA___KOG1728	0.891	0.571	0.891	0.891	0.891	0.878	0.891	0.891	0.891	0.891	0.910	0.878	0.891	0.981
CG8877-PA___KOG1795	0.954	0.901	0.940	0.956	0.954	0.954	0.900	0.954	0.920	0.941	0.343	0.571	0.690	0.952
CG8885-PA___KOG2792	0.972	0.857	0.865	0.968	0.853	0.988	0.833	0.968	0.905	0.984	0.885	0.825	0.849	0.952
CG8891-PA___KOG3222	0.964	0.943	0.943	0.943	0.943	0.943	0.943	0.964	0.948	0.958	0.964	0.948	0.943	0.943
CG8900-PB___KOG3311	0.850	0.856	0.850	0.850	0.850	0.850	0.850	0.850	0.850	0.810	0.000	0.850	0.850	0.850
CG8905-PA___KOG0876	0.913	0.931	0.936	0.853	0.849	0.830	0.839	0.844	0.936	0.858	0.835	0.830	0.830	0.959
CG8922-PA___KOG3291	0.843	0.843	0.843	0.843	0.843	0.843	0.843	0.843	0.886	0.834	0.843	0.843	0.843	0.843
CG8939-PA___KOG1098	0.650	0.644	0.720	0.698	0.687	0.683	0.680	0.683	0.672	0.699	0.246	0.682	0.682	0.677
CG8975-PA___KOG1567	0.830	0.959	0.962	0.992	0.967	0.802	0.954	0.898	0.832	0.815	0.843	0.832	0.815	0.827

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG8977-PA___KOG0364	0.813	0.974	0.817	0.952	0.859	0.433	0.538	0.974	0.939	0.965	0.952	0.965	0.622	0.956
CG8978-PA___KOG1523	0.997	0.963	0.963	0.963	0.960	0.960	0.963	0.997	0.963	0.963	0.960	0.963	0.963	0.963
CG8996-PB___KOG3954	0.958	0.958	0.994	0.958	0.979	0.958	0.958	0.698	0.816	0.958	0.955	0.955	0.955	0.958
CG9000-PA___KOG2719	0.892	0.892	0.958	0.892	0.940	0.892	0.892	0.936	0.896	0.892	0.905	0.892	0.892	0.892
CG9012-PB___KOG0985	0.916	0.952	0.952	0.952	0.949	0.952	0.821	0.828	0.953	0.952	0.952	0.955	0.879	0.952
CG9022-PA___KOG2754	0.922	0.949	0.947	0.927	0.922	0.929	0.884	0.944	0.902	0.918	0.980	0.940	0.931	0.964
CG9042-PB___KOG2711	0.889	0.889	0.934	0.961	0.889	0.889	0.521	0.889	0.909	0.917	0.889	0.765	0.942	0.875
CG9060-PA___KOG2703	0.882	0.747	0.786	0.716	0.841	0.795	0.417	0.705	0.867	0.825	0.810	0.467	0.566	0.860
CG9075-PA___KOG0327	0.993	0.960	0.998	0.946	0.948	0.948	0.978	0.965	0.948	0.960	0.946	0.946	0.946	0.946
CG9090-PA___KOG0767	0.757	0.800	0.765	0.795	0.808	0.816	0.699	0.736	0.760	0.816	0.696	0.808	0.792	0.699

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG9091-PA___KOG3475	0.968	0.777	0.968	0.968	0.968	0.957	0.989	0.968	0.968	0.968	0.000	0.968	0.968	0.957
CG9099-PA___KOG3239	0.874	0.716	0.784	0.711	0.779	0.779	0.784	0.711	0.721	0.711	0.795	0.784	0.868	0.779
CG9113-PB___KOG1062	0.651	0.602	0.640	0.655	0.605	0.454	0.611	0.575	0.646	0.643	0.518	0.644	0.404	0.647
CG9128-PA___KOG1889	0.720	0.767	0.777	0.823	0.656	0.767	0.841	0.708	0.823	0.779	0.737	0.799	0.771	0.782
CG9177-PG___KOG2767	0.589	0.695	0.000	0.744	0.718	0.697	0.303	0.587	0.645	0.740	0.701	0.553	0.559	0.748
CG9193-PB___KOG1636	1.000	1.000	0.996	0.996	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG9207-PA___KOG3149	0.899	0.930	0.930	0.939	0.943	0.939	0.934	0.899	0.921	0.895	0.974	0.904	0.899	0.939
CG9253-PA___KOG0330	0.726	0.642	0.726	0.726	0.726	0.726	0.648	0.726	0.736	0.726	0.726	0.726	0.726	0.754
CG9281-PC___KOG0927	0.833	0.887	0.894	0.894	0.894	0.894	0.703	0.894	0.894	0.894	0.894	0.892	0.894	0.894
CG9282-PA___KOG1722	0.699	0.692	0.699	0.692	0.699	0.692	0.667	0.699	0.699	0.699	0.692	0.699	0.699	0.699

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG9330-PA___KOG0062	0.843	0.842	0.838	0.894	0.858	0.848	0.745	0.714	0.770	0.894	0.841	0.904	0.890	0.890
CG9364-PC___KOG0602	0.896	0.906	0.794	0.896	0.906	0.926	0.864	0.896	0.896	0.893	0.896	0.918	0.898	0.918
CG9388-PA___KOG0937	1.000	1.000	1.000	0.993	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.991
CG9433-PA___KOG1131	0.888	0.942	0.953	0.966	0.975	0.912	0.332	0.918	0.891	0.732	0.955	0.914	0.957	0.966
CG9475-PA___KOG0727	0.950	0.927	0.934	0.941	0.936	0.919	0.953	0.924	0.927	0.943	0.711	0.957	0.744	0.924
CG9539-PA___KOG1373	0.998	1.000	0.996	0.998	0.818	0.834	1.000	0.998	0.998	0.998	0.966	0.998	0.998	1.000
CG9553-PB___KOG1755	1.000	1.000	1.000	1.000	1.000	1.000	0.717	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CG9742-PA___KOG1780	0.896	0.870	1.000	0.870	0.870	0.870	1.000	0.870	0.870	0.870	1.000	0.870	0.870	0.870
CG9750-PA___KOG2680	0.890	0.896	0.896	0.896	0.739	0.896	0.737	0.828	0.896	0.566	0.892	0.573	0.900	0.876
CG9779-PA___KOG3229	1.000	0.821	0.804	0.772	0.759	0.768	0.938	0.821	0.879	0.772	0.799	0.821	0.960	0.455

Essential_protein	*Achalarus lyciades*	*Papilio glaucus*	*Papilio polytes*	*Papilio xuthus*	*Danaus plexippus*	*Heliconius melpomene*	*Melitaea cinxia*	*Lerema accius*	*Bombyx mori*	*Manduca sexta*	*Plutella xylostella*	*Phoebis sennae*	*Calycopis cecrops*	*Pieris rapae*
CG9799-PA___KOG1539	0.918	0.930	0.970	0.971	0.936	0.952	0.970	0.923	0.943	0.964	0.967	0.933	0.807	0.965
CG9802-PA___KOG0964	0.949	0.946	0.948	0.949	0.940	0.946	0.697	0.946	0.951	0.954	0.833	0.948	0.911	0.952
CG9836-PA___KOG3361	0.787	0.774	0.774	0.806	0.819	0.787	0.819	0.819	0.774	0.774	0.832	0.774	0.781	0.800
CG9878-PB___KOG3480	0.968	0.978	0.978	0.978	0.914	0.978	0.978	0.968	0.978	0.946	0.849	0.978	0.978	0.978
CG9888-PA___KOG1596	0.661	0.661	0.664	0.681	0.658	0.658	0.672	0.655	0.664	0.391	0.661	0.649	0.661	0.655
CG9940-PA___KOG2303	0.874	0.888	0.613	0.902	0.874	0.871	0.873	0.811	0.871	0.872	0.873	0.872	0.581	0.702
CG9946-PA___KOG2916	0.795	0.792	0.795	0.795	0.795	0.789	0.681	0.789	0.789	0.792	0.801	0.804	0.792	0.792
CG9947-PA___KOG2952	0.824	0.930	0.902	0.902	0.899	0.919	0.899	0.885	0.888	0.821	0.888	0.894	0.894	0.869
total	0.858	0.857	0.832	0.879	0.860	0.857	0.757	0.847	0.857	0.848	0.818	0.854	0.833	0.877
average	0.871	0.869	0.858	0.888	0.874	0.865	0.792	0.868	0.868	0.864	0.841	0.874	0.853	0.887

Supplementary Table S2. Statistics for sequencing data and data processing related to experimental procedures and genome annotation

This file contains multiple sheets and each sheet corresponds to one supplement table.

S2A Supplementary Table S2A. Amount of data in sequence libraries used for genome assembly

S2B Supplementary Table S2B. Repeats in the *Achalarus lyciades* genome

S2C Supplementary Table S2C. Methods used for protein coding gene annotation

S2D Supplementary Table S2D. All predicted proteins in the *Achalarus lyciades* genome and their function annotations

Table S2A. Amount of data in sequence libraries used for genome assembly

Library	Raw sequence length	Processed sequence length
250 bp paired-end	24.68 Gb (46.7X)	24.21 Gb (42.7X)
500 bp paired-end	7.80 Gb (13.8X)	6.48 Gb (11.4X)
2 kb mate-pair	11.99 Gb (21.2X)	3.83 Gb (6.8X)
6 kb mate-pair	5.84 Gb (10.3X)	1.66 Gb (2.9X)
15 kb paired-end	8.21 Gb (14.5X)	1.51 Gb (2.7X)
pair-end reads in mate-pair libraries	n/a	7.58 Gb (13.4X)
single-end	n/a	2.35 Gb (4.2X)
total	60.33 Gb (106.4X)	47.63 Gb (84.0X)

Table S2B. Repeats in the Achalarus lyciades genome

Type of repeat	Total number	Total length	% of genome
DNA transposon	157970	47967785	8.463
Helitron	99516	28310554	4.995
hAT	14540	4171646	0.736
Mariner	12032	5575543	0.984
Sola	1935	887163	0.157
Harbinger	1718	769730	0.136
Polinton	1460	602090	0.106
PiggyBac	1400	584358	0.103
EnSpm	1359	583959	0.103
Other	6579	1622027	0.286

Unknown	17431	4860715	0.858
Endogenous Retrovirus	630	291958	0.052
ERV1	131	47949	0.008
ERV2	36	20093	0.004
Gypsy	15	4638	0.001
Other	11	7637	0.001
Unknown	437	211641	0.037
LTR Retrotransposon	15178	4316479	0.762
Gypsy	8287	2615764	0.461
Copia	3762	888810	0.157
BEL	1243	509650	0.090

Other	1471	170852	0.030
Unknown	415	131403	0.023
Non-LTR Retrotransposon	306725	73642878	12.992
CR1	172466	41012661	7.236
SINE	91246	18563377	3.275
R1	13549	4196140	0.740
RTE	9564	3145849	0.555
Jockey	5855	1830907	0.323
Daphne	4248	1701914	0.300
Other	9660	3142281	0.554
Unknown	137	49749	0.009

Pseudogene	7452	1551528	0.274
Simple Repeat	131920	6352520	1.121
Integrated Virus/Caulimovirus	172	52707	0.009
Low_complexity	20372	1013614	0.179
Unknown	25498	6345271	1.119
Total	665917	141534740	24.970

Table S2C. Methods used for protein coding gene annotation

Approach	Program	Organism	Number of gene models	Weight
homology	exonerate	Heliconius Melpomene	16732	2
homology	exonerate	Danaus plexippus	18202	6
homology	exonerate	Papilio Xuthus	39930	2
homology	exonerate	Drosophila melanogaster	6226	4
homology	exonerate	Bombyx mori	24193	4
homology	exonerate	Lerema accius	25195	8
homology	genBlastG	all in Uniref90	231448	4
transcript	cufflinks	Achalarus lyciades	19550	12
transcript	PASA	Achalarus lyciades	35532	18
de novo	Maker	na	19759	10
de novo	AUGUSTUS	na	16850	4
de novo	SNAP	na	55537	3
de novo	GeneMark	na	70947	2
de novo	GlimmerHMM	na	528714	1
consensus	EvidenceModeller	na	15881	na
official gene set	EvidenceModeller and manual	na	15881	na

Table S2C. All predicted proteins in the Achalarus lyciades genome and their function annotations

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
proteinID	annotation	go-terms	ortholog_in_flybase	Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius-TM	TMHMM	Phobius-SP	SignalP_EUK
aly1.1	Unknown		n/a																				
aly1.2	Zinc finger homeobox protein 3	GO:0019899,GO:0008270,GO:0003677,GO:0007417,GO:0043565,GO:0007517,GO:0005730,GO:0005634,GO:0007476,GO:0005739,GO:0005654,GO:0045664,GO:0045663,GO:0045662,GO:0046872,GO:0006366,GO:0007050,GO:0045892,GO:0035220,GO:0043231,GO:0044212,GO:0007420,GO:0007399,GO:0003700,GO:0000122,GO:0003705,GO:0006355,GO:0000977,GO:0005667	CG1449-PA				SM00389,SM00389,SM00389,SM00389,SM00389,SM00451,SM00451,SM00451,SM00451,SM00451,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF05605,PF00046,PF00046,PF00046,PF00046	PS50157,PS50157,PS50157,PS50157,PS50157,PS50071,PS50071,PS50157,PS50157,PS50071,PS50071,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00027,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00027,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:1.10.10.60,G3DSA:1.10.10.60,G3DSA:1.10.10.60,G3DSA:1.10.10.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF46689,SSF57667,SSF46689,SSF57667,SSF57667,SSF46689,SSF57667,SSF57667,SSF57667,SSF46689,SSF57667,SSF57667	922~942								
aly10.1	Unknown		n/a																				
aly10.2	Glutaryl-CoA dehydrogenase, mitochondrial	GO:0050660,GO:0004361,GO:0006554,GO:0006568,GO:0005743,GO:0005875,GO:0046948,GO:0008152,GO:0005759,GO:0016627,GO:0055114	CG9547-PA						PF02770,PF02771,PF00441			PS00073	G3DSA:1.20.140.10,G3DSA:1.10.540.10,G3DSA:2.40.110.10	SSF56645,SSF47203									
aly10.3	Glutaryl-CoA dehydrogenase, mitochondrial	GO:0050660,GO:0004361,GO:0006554,GO:0006568,GO:0005743,GO:0046948,GO:0005759,GO:0005875,GO:0055114	CG9547-PA						PF02770,PF02771,PF00441			PS00073	G3DSA:2.40.110.10,G3DSA:1.10.540.10,G3DSA:1.20.140.10	SSF47203,SSF56645									
aly10.4	UDP-glucuronosyltransferase 1-10	GO:0045922,GO:0051552,GO:0052695,GO:0052696,GO:0052697,GO:0005080,GO:0016021,GO:0009813,GO:0019899,GO:0005789,GO:0042803,GO:0032870,GO:0008152,GO:0015020,GO:0046982,GO:1904224,GO:2001030,GO:0005783	CG4302-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									
aly10.5	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG6475-PD						PF00201,PF00201				G3DSA:3.40.50.2000,G3DSA:3.40.50.2000,G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756,SSF53756									
aly1000.1	Unknown	GO:0016505	CG30116-PA										G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1000.2	Rho GTPase-activating protein 100F	GO:0048789,GO:0048846,GO:0090630,GO:0048786,GO:0005096,GO:0048790,GO:0005622,GO:0045467,GO:0007165,GO:0005515,GO:0005100,GO:0007266,GO:0097479	CG1976-PD				SM00239,SM00324,SM00228		PF00168,PF00620,PF00595	PS50238,PS50106			G3DSA:2.30.42.10,G3DSA:2.60.40.150,G3DSA:1.10.555.10	SSF49562,SSF48350,SSF50156			REACT_11044						
aly1000.3	Dedicator of cytokinesis protein 3	GO:0005089,GO:0005737,GO:0005085,GO:0045466,GO:0032863,GO:0005886,GO:0007264,GO:0007417	CG31048-PE				SM00326		PF06920,PF14429,PF16172	PS51651,PS51650,PS50002			G3DSA:2.30.30.40	SSF50044	1256~1276								
aly1000.4	Ubiquitin carboxyl-terminal hydrolase	GO:0005737,GO:0004221,GO:0005875,GO:0006511,GO:0005622,GO:0016579,GO:0004843	CG4265-PB						PF01088		PR00707,PR00707,PR00707,PR00707,PR00707		G3DSA:3.40.532.10	SSF54001									
aly1000.5	Unknown		n/a																				
aly1000.6	Innexin inx3	GO:0005737,GO:0010496,GO:0016328,GO:0016021,GO:0016327,GO:0007391,GO:0055085,GO:0005886,GO:0005243,GO:0006811,GO:0005921	CG1448-PA						PF00876	PS51013	PR01262,PR01262,PR01262,PR01262,PR01262,PR01262												
aly100186.1	Unknown		n/a											SSF54001									
aly10022.1	Unknown		n/a						PF13359														
aly10029.1	THAP domain containing protein 4	GO:0046872,GO:0003677	n/a						PF08768					SSF50814									
aly1003.1	Unknown		n/a																				
aly1003.2	Unknown	GO:0005886,GO:0007561,GO:0019898	CG2723-PB																				
aly1003.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10035.1	Insulin-degrading enzyme	GO:0045926,GO:0051260,GO:0005886,GO:0008270,GO:0050829,GO:0045089,GO:0050435,GO:0042277,GO:0005615,GO:0090062,GO:0005777,GO:0005739,GO:0005654,GO:1901143,GO:0046872,GO:0032461,GO:0005524,GO:0010992,GO:0004222,GO:0009986,GO:0010815,GO:0003824,GO:0006508,GO:0008340,GO:0046662,GO:0051603,GO:0005829	CG5517-PB						PF00675,PF05193,PF16187			PS00143	G3DSA:3.30.830.10,G3DSA:3.30.830.10	SSF63411,SSF63411									
aly10036.1	Unknown		n/a																				
aly100621.1	Activin receptor type-1	GO:0007507,GO:0032924,GO:0042078,GO:0008101,GO:0035222,GO:0007300,GO:0030509,GO:0008358,GO:0007304,GO:0050829,GO:0001745,GO:0050431,GO:0001701,GO:0007368,GO:0007476,GO:0030707,GO:0004674,GO:0004672,GO:0016361,GO:0046872,GO:0048477,GO:0005524,GO:0006468,GO:0007015,GO:0007281,GO:0001655,GO:0005887,GO:0005886,GO:0001755,GO:0030514,GO:0030512,GO:0007179,GO:0048179,GO:0030718,GO:0009953,GO:0007448,GO:0045887,GO:0005025,GO:0045824,GO:0005515,GO:0004702	CG1891-PC																				
aly1007.1	Unknown	GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0008066,GO:0050907,GO:0004970	CG31718-PC										G3DSA:1.10.287.70	SSF53850									
aly1007.2	Lachesin	GO:0004714,GO:0005515,GO:0005886,GO:0007155,GO:0007169,GO:0031225	CG34391-PD				SM00409		PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly10073.1	Unknown		n/a																				
aly10073.2	Unknown		n/a																				
aly10073.3	Unknown		n/a																				
aly100804.1	Unknown		n/a																				
aly100860.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly100872.1	Unknown		n/a																				
aly100895.1	Unknown		n/a																				
aly10092.1	Unknown		n/a																				
aly10092.2	LMBR1 domain-containing protein 2 homolog	GO:0005575,GO:0003674,GO:0016021,GO:0008150	CG8135-PA						PF04791						561~581								
aly10092.3	Proteasome-associated protein ECM29 homolog	GO:0005737,GO:0005634,GO:0008150,GO:0005488,GO:0000502,GO:0003674	CG8858-PA										G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371	336~356								
aly1011.1	Unknown		n/a																				
aly1011.10	Unknown		n/a																				
aly1011.11	ATP-sensitive inward rectifier potassium channel 12	GO:0042391,GO:0071805,GO:0006813,GO:0015272,GO:0016021,GO:0051289,GO:0035220,GO:0045475,GO:0005886,GO:0005242,GO:0031224	CG44159-PF						PF01007		PR01320,PR01320,PR01320,PR01320,PR01320,PR01320		G3DSA:1.10.287.70,G3DSA:2.60.40.1400	SSF81324,SSF81296										
aly1011.12	Unknown		n/a																				
aly1011.13	Targeting protein for Xklp2 homolog	GO:0005737,GO:0007067,GO:0005819,GO:0005874,GO:0005634	n/a						PF12214,PF06886						347~367,445~488								
aly1011.2	Viral cathepsin	GO:0003674,GO:0035071,GO:0035220,GO:0045169,GO:0005575,GO:0048102,GO:0004197,GO:0008150,GO:0004869,GO:0006508,GO:0008234,GO:0022416	CG12163-PA				SM00848		PF08246				G3DSA:3.90.70.10	SSF54001										
aly1011.3	Viral cathepsin	GO:0008234	n/a				SM00848		PF08246				G3DSA:3.90.70.10	SSF54001										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1011.4	Sodium-independent sulfate anion transporter	GO:0045434,GO:0005794,GO:0005783,GO:0015301,GO:0016021,GO:0005886,GO:0015116,GO:0005765,GO:0008271,GO:0008272,GO:0008509,GO:0070062	CG7005-PA						PF00916														
aly1011.5	Serine/threonine-protein kinase ATR	GO:0009314,GO:0030261,GO:0004672,GO:0003677,GO:0000723,GO:0007126,GO:0000075,GO:0005634,GO:0007348,GO:0007349,GO:0000706,GO:0004674,GO:0016310,GO:0007088,GO:0048477,GO:0005524,GO:0033314,GO:0006468,GO:0006281,GO:0016301,GO:0016321,GO:0031000,GO:0006974,GO:0008360,GO:0001700,GO:0007133,GO:0007131,GO:0007015,GO:0000077,GO:0000076,GO:0045003,GO:0045002,GO:0007444,GO:0005515,GO:0007095,GO:0046983,GO:0007093	CG4252-PA				SM00802,SM00146		PF08064,PF02260,PF00454,PF02259	PS50290,PS51190,PS51189		PS00916	G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:3.30.1010.10,G3DSA:1.10.1070.11,G3DSA:1.10.1070.11	SSF56112,SSF56112	2461~2461								
aly1011.6	Unknown		n/a																				
aly1011.7	Hepatocyte growth factor-regulated tyrosine kinase substrate	GO:0008021,GO:0005770,GO:0008333,GO:0033619,GO:0042059,GO:0007298,GO:1990182,GO:0005737,GO:0006886,GO:0006887,GO:0033565,GO:0045743,GO:0031398,GO:0048471,GO:0046872,GO:0032509,GO:2000274,GO:0016082,GO:0016322,GO:0005938,GO:0007269,GO:0008593,GO:0016197,GO:0006897,GO:0051726,GO:0016079,GO:0016050,GO:0043130,GO:0045752,GO:0008293,GO:0001933,GO:0005768,GO:0005769	CG2903-PB				SM00288,SM00064		PF00790,PF01363,PF12210	PS50178,PS50179,PS50330			G3DSA:1.25.40.90,G3DSA:3.30.40.10	SSF48464,SSF57903	420~443,246~266,482~506								
aly1011.8	Inward rectifier potassium channel 2	GO:0042391,GO:0055119,GO:0014861,GO:0086002,GO:0051289,GO:0006813,GO:0090099,GO:0016021,GO:0090076,GO:0015467,GO:0035220,GO:0060306,GO:0015693,GO:0048812,GO:0005546,GO:0086008,GO:0010107,GO:0008076,GO:0005242,GO:0031224,GO:0086091	CG4370-PD			PIRSF005465			PF01007		PR01320,PR01320,PR01320,PR01320,PR01320,PR01320		G3DSA:2.60.40.1400,G3DSA:1.10.287.70	SSF81324,SSF81296									
aly1011.9	ATP-sensitive inward rectifier potassium channel 12	GO:0042391,GO:0071805,GO:0006813,GO:0090099,GO:0016021,GO:0051289,GO:0015467,GO:0035220,GO:0048812,GO:0005886,GO:0005242,GO:0031224	CG4370-PD						PF01007		PR01320,PR01320,PR01320,PR01320,PR01320,PR01320		G3DSA:2.60.40.1400,G3DSA:1.10.287.70	SSF81296,SSF81324									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1012.1	Unknown		n/a																				
aly1012.2	Probable cytochrome P450 9f2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0035220,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG11466-PA						PF00067		PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264	347~367		REACT_13433						
aly1012.3	Probable cytochrome P450 9f2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0035220,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG11466-PA						PF00067		PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly1012.4	Cytochrome P450 9b2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG4486-PA						PF00067				G3DSA:1.10.630.10	SSF48264	63~83		REACT_13433						
aly1012.5	Probable cytochrome P450 9f2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0035220,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG11466-PA										G3DSA:1.10.630.10				REACT_13433						
aly1012.6	Cytochrome P450 9e2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0035220,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG11466-PA						PF00067		PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264	218~238		REACT_13433						
aly10128.1	Hemicentin-2	GO:0005887,GO:0030425,GO:0030424,GO:0004872,GO:0008045,GO:0007411,GO:0030054,GO:0022409,GO:0003151,GO:0007432,GO:0031982,GO:0008406,GO:0071666,GO:0001964,GO:0005509,GO:0043025,GO:0031987,GO:0035385,GO:2000274,GO:0072499,GO:0035050,GO:0044295,GO:0008038,GO:0046716,GO:0009649,GO:0005886,GO:0008201,GO:0043234,GO:0007427,GO:0005604,GO:0050773,GO:0048854,GO:0050896,GO:0070983,GO:0016199,GO:0048813,GO:0005576,GO:0005515,GO:0005938	CG13521-PA				SM00409,SM00409,SM00409,SM00408,SM00409,SM00408,SM00408,SM00408		PF07679,PF07679,PF07679,PF07679	PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10128.2	Hemicentin-1	GO:0016319,GO:0005938,GO:0005604,GO:0070062,GO:0007601,GO:0050896,GO:0008406,GO:0008038,GO:0007419,GO:0008046,GO:0048036,GO:0005886,GO:0007411,GO:0030424,GO:0030054,GO:0005509	CG5423-PA				SM00408,SM00408,SM00409,SM00409		PF07679,PF07679	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly10128.3	Peroxidasin-like protein	GO:0005887,GO:0030425,GO:0030424,GO:0042744,GO:0004872,GO:0008045,GO:0007411,GO:0022409,GO:0003151,GO:0007432,GO:0031982,GO:0008406,GO:0006979,GO:0071666,GO:0001964,GO:0046872,GO:0043025,GO:0031987,GO:0035385,GO:0020037,GO:0200274,GO:0072499,GO:0035000,GO:0044295,GO:0008038,GO:0046716,GO:0009649,GO:0005886,GO:0008201,GO:0055114,GO:0005615,GO:0043234,GO:0007427,GO:0050773,GO:0048854,GO:0070983,GO:0016199,GO:0005737,GO:0048813,GO:0005515,GO:0004519,GO:0004601	CG13521-PA				SM00409,SM00408		PF07679	PS50835			G3DSA:2.60.40.10	SSF48726									
aly10128.4	Unknown		n/a																				
aly10128.5	Contactin-5	GO:0016319,GO:0048675,GO:0050808,GO:0045924,GO:0030175,GO:0008049,GO:0031225,GO:0005737,GO:0019991,GO:0048812,GO:0060857,GO:0005509,GO:0008366,GO:0035151,GO:0016328,GO:0007605,GO:0072499,GO:0035011,GO:0008050,GO:0007173,GO:0048036,GO:0007409,GO:0005886,GO:0007155,GO:0005919,GO:0005918,GO:0007560,GO:0048813,GO:0061343,GO:0005515,GO:0021682,GO:0007158	CG1634-PG							PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726									
aly10129.1	Unknown		n/a																				
aly1014.1	Unknown		CG7518-PH												123~167,24~44,77~1								
aly1014.2	Bromodomain-containing protein 8	GO:0043967,GO:0043968,GO:0040008,GO:0005739,GO:0000812,GO:0005654,GO:0006355,GO:0010629,GO:0035267,GO:0005515,GO:0006351	CG14514-PA				SM00297		PF00439	PS50014	PR00503,PR00503,PR00503,PR00503		G3DSA:1.20.920.10	SSF47370	104~124								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1014.3	Unknown	GO:0005634,GO:0008270,GO:0003676	n/a				SM00451,SM00451,SM00451,SM00451,SM00451,SM00451,SM00451,SM00451,SM00451			PS50171				SSF57667									
aly1014.4	Unknown		n/a										G3DSA:3.30.60.30										
aly1014.5	Protein prune homolog	GO:0005737,GO:0046872,GO:0004427,GO:0019889,GO:0005634,GO:0030145,GO:0048072,GO:0016462,GO:0004309,GO:0005925,GO:0006798	CG3461-PA						PF01368				G3DSA:3.90.1640.10	SSF64182		00190+3.6.1.1							
aly1014.6	Solute carrier family 2, facilitated glucose transporter member 1	GO:0005355,GO:0042470,GO:0016021,GO:0006461,GO:0030864,GO:0015758,GO:0005887,GO:0055085,GO:0043621	CG43946-PP					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171,PR00171,PR00171	PS00216,PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473			REACT_15518						
aly1014.7	Zinc finger and BTB domain-containing protein 24	GO:0003700,GO:0005634,GO:0006355,GO:0002244,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG2129-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028		SSF57667,SSF57667									
aly1014.8	Unknown		n/a																				
aly101417.1	Unknown		n/a																				
aly101542.1	Cytoplasmic FMR1-interacting protein	GO:0005737,GO:0045177,GO:0006909,GO:0000902,GO:0033627,GO:0030031,GO:0050807,GO:0030866,GO:0017048,GO:0008360,GO:0045202,GO:0007411,GO:0001745,GO:0022416,GO:0031209	CG4931-PA						PF07159		PR01698,PR01698												
aly1016.1	Neuroligin-4, Y-linked	GO:0042043,GO:0071625,GO:0035176,GO:0009986,GO:0007612,GO:0052689,GO:0097110,GO:0045211,GO:0050808,GO:0030054,GO:0045202,GO:0005887,GO:0004872,GO:0014069,GO:0007158,GO:0050839,GO:0051932,GO:0007416,GO:0030431	CG34139-PD						PF00135			PS00941	G3DSA:3.40.50.1820	SSF53474									
aly10178.1	Fructose-bisphosphate aldolase	GO:0031430,GO:0007498,GO:0005829,GO:0004332,GO:0007095,GO:0006096,GO:0030018	CG6058-PE						PF00274			PS00158	G3DSA:3.20.20.70	SSF51569		00030+4.1.2.13,00710+4.1.2.13,00010+4.1.2.13,00051+4.	REACT_474	PWY-1042,PWY-6142,PWY-5484,PWY-1861,PWY-7385	UPA00109				
aly1018.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1018.10	Unknown		n/a																				
aly1018.11	Unknown		n/a												444~468								
aly1018.12	Nuclear receptor-binding protein homolog	GO:0042127,GO:0005794,GO:0006468,GO:0006888,GO:0009306,GO:0005829,GO:0004674,GO:0008361,GO:0005938,GO:0004672,GO:0042803,GO:0005524,GO:0012505	CG1098-PA						PF00069	PS50011			G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly1018.13	Somatostatin receptor type 2	GO:0005887,GO:0005886,GO:0071385,GO:0042594,GO:0008188,GO:0005737,GO:0004930,GO:0016021,GO:0016020,GO:0042923,GO:0043005,GO:0004994,GO:0007186,GO:0008285,GO:0006937,GO:0071392,GO:0007218,GO:0038170,GO:0007283,GO:0030165,GO:0030432,GO:0008261,GO:0021549,GO:0030900,GO:0007193	CG13702-PD						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00246,PR00246,PR00246,PR00246	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1018.14	Brahma-associated protein of 60 kDa	GO:0035060,GO:0001085,GO:0007517,GO:0048666,GO:0031453,GO:0006357,GO:0005634,GO:0006366,GO:0003713,GO:0017022,GO:0048813,GO:0010628,GO:0045944,GO:0045893,GO:0005515,GO:0003677,GO:0005719,GO:0008134	CG4303-PA				SM00151		PF02201				G3DSA:1.10.245.10	SSF47592									
aly1018.15	Aquaporin-4	GO:0005737,GO:0009992,GO:0070295,GO:0005887,GO:0009897,GO:0007605,GO:0016021,GO:0071346,GO:0006833,GO:0016323,GO:0015250,GO:0034220,GO:0015267,GO:0003014,GO:0015254,GO:0005911,GO:0015793,GO:0030104,GO:0005886,GO:0055085	CG17664-PC						PF00230		PR00783,PR00783,PR00783,PR00783	PS00221	G3DSA:1.20.1080.10	SSF81338									
aly1018.16	Ubiquitin-conjugating enzyme E2 S	GO:0010458,GO:0016874,GO:0007476,GO:0031145,GO:0016567,GO:0051301,GO:0004842,GO:0005524	CG8188-PA				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				
aly1018.17	Unknown		n/a																				
aly1018.18	Unknown		n/a																				
aly1018.2	60S ribosomal protein L30	GO:0040007,GO:0022625,GO:0007422,GO:0003735,GO:0007052,GO:0005840,GO:0000022,GO:0006412,GO:0051298	CG10652-PE						PF01248			PS00709	G3DSA:3.30.1330.30	SSF55315									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1018.3	Unknown		n/a																				
aly1018.4	Protein tiptop	GO:0048749,GO:0061330,GO:0000122,GO:0003700,GO:0005634,GO:0006355,GO:0007380,GO:0008270,GO:0003677,GO:0048730,GO:0046872,GO:0006351	CG12630-PA				SM00355,SM00355,SM00355,SM00355		PF12756,PF12756,PF13912	PS50157,PS50157		PS00028,PS00028,PS00028,PS00028											
aly1018.5	Unknown		n/a																				
aly1018.6	Zinc finger protein 37 homolog	GO:0003700,GO:0005634,GO:0005811,GO:0006355,GO:0046331,GO:0006351,GO:0003676,GO:0003677,GO:0046872,GO:0008270	CG31612-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00451,SM00451,SM00451,SM00451			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667	868~868								
aly1018.7	Zinc finger protein 407	GO:0005634,GO:0005811,GO:0006355,GO:0046331,GO:0006351,GO:0003676,GO:0003677,GO:0046872,GO:0008270	CG31612-PA				SM00355,SM00355,SM00355		PF13909,PF13909	PS50157,PS50157		PS00028	G3DSA:3.30.160.60	SSF57667									
aly1018.8	Ankyrin repeat domain-containing protein 29	GO:0005515	CG3104-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796	PS50088,PS50088,PS50088,PS50088,PS50088,PS50297	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403									
aly1018.9	Lymphokine-activated killer T-cell-originated protein kinase	GO:0018107,GO:0006468,GO:0018105,GO:0032435,GO:0004672,GO:0050728,GO:0032873,GO:0004674,GO:0034644,GO:0001933,GO:0005524	CG8173-PA				SM00220		PF00069	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly101847.1	Unknown		n/a																				
aly10189.1	Nuclear envelope integral membrane protein 1a		CG9723-PA						PF10225														
aly1019.1	Sodium-coupled monocarboxylate transporter 2	GO:0006810,GO:0016021,GO:0070062,GO:0015129,GO:0016324,GO:0005215,GO:0008523,GO:0016020,GO:0035873,GO:0006814,GO:0051780,GO:0015293,GO:0008343,GO:0055085	CG8451-PA						PF00474,PF00474	PS50283													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1019.10	Probable ATP-dependent RNA helicase DDX5	GO:0008026,GO:0050681,GO:0009299,GO:0003676,GO:2001014,GO:0005875,GO:0072332,GO:0036002,GO:0001701,GO:0016049,GO:0070062,GO:0005730,GO:0005634,GO:0016020,GO:0003713,GO:0030529,GO:0005654,GO:0045667,GO:0010501,GO:0044822,GO:0005524,GO:0007623,GO:0033031,GO:0071013,GO:0033148,GO:0004004,GO:0000381,GO:0043517,GO:0060765,GO:0045069,GO:0000122,GO:0000398,GO:0003724,GO:0045944	CG10077-PA				SM00490,SM00487		PF00271,PF00270	PS51192,PS51194,PS51195		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									
aly1019.11	Polycomb protein Asx	GO:0007469,GO:0006351,GO:2000158,GO:0046872,GO:0035186,GO:0006342,GO:0005634,GO:0001709,GO:0007475,GO:2000152,GO:0045498,GO:0000785,GO:0045893,GO:0035522,GO:0045892,GO:0035800,GO:0003682,GO:0003677,GO:0010468,GO:0035517	CG8787-PC						PF13919,PF13922														
aly1019.12	Abhydrolase domain-containing protein 2	GO:0006629,GO:0016021,GO:0035220,GO:0022416,GO:0052689,GO:0016298	CG3488-PA			PIRSF005211			PF00561			PS01133	G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474									
aly1019.13	Plexin-B	GO:0016021,GO:0016020,GO:0005622,GO:0035025,GO:0007165,GO:0005515,GO:0008045,GO:0007411,GO:0005886,GO:0017154,GO:0071678,GO:0035021	CG17245-PA				SM00423,SM00423,SM00423,SM00630,SM00429,SM00429,SM00429,SM00429		PF01833,PF01833,PF01833,PF01833,PF01437,PF08337,PF01403	PS51004			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.30.1680.10,G3DSA:2.130.10.10,G3DSA:3.30.1680.10,G3DSA:2.60.40.10,G3DSA:3.10.20.90	SSF81296,SSF103575,SSF81296,SSF48350,SSF48350,SSF101912,SSF81296,SSF81296	1279~1299		REACT_18266						
aly1019.14	Transformation/transcription domain-associated protein	GO:0006909,GO:0016310,GO:0035222,GO:0003712,GO:0005488,GO:0005875,GO:0005737,GO:0000124,GO:0000123,GO:0033276,GO:0006325,GO:0005634,GO:0043967,GO:0003713,GO:0000281,GO:0030914,GO:0005654,GO:0045747,GO:0016573,GO:0004672,GO:0016578,GO:0005794,GO:0006281,GO:0043968,GO:0016301,GO:0000125,GO:0016773,GO:0005703,GO:0005700,GO:0000812,GO:0006355,GO:0006351,GO:0007093,GO:0035267	CG33554-PE				SM00146		PF00454,PF02259	PS51190,PS50290,PS51189			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.10.1070.11,G3DSA:1.10.1070.11	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48452,SSF48452,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF56112,SSF56112,SSF48371,SSF48371,SSF48371,SSF48371									
aly1019.15	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1019.16	Fibronectin type-III domain-containing protein 3a	GO:0016021,GO:0000139,GO:0005575,GO:0003674,GO:0005515,GO:0008150	CG42389-PE				SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060		PF00041,PF00041,PF00041,PF00041,PF00041	PS50853,PS50853,PS50853,PS50853,PS50853,PS50853,PS50853,PS50853	PR00014,PR00014,PR00014,PR00014		G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF49265,SSF49265,SSF49265,SSF49265,SSF49265,SSF49265	203~226									
aly1019.17	Protein eyes shut	GO:0005201,GO:0000902,GO:0005615,GO:0009986,GO:0010378,GO:0031513,GO:0005576,GO:0005509,GO:0005515,GO:0005886,GO:0016021,GO:0042052	CG33955-PE				SM00282,SM00282,SM00282,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179		PF02210,PF02210,PF02210,PF00008,PF00008,PF00008,PF00008,PF00008	PS50026,PS50026,PS50026,PS50026,PS50025,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50025	PR00010,PR00010,PR00010,PR00010	PS00022,PS00022,PS01186,PS00022,PS01187,PS00022,PS01187,PS00010,PS00022,PS00022,PS00022,PS00010,PS00022,PS00010,PS00022,PS01186,PS01186,PS01186,PS01186,PS00022,PS00010,PS00022,PS01187,PS00022,PS01186,PS00022,PS00010,PS01187	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.170.300.10	SSF57196,SSF57196,SSF57196,SSF57196,SSF49899,SSF57196,SSF57196,SSF57196,SSF49899,SSF57196									
aly1019.18	MKRN2 opposite strand protein		CG9967-PB						PF16044														
aly1019.19	Putative defense protein Hdd11 like	GO:0004252,GO:0045087,GO:0042832,GO:0042742,GO:0005576	CG7532-PA						PF02014	PS51019													
aly1019.2	Leucine-rich repeat-containing protein 43	GO:0016021,GO:0005886,GO:0006952,GO:0004888,GO:0007165,GO:0005515,GO:0048935,GO:0002227,GO:0060049	CG6890-PA							PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									
aly1019.20	Transcription elongation factor S-II	GO:0005634,GO:0032784,GO:0006355,GO:0006357,GO:0006351,GO:0003676,GO:0003677,GO:0006368,GO:0008270	CG3710-PA			PIRSF006704	SM00509,SM00440,SM00510	TIGR01385	PF01096,PF08711,PF07500	PS51321,PS51133,PS51319		PS00466	G3DSA:2.20.25.10,G3DSA:1.20.930.10,G3DSA:1.10.472.30	SSF46942,SSF47676,SSF57783									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1019.21	Zinc finger protein 91	GO:0003700,GO:0005634,GO:0003677,GO:0035220,GO:0022416,GO:0045892,GO:0006351,GO:0070895,GO:0046872,GO:0008270	CG9932-PA				SM00355,SM00355		PF13909,PF13909,PF13909,PF13909,PF13909,PF13909,PF13909	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	130~150								
aly1019.22	Unknown		n/a																				
aly1019.23	Unknown		n/a																				
aly1019.24	Unknown	GO:0030246	CG3244-PA				SM00034			PS50041		PS00615	G3DSA:3.10.100.10	SSF56436									
aly1019.25	NHL repeat-containing protein 2	GO:0005515	CG12547-PA						PF01436,PF01436,PF13905	PS51125,PS51125,PS51352,PS51125			G3DSA:3.40.30.10,G3DSA:2.120.10.30	SSF52833,SSF101898									
aly1019.26	Cysteine protease ATG4B	GO:0005737,GO:0006995,GO:0005829,GO:0000422,GO:0004175,GO:0006914,GO:0006612,GO:0044804,GO:0000045,GO:0006501,GO:0010508,GO:0004197,GO:0016485,GO:0006508,GO:0008233,GO:0010506,GO:0008234,GO:0051697	CG4428-PA						PF03416					SSF54001									
aly1019.27	Protein phosphatase 1L	GO:0030148,GO:0070062,GO:0006470,GO:0016021,GO:0000165,GO:0004722,GO:0005789,GO:0003824,GO:0008360,GO:0044281,GO:0007155,GO:0046872,GO:0006665,GO:0007178	CG7115-PA				SM00332		PF00481,PF00481	PS51746		PS01032	G3DSA:3.60.40.10,G3DSA:3.60.40.10	SSF81606,SSF81606									
aly1019.28	Dedicator of cytokinesis protein 9	GO:0005089,GO:0043547,GO:0016020,GO:0017048,GO:0005622,GO:0005575,GO:0012505,GO:0035023,GO:0007264	CG42533-PK						PF06920	PS51651													
aly1019.29	Dedicator of cytokinesis protein 9	GO:0005089,GO:0016020,GO:0005829,GO:0007596,GO:0005575,GO:0012505,GO:0035023,GO:0007264	CG42533-PK				SM00233		PF14429,PF06920,PF11878,PF00169	PS50003,PS51650			G3DSA:2.30.29.30	SSF50729									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1019.3	Sodium- and chloride-dependent glycine transporter 1	GO:0005328,GO:0007287,GO:0016007,GO:0005283,GO:0016021,GO:0016020,GO:0016006,GO:0005739,GO:0007291,GO:0005326,GO:0006836,GO:0005887,GO:0015187,GO:0030317,GO:0005634	CG7075-PA						PF00209	PS50267	PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176	PS00610		SSF161070									
aly1019.30	Tyrosine-protein kinase transmembrane receptor Ror	GO:0000186,GO:0048565,GO:0042051,GO:0007498,GO:0018108,GO:0007169,GO:0007411,GO:0090328,GO:0007417,GO:0040008,GO:0004716,GO:0004714,GO:0004713,GO:0071212,GO:0005524,GO:0006468,GO:0043410,GO:0061177,GO:0061176,GO:0005886,GO:0007522,GO:0045792,GO:1900074,GO:0070374,GO:0045610,GO:0016021	CG8250-PA				SM00219		PF07714	PS50011		PS00107	G3DSA:3.30.200.20	SSF56112									
aly1019.31	Unknown	GO:0016021	CG18635-PA						PF09815														
aly1019.32	Mitochondrial assembly of ribosomal large subunit protein 1	GO:0005737,GO:0042273,GO:0070130,GO:0090071,GO:0005739,GO:0005575,GO:0003674,GO:0017148,GO:0005759,GO:0008150,GO:0043023	CG9166-PA	MF_01477				TIGR00090	PF02410				G3DSA:3.30.460.10	SSF81301									
aly1019.33	Cyclin-Y-like protein 1	GO:0019901,GO:0000079,GO:0048589	CG14939-PA				SM00385		PF00134				G3DSA:1.10.472.10	SSF47954									
aly1019.34	Apoptotic chromatin condensation inducer in the nucleus	GO:0061574,GO:0003676,GO:0006921,GO:0019899,GO:0098779,GO:0030263,GO:0016887,GO:0048025,GO:0005737,GO:0043065,GO:0005730,GO:0005634,GO:0000166,GO:0005654,GO:0030218,GO:0010506,GO:0008380,GO:0016607,GO:0071011,GO:0071013,GO:0006915,GO:0044822,GO:0006622,GO:0012501,GO:0005886,GO:0005829,GO:0000398,GO:0045657,GO:0002230,GO:0005515,GO:0006397	CG10473-PA						PF13893,PF16294	PS50102			G3DSA:3.30.70.330	SSF54928	741~761								
aly1019.35	Venom dipeptidyl peptidase 4	GO:0004177,GO:0016020,GO:0008239,GO:0005576,GO:0006508,GO:0008236	CG11034-PB						PF00326,PF00930				G3DSA:2.140.10.30,G3DSA:3.40.50.1820	SSF53474,SSF82171									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1019.36	Venom dipeptidyl peptidase 4	GO:0004177,GO:0016020,GO:0008239,GO:0005576,GO:0006508,GO:0008236	CG11034-PB						PF00326,PF01593,PF00930				G3DSA:3.40.50.1820,G3DSA:3.90.660.10,G3DSA:3.50.50.60,G3DSA:2.140.10.30	SSF54373,SSF82171,SSF53474,SSF51905,SSF51905										
aly1019.37	Unknown		n/a										G3DSA:3.30.40.10	SSF57903	136~187								
aly1019.38	Unknown		n/a																				
aly1019.39	Venom acid phosphatase Acph-1	GO:0005576,GO:0003993	CG7899-PB						PF00328				G3DSA:3.40.50.1240	SSF53254									
aly1019.4	Unknown		n/a																				
aly1019.40	Prostatic acid phosphatase	GO:0052642,GO:0051930,GO:0016791,GO:0005615,GO:0060168,GO:0016311,GO:0042131,GO:0016021,GO:0008253,GO:0006144,GO:0030175,GO:0005765,GO:0009117,GO:0012506,GO:0005886,GO:0006772,GO:0005634,GO:0046085,GO:0003993,GO:0070062	CG7899-PB						PF00328				G3DSA:3.40.50.1240	SSF53254									
aly1019.41	Venom acid phosphatase Acph-1	GO:0005576,GO:0003993	CG7899-PB						PF00328				G3DSA:3.40.50.1240	SSF53254									
aly1019.5	Unknown		CG7196-PA												47~67								
aly1019.6	Uricase	GO:0005777,GO:0019628,GO:0004846,GO:0019428,GO:0006144,GO:0055114	CG7171-PA			PIRSF000241		TIGR03383	PF01014,PF01014		PR00093,PR00093,PR00093,PR00093,PR00093	PS00366	G3DSA:3.10.270.10	SSF55620,SSF55620		00230+1.7.3.3,00232+1.7.3.3		PWY-5691	UPA00394				
aly1019.7	MAGUK p55 subfamily member 6	GO:0035151,GO:0019991,GO:0016328,GO:0070062,GO:0007424,GO:0035159,GO:0016021,GO:0016020,GO:0004385,GO:0046939,GO:0035001,GO:0005886,GO:0005918	CG9326-PB				SM00326,SM00228,SM00072		PF07653,PF00625,PF00595	PS50002,PS50106,PS50052		PS00856	G3DSA:3.30.63.10,G3DSA:2.30.30.40,G3DSA:2.30.42.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF50044,SSF50156		00230+2.7.4.8		PWY-7221					
aly1019.8	Tubulin polyglutamylase complex subunit 2	GO:0005737,GO:0005874	CG6931-PA																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1019.9	tRNA-dihydrouridine (47) synthase [NAD(P)(+)]-like	GO:0017150,GO:0046872,GO:0050660,GO:0008033,GO:0055114	CG10463-PA						PF01207	PS50103,PS50103		PS01136	G3DSA:3.20.20.70	SSF51395									
aly102.1	Hemocytin	GO:0007599,GO:0042381,GO:0008270,GO:0030246,GO:0042060,GO:0005576,GO:0035006,GO:0008061,GO:0003676,GO:0007155,GO:0006030,GO:0042803	CG7002-PA				SM00832,SM00832,SM00216		PF08742,PF08742,PF00094,PF00094	PS51233,PS51233			G3DSA:2.10.25.10	SSF57567									
aly102.10	Sesquipedalian 1	GO:0007032,GO:0055037,GO:0005802,GO:0042147,GO:0030136,GO:0001881,GO:0005769,GO:0042803	CG12393-PB				SM00233		PF00169	PS50003			G3DSA:2.30.29.30	SSF50729	112~139								
aly102.11	Unknown	GO:0003676	n/a				SM00980,SM00692		PF12017,PF05485	PS50950				SSF57716									
aly102.12	Mediator of RNA polymerase II transcription subunit 13	GO:0048749,GO:0004252,GO:0045165,GO:0048190,GO:0045498,GO:0005634,GO:0005654,GO:0036011,GO:0006367,GO:0001104,GO:0009790,GO:0030177,GO:0006357,GO:0007526,GO:0005515,GO:0006366,GO:0016592,GO:0022416	CG9936-PE						PF11597,PF06333,PF06333														
aly102.13	39S ribosomal protein L50, mitochondrial	GO:0003735,GO:0005762,GO:0032543,GO:0005739,GO:0005840	CG8612-PA						PF10501														
aly102.14	Unknown		CG14967-PB																				
aly102.15	Protein KIAA0100	GO:0005576	CG14967-PB						PF10351,PF10347,PF10293						1014~1034,285~312								
aly102.16	Protein KIAA0100	GO:0005576	CG14967-PB						PF10351														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly102.17	Integrin alpha-PS2	GO:0007494,GO:0050840,GO:0035160,GO:0007160,GO:0004872,GO:0007411,GO:0007298,GO:0005925,GO:0007414,GO:0007157,GO:0007435,GO:0007431,GO:0034446,GO:0007476,GO:0051492,GO:0007475,GO:0009925,GO:0016477,GO:0033627,GO:0016203,GO:0042383,GO:0007608,GO:0030239,GO:0016324,GO:0016328,GO:0008305,GO:0045185,GO:0008360,GO:0045214,GO:0005887,GO:0005886,GO:0007155,GO:0016337,GO:0050839,GO:0035099,GO:0021551,GO:0007427,GO:0007426,GO:0007229,GO:0046982	CG9623-PB				SM00191,SM00191,SM00191,SM00191,SM00191		PF08441,PF01839,PF01839	PS51470,PS51470,PS51470,PS51470,PS51470,PS51470,PS51470	PR01185,PR01185,PR01185,PR01185,PR01185,PR01185,PR01185		G3DSA:2.60.40.1460,G3DSA:2.60.40.1510,G3DSA:2.130.10.130,G3DSA:1.20.5.930,G3DSA:2.60.40.1530,G3DSA:2.60.40.1530	SSF69318,SSF69179,SSF69179,SSF69179,SSF69179			REACT_13552							
aly102.18	Unknown		n/a																				
aly102.19	Beta-1,3-glucosyltransferase	GO:0006486,GO:0016021,GO:0016020,GO:0005789,GO:0016757,GO:0006004	CG9109-PC						PF02434														
aly102.2	Hemocytin	GO:0007599,GO:0042381,GO:0008270,GO:0030246,GO:0042060,GO:0005576,GO:0035006,GO:0008061,GO:0003676,GO:0007155,GO:0006030,GO:0042803	CG7002-PA				SM00215,SM00215,SM00216,SM00216,SM00216,SM00231,SM00231,SM00494,SM00494,SM00181,SM00181,SM00181,SM00181,SM00832,SM00832,SM00832		PF08742,PF08742,PF08742,PF13330,PF00094,PF00094,PF00094,PF01826,PF01826,PF01826,PF01826,PF01826,PF00754,PF00754	PS51233,PS50022,PS50026,PS51233,PS51233,PS50026,PS50940,PS50022		PS00022,PS01285,PS00022	G3DSA:2.60.120.260,G3DSA:2.60.120.260,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10	SSF57196,SSF49785,SSF57625,SSF57567,SSF57567,SSF49785,SSF57567										
aly102.20	Peroxisomal acyl-coenzyme A oxidase 3	GO:0050660,GO:0006909,GO:0006635,GO:0016020,GO:0005777,GO:0005102,GO:0005739,GO:0033540,GO:0044281,GO:0016402,GO:0003995,GO:0005782,GO:0003997,GO:0044255,GO:0055114	CG9527-PB						PF02770,PF01756				G3DSA:1.20.140.10,G3DSA:2.40.110.10,G3DSA:1.20.140.10	SSF47203,SSF56645,SSF47203	658~658	00071+1.3.3.6,00592+1.3.3.6		PWY-6920,PWY-7291,PWY-7340,PWY-7606,PWY-7338,PWY-6837,PWY-735,PWY-5136,PWY-7007,PWY-					
aly102.21	Glutamate receptor ionotropic, delta-2	GO:0045211,GO:0009593,GO:0008328,GO:0035235,GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0034220,GO:0030054,GO:0005886,GO:0030425,GO:0035249,GO:0004970	CG6185-PA				SM00918		PF00060,PF10613				G3DSA:3.40.190.10,G3DSA:1.10.287.70	SSF53850,SSF53850,SSF53850										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly102.22	Aurora kinase A	GO:0008105,GO:0031647,GO:0032436,GO:0000212,GO:0032355,GO:0007279,GO:0000226,GO:0031616,GO:0007067,GO:0051301,GO:0000278,GO:0050767,GO:0007100,GO:0072686,GO:0051233,GO:1990138,GO:0009948,GO:0005813,GO:0005634,GO:0005815,GO:0043146,GO:0004674,GO:0043066,GO:0004712,GO:0005876,GO:0004672,GO:0032465,GO:0071539,GO:0048471,GO:0032133,GO:0035174,GO:0005524,GO:0006468,GO:0015630,GO:0051299,GO:0051298,GO:0032091,GO:0051294,GO:0051297,GO:0007126,GO:0043203,GO:0019901,GO:0035404,GO:0031625,GO:0042585,GO:0007057,GO:0051642,GO:0045167,GO:0007017,GO:0000780,GO:0045120,GO:1900195,GO:0007052,GO:0072687,GO:000709	CG3068-PA				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112										
aly102.23	RWD domain-containing protein 4	GO:0005515	CG10343-PA				SM00591		PF05773	PS50908			G3DSA:3.10.110.10	SSF54495									
aly102.24	Cytochrome b5 domain-containing protein 1	GO:0046872,GO:0046331,GO:0020037	CG15429-PA						PF00173				G3DSA:3.10.120.10,G3DSA:3.10.120.10	SSF55856									
aly102.25	TNF receptor-associated factor 4	GO:0030323,GO:0006909,GO:0019901,GO:0034332,GO:0005164,GO:0003384,GO:0009790,GO:0008270,GO:0008063,GO:0050829,GO:0042981,GO:0005923,GO:0002168,GO:0005737,GO:0045177,GO:0007250,GO:0005634,GO:0050699,GO:0045179,GO:0043065,GO:0048471,GO:0046529,GO:0005856,GO:0007585,GO:0035071,GO:0007370,GO:0006915,GO:0006952,GO:0046330,GO:0001654,GO:0005886,GO:0004842,GO:0045167,GO:0031625,GO:0031996,GO:0048102,GO:0090073,GO:0007391,GO:001656	CG3048-PA				SM00061		PF02176	PS50145,PS50144,PS50145			G3DSA:2.60.210.10,G3DSA:3.90.890.10	SSF49599,SSF49599,SSF49599										
aly102.26	Probable DNA replication complex GINS protein PSF2	GO:0000727,GO:0032784,GO:0006271,GO:0000811,GO:0030261,GO:0031298,GO:0046331,GO:1902975,GO:0022008,GO:0043138,GO:0032508,GO:0005634,GO:1900087	CG18013-PB			PIRSF028998			PF05916					SSF160059,SSF158573										
aly102.27	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly102.28	Leucine-rich repeat-containing protein 74A	GO:0005737,GO:0005098,GO:0006611,GO:0045132,GO:0006913,GO:0032853,GO:0048471,GO:0022008	CG9999-PA				SM00368,SM00368,SM00368,SM00368						G3DSA:3.80.10.10	SSF52047										
aly102.29	Leucine-rich repeat-containing protein 74A	GO:0005737,GO:0005098,GO:0006611,GO:0045132,GO:0006913,GO:0032853,GO:0048471,GO:0022008	CG9999-PA				SM00368,SM00368,SM00368,SM00368						G3DSA:3.80.10.10	SSF52047										
aly102.3	Tumor protein p63-regulated gene 1-like protein	GO:0008021,GO:0070062,GO:0030054	n/a						PF12456														
aly102.30	Unknown		n/a																				
aly102.4	Unknown	GO:0019028	CG42749-PD						PF03067														
aly102.5	Sin3 histone deacetylase corepressor complex component SDS3	GO:0005737,GO:0070822,GO:0016580,GO:0000122,GO:0005634,GO:0006915,GO:0019899,GO:0016575,GO:0043065,GO:0045892,GO:0006351,GO:0042826,GO:0042802,GO:0042803	CG14220-PA						PF08598						75~95,134~176								
aly102.6	F-BAR domain only protein 2	GO:0005737,GO:0072659,GO:0035091,GO:0005543,GO:0072583,GO:0010324,GO:0048268,GO:0005905,GO:0005886,GO:0035612,GO:0043009,GO:0005546,GO:0001786	CG8176-PC				SM00055		PF10291,PF00611	PS51741,PS51072				SSF49447,SSF103657	430~450,160~180,187~214									
aly102.7	SH3 domain-binding protein 5 homolog	GO:0005737,GO:0007517,GO:0009952,GO:0007498,GO:0017124,GO:0004860,GO:0012501,GO:0035556,GO:0005886,GO:0061099,GO:0030292,GO:0048644,GO:0042694	CG7761-PB						PF05276						302~325,22~49,186~213								
aly102.8	Peroxisomal acyl-coenzyme A oxidase 3	GO:0050660,GO:0005782,GO:0006635,GO:0016627,GO:0016020,GO:0005777,GO:0005102,GO:0005739,GO:0033540,GO:0044281,GO:0016402,GO:0003995,GO:0003997,GO:0044255,GO:0055114	CG17544-PA			PIRSF000168			PF00441,PF01756,PF02770				G3DSA:2.40.110.10,G3DSA:1.20.140.10,G3DSA:1.20.140.10	SSF47203,SSF47203,SSF56645		00071+1.3.3.6,00592+1.3.3.6		PWY-6920,PWY-7291,PWY-7340,PWY-7606,PWY-7338,PWY-6837,PWY-735,PWY-5136,PWY-					
aly102.9	Protein outspread	GO:0005575,GO:0008150,GO:0003674	CG3479-PF				SM00233,SM00233		PF00169,PF00169	PS50003,PS50003			G3DSA:2.30.29.30,G3DSA:2.30.29.30	SSF50729,SSF50729	929~956,1791~1833,1670~1736,894~914,8								
aly1020.1	Unknown		n/a																				
aly1020.10	Unknown		n/a												186~206								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1020.2	Unknown		n/a																				
aly1020.3	Unknown		n/a																				
aly1020.4	40S ribosomal protein SA	GO:0000028,GO:0005840,GO:0030686,GO:0005875,GO:0003735,GO:0000461,GO:0007052,GO:0015935,GO:0000447,GO:0000022,GO:0043022,GO:0022627,GO:0006412,GO:0006407	CG14792-PA	MF_03015				TIGR01012	PF00318,PF00318		PR00395,PR00395,PR00395,PR00395,PR00395,PR00395	PS00962,PS00963	G3DSA:3.40.50.10490	SSF52313									
aly1020.5	Protein E(sev)2B	GO:0007614,GO:0007613,GO:0004871,GO:0038202,GO:0008355,GO:0005070,GO:0001700,GO:0045500,GO:0009967,GO:0007476,GO:0005118,GO:0043410,GO:0008595,GO:0007175,GO:0008360,GO:0005886,GO:0007265,GO:0007015,GO:0008306,GO:0005515,GO:0008293,GO:0045678	CG6033-PC				SM00252,SM00326,SM00326		PF14604,PF00017,PF00018	PS50002,PS50001,PS50002	PR00499,PR00499,PR00499,PR00499,PR00452,PR00452,PR00452,PR00452,PR00401,PR00401,PR00401,PR00401		G3DSA:2.30.30.40,G3DSA:3.30.505.10,G3DSA:2.30.30.40	SSF50044,SSF50044,SSF55550										
aly1020.6	Mitochondrial uncoupling protein 4	GO:0035356,GO:0044281,GO:0006091,GO:0051562,GO:0045177,GO:0015992,GO:0070997,GO:0016021,GO:0005740,GO:0005739,GO:0043066,GO:0022904,GO:0017077,GO:0043025,GO:0008284,GO:0010917,GO:0006839,GO:0048839,GO:0044237,GO:0005743,GO:0022857,GO:0046324	CG6492-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly1020.7	Unknown	GO:0048749,GO:0005634,GO:0022416,GO:0035220	CG2446-PB																				
aly1020.8	Protein asunder	GO:0005737,GO:0007346,GO:0030317,GO:0051321,GO:0034472,GO:0048471,GO:0005634,GO:0030154,GO:0032039,GO:0080154,GO:0007283,GO:0003674,GO:0007067,GO:0051642,GO:0007275,GO:0051301	CG6814-PA						PF10221														
aly1020.9	Ubiquitin carboxyl-terminal hydrolase 7	GO:0007275,GO:0005737,GO:0016605,GO:0006342,GO:0005634,GO:0043065,GO:0006511,GO:0016579,GO:0016578,GO:0042803,GO:0010216,GO:0006283,GO:0061136,GO:0035328,GO:0004843,GO:0043234,GO:0051090,GO:0031647,GO:0005700,GO:0006355,GO:0004197,GO:0043161	CG1490-PB				SM00061		PF00917,PF14533,PF12436,PF00443	PS50235,PS50144		PS00973,PS00972	G3DSA:2.60.210.10,G3DSA:2.20.210.10	SSF54001,SSF49599	1206~1207									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10202.1	Venom serine protease Bi-VSP	GO:0004252,GO:0045087,GO:0006952,GO:0050830,GO:0005576,GO:0045752,GO:0016504,GO:0006508	CG5896-PB				SM00680		PF12032,PF00089			PS00134	G3DSA:2.40.10.10	SSF50494									
aly10202.2	Unknown		n/a																				
aly102139.1	Cell death specification protein 2	GO:0043565,GO:0003700,GO:0005634,GO:0006915,GO:0001012,GO:0006355,GO:0006351,GO:0043068,GO:0042803	CG7786-PA				SM00338		PF07716	PS50217			G3DSA:1.20.5.170	SSF57959									
aly1022.1	Dual 3',5'-cyclic-AMP and -GMP phosphodiesterase 11	GO:0046058,GO:0047555,GO:0004115,GO:0005829,GO:0005575,GO:0046331,GO:0007165,GO:0046068,GO:0046872	CG34341-PF				SM00065,SM00065,SM00471		PF00233,PF01590,PF01590		PR00387,PR00387,PR00387,PR00387,PR00387,PR00387	PS00126	G3DSA:3.30.450.40,G3DSA:3.30.450.40,G3DSA:1.10.1300.10	SSF55781,SSF55781,SSF109604									
aly1022.2	Unknown		n/a																				
aly1022.3	Long-chain-fatty-acid--CoA ligase 1	GO:0033211,GO:0005778,GO:0034201,GO:0005741,GO:0006641,GO:0016021,GO:0016020,GO:0042493,GO:0005739,GO:0005789,GO:0014070,GO:0004467,GO:0044539,GO:0005886,GO:0001676,GO:0071902,GO:0042178,GO:0007584,GO:0005524,GO:0008610	CG3961-PA						PF00501			PS00455	G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.40.50.980,G3DSA:3.40.50.980	SSF56801,SSF56801	31~51									
aly1022.4	Unknown		n/a																				
aly1022.5	cGMP-dependent protein kinase, isozyme 2 forms cD4/T1/T3A/T3B	GO:0030553,GO:0007631,GO:0006468,GO:0030536,GO:0032095,GO:0007616,GO:0007614,GO:0008016,GO:0009744,GO:0004674,GO:0046959,GO:0005886,GO:0004692,GO:0004690,GO:0008345,GO:0005829,GO:0005524	CG10033-PH			PIRSF000559	SM00100,SM00100,SM00133,SM00220		PF00027,PF00027,PF00069,PF16808	PS51285,PS50042,PS50011,PS50042	PR00104,PR00104,PR00104,PR00104,PR00104,PR00104	PS00888,PS00889,PS00107,PS00108,PS00888,PS00889	G3DSA:3.30.200.20,G3DSA:2.60.120.10,G3DSA:2.60.120.10,G3DSA:1.10.510.10	SSF51206,SSF56112,SSF51206	403~423,88~115									
aly1022.6	Unknown		n/a																				
aly1022.7	Unknown		n/a												43~63								
aly1022.8	cGMP-dependent protein kinase, isozyme 2 forms cD5/T2	GO:0030553,GO:0007631,GO:0006468,GO:0030536,GO:0032095,GO:0008016,GO:0007616,GO:0005829,GO:0005886,GO:0009744,GO:0004674,GO:0046959,GO:0004692,GO:0004690,GO:0008345,GO:0007614,GO:0005524	n/a												99~119								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10226.1	Annexin B11	GO:0003779,GO:0005544,GO:0005575,GO:0008360,GO:0005509,GO:0007155	CG9968-PB				SM00335,SM00335,SM00335,SM00335		PF00191,PF00191,PF00191		PR00196,PR00196,PR00196,PR00196,PR00196,PR00196	PS00223,PS00223,PS00223	G3DSA:1.10.220.10,G3DSA:1.10.220.10,G3DSA:1.10.220.10,G3DSA:1.10.220.10	SSF47874									
aly10226.10	NADPH oxidase 4	GO:0048085,GO:0016175,GO:0035220,GO:0005789,GO:0043406,GO:0042742,GO:0005925,GO:0051897,GO:0002385,GO:0042554,GO:0050667,GO:0000902,GO:0016021,GO:0006979,GO:0010467,GO:0043066,GO:0005509,GO:0071333,GO:0048471,GO:2000573,GO:0008285,GO:0020037,GO:0055007,GO:0072593,GO:0008365,GO:0005886,GO:0045453,GO:0055114,GO:0072341,GO:0007569,GO:0070374,GO:0004601	CG3131-PC						PF01794														
aly10226.11	Unknown	GO:0033260,GO:0005634,GO:0007307,GO:0003674,GO:0008283	CG2669-PA																				
aly10226.12	Protein downstream neighbor of son homolog	GO:0008283,GO:0005634,GO:0033260,GO:0003674,GO:0007307,GO:0007275,GO:0051301	CG2669-PA																				
aly10226.13	Chromodomain-helicase-DNA-binding protein Mi-2 homolog	GO:0008026,GO:0031491,GO:0008270,GO:0016887,GO:0003677,GO:0003678,GO:0042766,GO:0007517,GO:0000122,GO:0005634,GO:0043044,GO:0005524,GO:0004003,GO:0032508,GO:0071923,GO:0004386,GO:0007283,GO:0045892,GO:0051312,GO:0016581,GO:0070615,GO:0005829,GO:0051276,GO:0006333,GO:0005700,GO:0048813,GO:0006357,GO:0006351,GO:0005515,GO:0035327,GO:0003682	CG8103-PB				SM00487,SM00490,SM00298,SM00298,SM00249,SM00249		PF00271,PF00385,PF08074,PF06461,PF08073,PF00628,PF00628,PF06465,PF00176	PS50013,PS51194,PS50013,PS50016,PS50016,PS51192		PS00690	G3DSA:3.40.50.300,G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:2.40.50.40,G3DSA:2.40.50.40,G3DSA:3.40.50.300	SSF52540,SSF57903,SSF54160,SSF57903,SSF54160,SSF52540									
aly10226.14	Unknown	GO:0046872,GO:0006281	CG42382-PA						PF00642	PS50103			G3DSA:4.10.1000.10	SSF90229									
aly10226.15	Unknown		CG30118-PC						PF13521				G3DSA:2.40.320.10	SSF55154									
aly10226.16	DNA repair protein RAD51 homolog 4	GO:0033063,GO:0000781,GO:0003677,GO:0005737,GO:0000724,GO:0005813,GO:0005634,GO:0005657,GO:0003697,GO:0005524,GO:0000723,GO:0006281,GO:0006289,GO:0006974,GO:0042148,GO:0006310,GO:0008094,GO:0000400,GO:0051276,GO:0051726,GO:0000150,GO:0036297,GO:0043015	CG2412-PB						PF08423	PS50162			G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10226.17	FACT complex subunit spt16	GO:0006281,GO:0032968,GO:0035101,GO:0005694,GO:0001672,GO:0006351,GO:0003677,GO:0006260,GO:0022008,GO:0003682,GO:0006268,GO:0005634	CG1828-PA						PF08512,PF14826,PF00557,PF08644				G3DSA:3.40.350.10,G3DSA:3.90.230.10	SSF55920	470~497								
aly10226.18	Protoheme IX farnesyltransferase, mitochondrial	GO:0004129,GO:0005739,GO:0018343,GO:0006783,GO:0006784,GO:0016021,GO:0070069,GO:0008535,GO:1902600,GO:0000266,GO:0009060,GO:0008495,GO:0017004,GO:0048034,GO:0045333,GO:0031966,GO:0004311,GO:0007005	CG5037-PA	MF_00154		PIRSF001773		TIGR01473	PF01040			PS00943							UPA00834				
aly10226.19	E3 ubiquitin-protein ligase TRIM37	GO:0035518,GO:0005164,GO:0016235,GO:0008270,GO:0005737,GO:0070842,GO:0016874,GO:0005777,GO:0048471,GO:0042803,GO:0004842,GO:0046600,GO:0061630,GO:0036353,GO:0051092,GO:0051091,GO:0031625,GO:0005829,GO:0000122,GO:0032088,GO:0051865,GO:0006351,GO:0005515,GO:0003682	n/a				SM00502,SM00336,SM00061		PF00917,PF00643	PS50119,PS50144,PS50089			G3DSA:2.60.210.10,G3DSA:3.30.40.10,G3DSA:4.10.45.10	SSF49599,SSF57845,SSF57850	222~242,154~188,84~104								
aly10226.2	Uncharacterized protein C4orf22 homolog		CG8138-PA						PF14713														
aly10226.20	Unknown		n/a																				
aly10226.21	GTPase-activating protein pac-1	GO:0005737,GO:0008105,GO:0043547,GO:0007480,GO:0005096,GO:0005622,GO:0005575,GO:0007165,GO:0010470,GO:0005100,GO:0007266,GO:0007265,GO:0030054	CG1412-PD				SM00324		PF00620	PS50238			G3DSA:1.10.555.10	SSF48350			REACT_11044						
aly10226.22	Rho GTPase-activating protein 21	GO:0005856,GO:0005794,GO:0007030,GO:0007165,GO:0043547,GO:0007480,GO:0072384,GO:0005886,GO:0005096,GO:0005622,GO:0005575,GO:0030659,GO:0051684,GO:0005515,GO:0051683,GO:0005100,GO:0007266,GO:0051645,GO:0030100,GO:0030054,GO:0000139	CG1412-PD				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10226.23	Protein scarlet	GO:0006856,GO:0042626,GO:0031409,GO:0016887,GO:0043190,GO:0016021,GO:0006810,GO:0006727,GO:0006726,GO:0005395,GO:0005887,GO:0005524	CG4314-PA				SM00382		PF00005,PF01061	PS50893		PS00211	G3DSA:3.40.50.300	SSF52540									
aly10226.24	Protein white	GO:0006856,GO:0042626,GO:0031409,GO:0042332,GO:0042441,GO:0070731,GO:0043190,GO:0031410,GO:0016021,GO:0048072,GO:0006727,GO:0006726,GO:0042401,GO:0004888,GO:0005395,GO:0007165,GO:0016887,GO:0005887,GO:0008049,GO:0007613,GO:0005524	CG2759-PA				SM00382	TIGR00955	PF00005,PF01061	PS50893		PS00211	G3DSA:3.40.50.300	SSF52540									
aly10226.25	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit delta isoform	GO:0006954,GO:0051124,GO:0045927,GO:0030307,GO:0060326,GO:0017124,GO:0042059,GO:0046622,GO:0002164,GO:0035004,GO:0035005,GO:0006468,GO:0048169,GO:0002168,GO:0046934,GO:0001727,GO:0016049,GO:0005942,GO:0005943,GO:0007166,GO:0007552,GO:0005737,GO:0030335,GO:0036092,GO:0005886,GO:0016310,GO:0001782,GO:0045727,GO:0048477,GO:0010507,GO:0005524,GO:0042127,GO:0007436,GO:0008286,GO:0030154,GO:0046620,GO:0016303,GO:0006914,GO:0046854,GO:2000377,GO:0016322,GO:0042113,GO:0050832,GO:0008361,GO:0060074,GO:0009267,GO:0048872,GO:0014065,GO:0048015,GO:0006979,GO:0030168,GO:0055115,GO:0045793,GO:0030536,GO:0040014,GO:0050773,GO:0007390,GO:0048813,GO:0010628,GO:0045087,GO:0002250,GO:0051823,GO:0045572	CG4141-PA				SM00142,SM00145,SM00143,SM00146,SM00144		PF00794,PF02192,PF00454,PF00613,PF00792	PS50290,PS51546,PS51545,PS51547,PS51544		PS00916,PS00915	G3DSA:3.10.20.90,G3DSA:1.10.1070.11,G3DSA:3.30.1010.10,G3DSA:2.60.40.150,G3DSA:1.25.40.70,G3DSA:3.10.20.90	SSF54236,SSF49562,SSF56112,SSF48371	1055~1057									
aly10226.26	Probable 28S rRNA (cytosine-C(5))-methyltransferase	GO:0045089,GO:0005730,GO:0005634,GO:0006364,GO:0050829,GO:0008168,GO:0044822	CG42358-PA						PF01189	PS51686	PR02008,PR02008,PR02008,PR02008,PR02008		G3DSA:3.40.50.150	SSF53335									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10226.27	Echinoderm microtubule-associated protein-like CG42247	GO:0005737,GO:0007017,GO:0071683,GO:0007605,GO:0008017,GO:0035011,GO:0035556,GO:0005874,GO:0008344	CG42247-PG				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00537,SM00537		PF03451,PF03607,PF03607,PF00400	PS50309,PS50294,PS50082,PS50309,PS50082,PS50294		PS00678,PS00678	G3DSA:3.10.20.230,G3DSA:3.10.20.230,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50998,SSF50998,SSF50998,SSF89837,SSF89837,SSF50998									
aly10226.28	Alpha-ketoglutarate-dependent dioxygenase alkB homolog 4	GO:0005737,GO:0006482,GO:0031032,GO:0006355,GO:0016706,GO:0005634,GO:0030496,GO:0003779,GO:0032451,GO:0036090,GO:0070938,GO:0046872,GO:0055114,GO:0006351	CG4036-PA						PF03171				G3DSA:2.60.120.590,G3DSA:2.60.120.590	SSF51197,SSF51197									
aly10226.29	Tetraspanin-33	GO:0051604,GO:0016021,GO:0097197,GO:0019899,GO:0090002,GO:0008150,GO:0005886,GO:0003674,GO:0009986	CG9496-PB						PF00335		PR00259,PR00259,PR00259,PR00259			SSF48652									
aly10226.3	Nitric oxide synthase	GO:0031284,GO:0003958,GO:0006809,GO:0007416,GO:0050661,GO:0050660,GO:0005777,GO:0002027,GO:0010181,GO:0005506,GO:0008285,GO:0020037,GO:0046620,GO:0006952,GO:0008156,GO:0007263,GO:0055114,GO:0007399,GO:0004517,GO:0005829,GO:0007444,GO:0005516	CG6713-PA			PIRSF000333			PF00175,PF00667,PF00258,PF02898	PS50902,PS51384	PR00371,PR00371,PR00371,PR00371,PR00371,PR00369,PR00369,PR00369,PR00369,PR00369	PS60001	G3DSA:1.20.990.10,G3DSA:3.40.50.80,G3DSA:3.90.1230.10,G3DSA:3.90.340.10,G3DSA:3.40.50.360,G3DSA:3.40.50.360,G3DSA:2.40.30.10,G3DSA:2.40.30.10	SSF52343,SSF56512,SSF63380,SSF52218,SSF52218		00330+1.14.13.39		PWY-6845,PWY-4983					
aly10226.30	CD63 antigen	GO:0048757,GO:0007160,GO:0003674,GO:0031226,GO:0010008,GO:0070062,GO:0016021,GO:0005770,GO:0035646,GO:0031904,GO:0031902,GO:0043473,GO:2001046,GO:0050931,GO:0034613,GO:0008150,GO:0002092,GO:0097487,GO:2000680,GO:0009986,GO:0042470,GO:0016477,GO:0005764,GO:0005765,GO:1900746,GO:0015031	CG9496-PB			PIRSF002419			PF00335		PR00259,PR00259,PR00259,PR00259	PS00421		SSF48652									
aly10226.31	CD63 antigen	GO:0007596,GO:0048757,GO:0007160,GO:0003674,GO:0031226,GO:0010008,GO:0070062,GO:0016021,GO:0035646,GO:0031904,GO:0031902,GO:2001046,GO:0009986,GO:0034613,GO:0008150,GO:0002092,GO:0005887,GO:0005886,GO:0097487,GO:2000680,GO:0030168,GO:0042470,GO:0016477,GO:0031088,GO:0005765,GO:1900746,GO:0015031,GO:0002576	CG9494-PA			PIRSF002419			PF00335		PR00259,PR00259,PR00259,PR00259			SSF48652									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10226.32	CD63 antigen	GO:0042470,GO:2001046,GO:0016021,GO:0048757,GO:0007160,GO:0005765,GO:0003674,GO:0002092,GO:0035646,GO:0097487,GO:0015031,GO:0008150,GO:0016477,GO:0031226,GO:0031902,GO:1900746	CG9494-PA			PIRSF002419			PF00335		PR00259,PR00259,PR00259,PR00259			SSF48652									
aly10226.33	CD63 antigen	GO:0007596,GO:0048757,GO:0007160,GO:0003674,GO:0031226,GO:0010008,GO:0070062,GO:0016021,GO:0035646,GO:0031904,GO:0031902,GO:2001046,GO:0009986,GO:0034613,GO:0008150,GO:0002092,GO:0005887,GO:0005886,GO:0097487,GO:2000680,GO:0030168,GO:0042470,GO:0016477,GO:0031088,GO:0005765,GO:1900746,GO:0015031,GO:0002576	CG8666-PB			PIRSF002419			PF00335		PR00259,PR00259,PR00259,PR00259	PS00421		SSF48652									
aly10226.34	Ubiquitin-conjugating enzyme E2-24 kDa	GO:0016874,GO:0004842,GO:0000209,GO:0005524,GO:0019915	CG6720-PA				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				
aly10226.35	Peptidyl-prolyl cis-trans isomerase-like 2	GO:0005737,GO:0000413,GO:0005796,GO:0006457,GO:0061630,GO:0071013,GO:0007596,GO:0034450,GO:0000398,GO:0000209,GO:0005654,GO:0050900,GO:0003755,GO:0005886,GO:0072659,GO:0016874,GO:0005634	CG7747-PA				SM00504		PF00160,PF04641	PS50072,PS51698	PR00153,PR00153,PR00153,PR00153,PR00153	PS00170	G3DSA:3.30.40.10,G3DSA:2.40.100.10	SSF57850,SSF50891	437~467				UPA00143				
aly10226.36	Protein lin-7 homolog B	GO:0008105,GO:0007269,GO:0008582,GO:0007268,GO:0045199,GO:0035003,GO:0007163,GO:0045202,GO:0007298,GO:0005923,GO:0006887,GO:0097025,GO:0043005,GO:1903361,GO:0016323,GO:0045211,GO:0014069,GO:0019904,GO:0005911,GO:0005886,GO:0007264,GO:0005622,GO:0005515,GO:0097016,GO:0015031	CG7662-PC				SM00228,SM00569		PF02828,PF00595	PS51022,PS50106			G3DSA:2.30.42.10	SSF50156,SSF101288									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10226.37	Paxillin	GO:0005737,GO:0005856,GO:0032319,GO:1901739,GO:0007016,GO:0035220,GO:0035218,GO:0007160,GO:0008270,GO:0005886,GO:0005925,GO:0010506,GO:0046843	CG31794-PA				SM00132,SM00132,SM00132,SM00132		PF00412,PF00412,PF00412,PF00412	PS50023,PS50023,PS50023,PS50023		PS00478,PS00478,PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716,SSF57716,SSF57716,SSF57716										
aly10226.38	Unknown		n/a												158~159								
aly10226.39	X-box-binding protein 1	GO:0048010,GO:0071222,GO:0005783,GO:0031017,GO:0045348,GO:0031062,GO:0006366,GO:0035220,GO:0001158,GO:0035356,GO:0031490,GO:0045582,GO:0030176,GO:0001889,GO:0051024,GO:0060612,GO:0032869,GO:2000347,GO:1901985,GO:0001525,GO:0055092,GO:0005737,GO:0043565,GO:0007517,GO:0016049,GO:0071375,GO:0000122,GO:0031670,GO:0005634,GO:0071353,GO:0042993,GO:0010508,GO:0043066,GO:0071332,GO:0071333,GO:1990418,GO:0010506,GO:0000981,GO:0042803,GO:0048666,GO:0071230,GO:1901800,GO:0071499,GO:0071498,GO:2000353,GO:1903489,GO:0055089,GO:0046331,GO:0010832,GO:0001047,GO:0042149,GO:0042632,GO:0034599,GO:1902236,GO:0045579,GO:0002639,GO:0046982,GO:0031648,GO:0006990,GO:0030968,GO:0070059,GO:0003700,GO:0060691,GO:0005829,GO:0045600,GO:0001934,GO:0014065,GO:0006355,GO:0022416,GO:0045944,GO:0000977,GO:2000778,GO:0032008,GO:0006511,GO:1900100,GO:1900103,GO:1900102,GO:0001935,GO:0035924,GO:0034976	CG9415-PE				SM00338		PF07716	PS50217		PS00036	G3DSA:1.20.5.170	SSF57959	60~108									
aly10226.4	Nitric oxide synthase-like protein	GO:0031284,GO:0003958,GO:0006809,GO:0007416,GO:0050661,GO:0050660,GO:0005777,GO:0002027,GO:0010181,GO:0005506,GO:0008285,GO:0020037,GO:0046620,GO:0006952,GO:0008156,GO:0007263,GO:0055114,GO:0007399,GO:0004517,GO:0005829,GO:0007444,GO:0005516	CG6713-PA			PIRSF000333			PF02898,PF00258,PF00175,PF00667	PS51384,PS50902	PR00369,PR00369,PR00369,PR00369,PR00369,PR00371,PR00371,PR00371,PR00371,PR00371,PR00371,PR00371,PR00371	PS60001	G3DSA:3.40.50.80,G3DSA:3.40.50.360,G3DSA:3.40.50.360,G3DSA:3.90.123 0.10,G3DSA:1.20.990.10,G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:3.90.340.10	SSF52218,SSF52343,SSF56512,SSF63380		00330+1.14.13.39		PWY-6845,PWY-4983						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10226.40	COP9 signalosome complex subunit 5	GO:0035204,GO:0032435,GO:0048142,GO:0048140,GO:0050821,GO:0007275,GO:0008237,GO:0008180,GO:0005737,GO:0019784,GO:0045787,GO:0019781,GO:0001751,GO:0035207,GO:0046872,GO:0048477,GO:0034399,GO:2000600,GO:0000338,GO:0007281,GO:0007314,GO:0007409,GO:0007310,GO:0010388,GO:0036099,GO:0008347,GO:0005515,GO:0007095	CG14884-PA				SM00232		PF01398				G3DSA:3.40.140.10	SSF102712										
aly10226.41	AP-1 complex subunit gamma-like 2	GO:0008021,GO:0055037,GO:0006901,GO:0030131,GO:0030133,GO:0030135,GO:0010008,GO:0008565,GO:0016183,GO:0006886,GO:0016020,GO:0030136,GO:0048749,GO:0030141,GO:0005798,GO:0030659,GO:0007269,GO:0030121,GO:0016192,GO:0005802,GO:0000139,GO:0035652,GO:0033363	CG9113-PB				SM00809		PF02883	PS50180			G3DSA:2.60.40.1230	SSF49348										
aly10226.42	AP-1 complex subunit gamma-1	GO:0043231,GO:0008021,GO:0019894,GO:0030669,GO:0055037,GO:0006901,GO:0061024,GO:0030117,GO:0030131,GO:0030119,GO:0030135,GO:0030136,GO:0008565,GO:0016183,GO:0030742,GO:0006886,GO:0016020,GO:0090160,GO:0005737,GO:0045954,GO:0043323,GO:0035646,GO:0005215,GO:0048471,GO:0032438,GO:0048749,GO:0005794,GO:0019886,GO:0030141,GO:0017137,GO:0050690,GO:0030659,GO:0032588,GO:0007269,GO:0030121,GO:0030665,GO:0006892,GO:0016192,GO:0005829,GO:0005802,GO:0000139,GO:0005765,GO:0035652,GO:0016032,GO:0033363	CG9113-PB			PIRSF037094			PF01602				G3DSA:1.25.10.10	SSF48371										
aly10226.43	ADP-ribosylation factor-related protein 1	GO:0016020,GO:0034067,GO:0007369,GO:0003924,GO:0005622,GO:0005575,GO:0043001,GO:0008150,GO:0042147,GO:0005802,GO:0007264,GO:0005525	CG7039-PA				SM00177		PF00025				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540										
aly10226.44	Unknown		n/a										G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452										
aly10226.45	23 kDa integral membrane protein	GO:0003674,GO:0016021,GO:0008150	CG9033-PB			PIRSF002419			PF00335					SSF48652										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10226.46	CD63 antigen	GO:0048757,GO:0007160,GO:0003674,GO:0031226,GO:0005737,GO:0045785,GO:0016021,GO:0035646,GO:0030855,GO:0032403,GO:0016477,GO:0031902,GO:2001046,GO:0030658,GO:0008150,GO:0002092,GO:0005886,GO:0097487,GO:0043234,GO:0042470,GO:0010633,GO:0005764,GO:0005765,GO:1900746,GO:0015031,GO:0045807	CG12846-PA			PIRSF002419			PF00335		PR00259,PR00259,PR00259	PS00421		SSF48652									
aly10226.47	Ero1-like protein	GO:0005783,GO:0051085,GO:0005789,GO:0016671,GO:0003756,GO:0055114,GO:0016491	CG1333-PB			PIRSF017205			PF04137					SSF110019									
aly10226.48	Nck-associated protein 5	GO:0008340	CG42663-PB												47~67,98~125,15~42								
aly10226.49	Unknown		n/a																				
aly10226.5	Unknown		n/a																				
aly10226.50	Unknown		n/a																				
aly10226.51	Unknown		n/a																				
aly10226.52	Sodium-independent sulfate anion transporter	GO:0005794,GO:0005783,GO:0015301,GO:0005215,GO:0016021,GO:0005886,GO:0005765,GO:0008271,GO:0008272,GO:0098656,GO:0008509,GO:0015381,GO:0070062	CG5002-PA						PF01740,PF00916	PS50801			G3DSA:3.30.750.24	SSF52091									
aly10226.53	Unknown		n/a																				
aly10226.54	Unknown		n/a																				
aly10226.55	Leucine-rich repeat-containing protein 23	GO:0008599,GO:0000164,GO:0005515,GO:0005929	CG13125-PA				SM00365,SM00365			PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058	342~362								
aly10226.56	Unknown	GO:0050829,GO:0070072,GO:0045089	CG42359-PA						PF09446						110~111								
aly10226.6	UDP-glucuronosyltransferase 2B30	GO:0015020,GO:0016021,GO:0002121,GO:0008152,GO:0005789	CG17323-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10226.7	Vesicle transport protein SEC20	GO:0005737,GO:0005635,GO:0005783,GO:0007029,GO:0006914,GO:0006915,GO:0016320,GO:0043066,GO:0005739,GO:0097194,GO:0030176,GO:0016192,GO:0005484,GO:0031201,GO:0043231	CG2023-PB						PF03908						67~101								
aly10226.8	Odorant receptor 94b	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG6679-PA						PF02949														
aly10226.9	NADPH oxidase 4	GO:0071480,GO:0048085,GO:0014911,GO:0016175,GO:0016174,GO:0035220,GO:0005789,GO:0043406,GO:0042742,GO:0005925,GO:0051897,GO:0002385,GO:0016491,GO:0042554,GO:0001666,GO:0050667,GO:0000902,GO:0050664,GO:0051496,GO:0005739,GO:0006979,GO:0043065,GO:0010467,GO:0043066,GO:0005509,GO:0071333,GO:0043020,GO:0048471,GO:2000573,GO:0008285,GO:2000379,GO:0020037,GO:0055007,GO:0016324,GO:0072593,GO:0008365,GO:0045453,GO:0055114,GO:0072341,GO:0007568,GO:0007569,GO:0071320,GO:0071560,GO:0070374,GO:0004601,GO:0006801	CG3131-PC						PF08022,PF08030	PS51384	PR00466,PR00466		G3DSA:3.40.50.80,G3DSA:2.40.30.10	SSF63380,SSF52343									
aly10235.1	11-beta-hydroxysteroid dehydrogenase 1B	GO:0006694,GO:0016021,GO:0005811,GO:0008667,GO:0055114,GO:0008152,GO:0019290,GO:0070524,GO:0016491	CG31548-PA						PF00106		PR01397,PR01397		G3DSA:3.40.50.720	SSF51735				PWY-5901					
aly10235.2	Uncharacterized oxidoreductase YxbG	GO:0008670,GO:0016614,GO:0006635,GO:0008152,GO:0016491	CG3699-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10235.3	Uncharacterized oxidoreductase YxbG	GO:0008670,GO:0016614,GO:0006635,GO:0008152,GO:0016491	CG3699-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735									
aly10235.4	3-oxoacyl-[acyl-carrier-protein] reductase FabG	GO:0050661,GO:0051287,GO:0030497,GO:0004316,GO:0008152,GO:0016491	CG31548-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735	35~55								
aly10235.5	Nephrin	GO:0072015,GO:0007254,GO:0030838,GO:0070062,GO:0007588,GO:0032836,GO:0044062,GO:0007519,GO:0017022,GO:0005622,GO:0007520,GO:0046331,GO:0005887,GO:0005886,GO:0007155,GO:0042995,GO:0036057	CG12484-PB				SM00409,SM00409,SM00409,SM00409,SM00408,SM00408		PF08205,PF08205	PS50835,PS50835,PS50835,PS50835,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF49265,SSF48726										
aly102417.1	Unknown		n/a												27~47								
aly102424.1	Unknown		n/a																				
aly1026.1	Unknown		n/a																				
aly1026.2	Unknown		n/a																				
aly1026.3	Unknown		n/a																				
aly1026.4	Unknown		n/a																				
aly1026.5	Unknown		n/a												95~96								
aly1026.6	Unknown		n/a																				
aly1026.7	Unknown		n/a																				
aly1026.8	Unknown		n/a																				
aly1026.9	Unknown		n/a																				
aly10276.1	Unknown		n/a																				
aly10288.1	Acidic fibroblast growth factor intracellular-binding protein	GO:0070062,GO:0005634,GO:0016020,GO:0017134,GO:0005622,GO:0005654,GO:0012505,GO:0070527	CG8660-PB						PF05427,PF05427														
aly10288.2	Nucleic-acid-binding protein from transposon X-element	GO:0022008,GO:0006313,GO:0019013,GO:0008270,GO:0003676	CG5569-PA				SM00596		PF07530,PF04430				G3DSA:3.40.1230.10	SSF64076	392~412								
aly102915.1	Unknown		n/a																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly102915.2	ATP-dependent DNA helicase PIF1	GO:0000723,GO:0006310,GO:0042162,GO:0051880,GO:0006281,GO:0032204,GO:0032508,GO:0000287,GO:0033682,GO:0005739,GO:0004386,GO:0051974,GO:0000784,GO:0010521,GO:0043141,GO:0003678,GO:0000002,GO:0032211,GO:0017116,GO:0005524	CG3238-PA						PF02689,PF05970,PF14214				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540	208~235								
aly102988.1	Copper-transporting ATPase 2	GO:0016020,GO:0048085,GO:0007595,GO:0051208,GO:0005886,GO:0048066,GO:0002164,GO:0005739,GO:0006825,GO:0005737,GO:0016021,GO:0005770,GO:0006882,GO:0000166,GO:0046688,GO:0015677,GO:0005375,GO:0005507,GO:0005524,GO:0004008,GO:0006878,GO:0034220,GO:0005887,GO:0055065,GO:0055085,GO:0005802,GO:0000139,GO:0015680	CG1886-PB						PF00702			PS00154	G3DSA:3.40.1110.10	SSF81660									
aly103.1	Unknown	GO:0030246,GO:0007399	CG15765-PA											SSF56436									
aly103.10	Unknown	GO:0046872	CG7358-PA							PS50103			G3DSA:4.10.1000.10		505~525,309~329								
aly103.11	Pre-mRNA-splicing factor SYF1	GO:0016020,GO:0000381,GO:0006283,GO:0006281,GO:0071011,GO:0005634,GO:0001824,GO:0000398,GO:0006289,GO:0005654,GO:0006351,GO:0006909,GO:0071013	CG6197-PA				SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386		PF13181				G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452,SSF48452,SSF48452									
aly103.12	F-box only protein 42	GO:0005515	CG6758-PA				SM00256		PF13854,PF13418,PF12937	PS50181			G3DSA:1.20.1280.50,G3DSA:2.120.10.80	SSF81383,SSF117281									
aly103.13	Protein FAM73B	GO:0016021	CG12125-PA						PF10265,PF10265														
aly103.14	Unknown	GO:0005737,GO:0009790,GO:0046331,GO:0003723,GO:0003676,GO:0008190,GO:0045727,GO:0036099	CG2950-PD				SM00322		PF00013	PS50084			G3DSA:3.30.1370.10,G3DSA:1.25.40.180	SSF54791									
aly103.15	Piezo-type mechanosensitive ion channel component	GO:0007638,GO:0016021,GO:0005575,GO:0034220,GO:0005886,GO:0008381,GO:0071260	CG44122-PE						PF15917,PF12166,PF12166														

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly103.16	DNA-directed RNA polymerase II subunit RPB2	GO:0032549,GO:0005665,GO:0006351,GO:0006366,GO:0003899,GO:0046872,GO:0003677	CG3180-PA						PF04561,PF04560,PF04566,PF04567,PF04567,PF04565,PF00562,PF04563			PS01166	G3DSA:2.40.50.150,G3DSA:3.90.1110.10,G3DSA:3.90.1100.10,G3DSA:3.90.1100.10,G3DSA:3.90.1100.10,G3DSA:2.40.270.10,G3DSA:2.40.270.10	SSF64484,SSF64484,SSF64484		00240+2.7.7.6,00230+2.7.7.6	REACT_1788						
aly103.17	LIM domain-containing protein jub	GO:0045177,GO:0071539,GO:0046622,GO:0005622,GO:0003779,GO:0046966,GO:0008270,GO:0005911,GO:0007067,GO:0045572,GO:0016922,GO:0035329,GO:0005912	CG11063-PB				SM00132,SM00132,SM00132		PF00412,PF00412,PF00412	PS50023,PS50023,PS50023			G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716	475~499								
aly103.18	Uncharacterized protein C18orf19 homolog A	GO:0016021	CG14613-PA						PF06916						229~253,196~220								
aly103.19	Unknown	GO:0003824,GO:0008152	CG16854-PD						PF02995				G3DSA:1.20.1250.10,G3DSA:3.40.720.10	SSF53649	438~458								
aly103.2	Hypodermin-B	GO:0004252,GO:0005576,GO:0006508	CG32271-PA				SM00020,SM00020		PF00089,PF00089	PS50240,PS50240	PR00722,PR00722,PR00722	PS00134,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494,SSF50494									
aly103.20	Unknown	GO:0003824,GO:0008152	CG16854-PD						PF02995				G3DSA:3.40.720.10	SSF53649									
aly103.21	Unknown	GO:0003824,GO:0008152	CG16854-PD						PF02995				G3DSA:3.40.720.10	SSF53649									
aly103.22	Unknown	GO:0046872	CG4133-PA							PS50157		PS00028											
aly103.23	WD repeat-containing protein 59	GO:0035859,GO:0003674,GO:0008150,GO:0005515	CG4705-PB				SM00320,SM00320,SM00320,SM00320		PF00400	PS50082,PS50294,PS50082,PS50082,PS50294		PS00678	G3DSA:2.130.10.10	SSF50978									
aly103.24	Metallophosphoesterase 1	GO:0070971,GO:0016787,GO:0006888,GO:0005793,GO:0005794,GO:0005801,GO:0016021,GO:0034235,GO:0033116,GO:0030145,GO:0005575,GO:0008150,GO:0008081,GO:0006506,GO:0005654	CG8455-PB						PF00149				G3DSA:3.60.21.10	SSF56300									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly103.25	Cytochrome b5	GO:0043231,GO:0020037,GO:0016021,GO:0005811,GO:0005789,GO:0012505,GO:0035206,GO:0046872,GO:0045610,GO:0055114,GO:0009055	CG6870-PA						PF00173	PS50255	PR00363,PR00363,PR00363	PS00191	G3DSA:3.10.120.10	SSF55856									
aly103.26	Whirlin	GO:0032414,GO:0042052,GO:1990075,GO:0046716,GO:0010628,GO:0003674,GO:1990227,GO:0005929,GO:0002141,GO:0002142,GO:0005737,GO:0036064,GO:0021694,GO:0042803,GO:0032421,GO:0032420,GO:0032391,GO:0005515,GO:0032426,GO:0007605,GO:0072499,GO:0050953,GO:0030426,GO:0045184,GO:0060122,GO:0045475,GO:0001895,GO:0005575,GO:0001917,GO:1990696,GO:0046982,GO:0005884	CG43749-PG				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156									
aly103.27	Unknown		n/a																				
aly103.28	Whirlin	GO:0032414,GO:0042052,GO:1990075,GO:0046716,GO:0010628,GO:0003674,GO:1990227,GO:0005929,GO:0002141,GO:0002142,GO:0005737,GO:0036064,GO:0021694,GO:0042803,GO:0032421,GO:0032420,GO:0032391,GO:0005515,GO:0032426,GO:0007605,GO:0072499,GO:0050953,GO:0030426,GO:0045184,GO:0060122,GO:0045475,GO:0001895,GO:0005575,GO:0001917,GO:1990696,GO:0046982,GO:0005884	CG43749-PG				SM00228,SM00228		PF00595,PF00595	PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156									
aly103.29	Unknown	GO:0032414,GO:0042052,GO:0072499,GO:0046716,GO:0005575,GO:0003674,GO:0045475	CG43749-PG																				
aly103.3	Monocarboxylate transporter 12	GO:0005308,GO:0015293,GO:0008028,GO:0016021,GO:1902598,GO:0005887,GO:0055085	CG3456-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly103.30	Ral guanine nucleotide dissociation stimulator-like 1	GO:0007264,GO:0043547,GO:0005829,GO:0046578,GO:0008321,GO:0017016,GO:0005575,GO:0007165,GO:0044255,GO:0005622,GO:0032859,GO:0044281	CG8865-PE				SM00314,SM00229,SM00147		PF00788,PF00617,PF00618	PS50200,PS50212,PS50009		PS00720	G3DSA:3.10.20.90,G3DSA:1.10.840.10,G3DSA:1.20.870.10	SSF54236,SSF48366,SSF48366									
aly103.31	Unknown		n/a																				
aly103.32	mRNA cap guanine-N7 methyltransferase	GO:0006370,GO:0004482,GO:0005634,GO:0036265,GO:0003723	CG3688-PA			PIRSF028762			PF03291	PS51562			G3DSA:3.40.50.150,G3DSA:3.40.50.150	SSF53335,SSF53335	333~353,132~152			PWY-7375					
aly103.33	DNA topoisomerase 1	GO:0030261,GO:0003917,GO:0003916,GO:0003677,GO:0003918,GO:0005875,GO:0002168,GO:0005737,GO:0005719,GO:0005730,GO:0005634,GO:0007275,GO:0006265,GO:0031298,GO:0006260,GO:0004672,GO:0048477,GO:0006468,GO:0008283,GO:0045995,GO:0007059,GO:0006338,GO:0005829,GO:0005703,GO:0005700	n/a				SM00435		PF01028,PF14370,PF02919		PR00416,PR00416,PR00416,PR00416,PR00416	PS00176	G3DSA:3.90.15.10,G3DSA:2.170.11.10,G3DSA:2.170.11.10,G3DSA:1.10.10.41,G3DSA:1.10.132.10	SSF56741,SSF46596,SSF56349,SSF56349	505~532,838~865,877~904								
aly103.34	ATPase WRNIP1	GO:0005634,GO:0017111,GO:0031122,GO:0030174,GO:0005663,GO:0046331,GO:0006260,GO:0016887,GO:0003677,GO:0046872,GO:0005875,GO:0005524,GO:0000731	CG8142-PA				SM00382		PF16193,PF12002,PF00004				G3DSA:1.10.8.60,G3DSA:1.10.3710.10,G3DSA:3.40.50.300,G3DSA:1.20.272.10	SSF48019,SSF52540			REACT_152,REACT_216,REACT_22172,REACT_383,REACT_1538						
aly103.35	Protein O-mannosyltransferase 1	GO:0016203,GO:0007517,GO:0060025,GO:0005783,GO:0016021,GO:0016020,GO:0004169,GO:0007385,GO:0005789,GO:0045214,GO:0030259,GO:0035269,GO:0007525	CG6097-PA				SM00472,SM00472,SM00472		PF02366,PF16192,PF02815	PS50919,PS50919,PS50919			G3DSA:2.80.10.50	SSF82109									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly103.36	Proteasome subunit beta type-7	GO:0005737,GO:0051603,GO:0004175,GO:0005839,GO:0043161,GO:0005829,GO:0005654,GO:0010499,GO:0004298,GO:0006974,GO:1903955,GO:0000502,GO:0005634,GO:0070062	CG3329-PA						PF12465,PF00227	PS51476	PR00141,PR00141,PR00141,PR00141	PS00854	G3DSA:3.60.20.10	SSF56235			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045						
aly103.37	DnaJ homolog subfamily B member 11	GO:0005737,GO:0006457,GO:0005783,GO:0016556,GO:0005634,GO:0016020,GO:0051082,GO:0005788,GO:0009408,GO:0034663	CG4164-PA				SM00271		PF01556,PF00226	PS50076	PR00625,PR00625,PR00625,PR00625	PS00636	G3DSA:2.60.260.20,G3DSA:2.60.260.20,G3DSA:2.60.260.20,G3DSA:1.10.287.110	SSF49493,SSF49493,SSF46565,SSF49493									
aly103.38	Probable phosphorylase b kinase regulatory subunit beta	GO:0006468,GO:0005977,GO:0005964,GO:0005886,GO:0005575,GO:0003824,GO:0008150,GO:0005516,GO:0004553,GO:0003674,GO:0008607	CG8475-PC						PF00723				G3DSA:1.50.10.10	SSF48208			REACT_474						
aly103.39	Ubiquitin carboxyl-terminal hydrolase CYLD	GO:0042742,GO:0005874,GO:0055090,GO:0036064,GO:0005819,GO:1902017,GO:0005813,GO:0005634,GO:0031098,GO:0004843,GO:0048471,GO:0016579,GO:0070536,GO:0090090,GO:0004221,GO:0008017,GO:0005886,GO:0008340,GO:0006979,GO:0042347,GO:0003700,GO:0005829,GO:0016055,GO:0032088,GO:0097542,GO:0006511,GO:0008270	CG5603-PD				SM01052		PF01302	PS50235			G3DSA:2.30.30.190	SSF74924,SSF54001									
aly103.4	Rhodopsin, GQ-coupled	GO:0004930,GO:0009881,GO:0016021,GO:0007601,GO:0018298,GO:0007602	n/a							PS50262			G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly103.40	KDEL motif-containing protein 1	GO:0005788	CG31139-PA				SM00672		PF05686,PF00630				G3DSA:2.60.40.10	SSF81296									
aly103.41	39S ribosomal protein L3, mitochondrial	GO:0003735,GO:0006412,GO:0005762,GO:0005763	CG8288-PA						PF00297				G3DSA:4.10.960.10	SSF50447									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly103.42	Calcium-responsive transactivator	GO:0050775,GO:0006351,GO:0016604,GO:0005634,GO:0016358,GO:0000780,GO:0071565,GO:0016568,GO:0045893,GO:0000776,GO:0000777	CG10555-PA						PF05030						19~39								
aly103.43	JmjC domain-containing protein 4 homolog	GO:0005575,GO:0003674,GO:0008150	CG7200-PA				SM00558		PF13621	PS51184			G3DSA:2.60.120.650	SSF51197									
aly103.44	Alpha-methylacyl-CoA racemase	GO:0005737,GO:0008111,GO:0006631,GO:0001561,GO:0005777,GO:0005739,GO:0003824,GO:0008300,GO:0008152,GO:0006699,GO:0008206,GO:0005102	CG9319-PA						PF02515				G3DSA:3.40.50.10540,G3DSA:3.40.50.10540,G3DSA:3.30.1540.10	SSF89796									
aly103.45	Phosphorylated CTD-interacting factor 1	GO:0015630,GO:0045171,GO:0010923,GO:0005654,GO:0005515,GO:0048190	CG11399-PB				SM00456		PF12237,PF00397	PS50020			G3DSA:2.20.70.10	SSF51045									
aly103.46	Repressor of RNA polymerase III transcription MAF1 homolog	GO:0001030,GO:0001031,GO:0001032,GO:0043231,GO:0005730,GO:0005634,GO:0005813,GO:0005829,GO:0070217,GO:0005737,GO:0030425,GO:0030424,GO:0005654,GO:0006351,GO:0060077,GO:0005886,GO:0048471,GO:0005622,GO:0000994,GO:0016480	CG40196-PA			PIRSF037240			PF09174														
aly103.47	RanBP-type and C3HC4-type zinc finger-containing protein 1	GO:0043461,GO:0097039,GO:0004842,GO:0008270,GO:0043130,GO:0006351,GO:0003677,GO:0071797,GO:0016874,GO:0043123	CG8674-PA						PF07542	PS50089		PS00518	G3DSA:3.30.40.10,G3DSA:1.10.3580.10,G3DSA:3.30.2180.10	SSF160909,SSF57850,SSF57850,SSF57850	526~546								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly103.48	Small nuclear ribonucleoprotein-associated protein B	GO:0016070,GO:0046540,GO:0044822,GO:0030532,GO:0071011,GO:0005634,GO:0008406,GO:0000398,GO:0005682,GO:0007281,GO:0007052,GO:0071004,GO:0005686,GO:0005687,GO:0015030,GO:0005685,GO:0071013,GO:0005681,GO:0045495	CG5352-PB			PIRSF037187	SM00651		PF01423				G3DSA:2.30.30.100	SSF50182										
aly103.49	Krueppel homolog 1	GO:0035075,GO:0046872,GO:0003700,GO:0005634,GO:0007552,GO:0006355,GO:0010977,GO:0003676,GO:0003677,GO:0045316	CG45074-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF13912,PF12874,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly103.5	Visual pigment-like receptor peropsin	GO:0008020,GO:0042052,GO:0046673,GO:0030265,GO:0005791,GO:0004930,GO:0016028,GO:0042331,GO:0016023,GO:0016021,GO:0016027,GO:0009642,GO:0007186,GO:0009584,GO:0009589,GO:0007601,GO:0016029,GO:0018298,GO:0007602,GO:0008594,GO:0009881,GO:0005886,GO:0008344,GO:0043052,GO:0005767,GO:0005515,GO:0071632,GO:0005771	CG4550-PA						PF00001	PS50262	PR01244,PR01244,PR01244		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly103.50	Pre-mRNA-splicing factor CWC25 homolog	GO:0007052	CG2843-PA				SM01083		PF10197,PF12542						162~190,213~50,438~472								
aly103.51	E3 ubiquitin-protein ligase RNF31	GO:0035631,GO:0051092,GO:0050852,GO:0031625,GO:0060546,GO:0016874,GO:0005829,GO:0097039,GO:0009898,GO:0016567,GO:1903955,GO:0043130,GO:0008270,GO:0023035,GO:0071797,GO:0004842,GO:0000209,GO:0043123	CG11321-PE				SM00647,SM00647,SM00547		PF01485,PF16678	PS50089		PS01358		SSF57850,SSF57850,SSF57850	1364~1384,1224~1244,1315~1342									
aly103.52	Protein unzipped	GO:0007411,GO:0016021,GO:0007413,GO:0007409,GO:0005886	CG3533-PA						PF11901				G3DSA:2.170.15.10										
aly103.53	Unknown		n/a						PF13873						177~198								
aly103.54	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly103.55	Unknown		n/a																				
aly103.56	Piezo-type mechanosensitive ion channel component	GO:0007638,GO:0016021,GO:0005575,GO:0034220,GO:0005886,GO:0008381,GO:0071260	CG44122-PE						PF12166														
aly103.6	Protein msta, isoform B	GO:0008168,GO:0010629,GO:0042826,GO:0005515	CG18033-PA				SM00317		PF00856	PS50280			G3DSA:2.170.270.10,G3DSA:2.170.270.10	SSF82199									
aly103.7	Protein msta, isoform B	GO:0008168,GO:0010629,GO:0042826,GO:0005515	CG18033-PA				SM00317		PF00856	PS50280			G3DSA:2.170.270.10,G3DSA:2.170.270.10	SSF82199,SSF82199									
aly103.8	Unknown		n/a																				
aly103.9	Alpha-aspartyl dipeptidase	GO:0005737,GO:0006508,GO:0016805,GO:0008239,GO:0008236	CG2200-PA						PF03575				G3DSA:3.40.50.880	SSF52317									
aly10303.1	Unknown		n/a																				
aly1033.1	Unknown		n/a																				
aly1033.2	NACHT and WD repeat domain-containing protein 2	GO:0005575,GO:0008150,GO:0003674	CG10185-PA						PF13271,PF05729				G3DSA:3.40.50.300	SSF52540									
aly1033.3	Unknown		n/a																				
aly1033.4	Unknown		n/a																				
aly10338.1	Oxygen-dependent coproporphyrinogen-III oxidase	GO:0006783,GO:0006782,GO:0004109,GO:0005739,GO:0006779,GO:0055114,GO:0042803	CG3433-PA						PF01218		PR00073,PR00073,PR00073		G3DSA:3.40.1500.10	SSF102886		00860+1.3.3.3		PWY-5531,PWY-7159	UPA00251				
aly10347.1	Unknown		n/a																				
aly1036.1	Thyrotropin-releasing hormone receptor	GO:0009755,GO:0008528,GO:0016021,GO:0005886,GO:0048812,GO:0005887,GO:0008188,GO:0042654,GO:0022008,GO:0004997,GO:0007186,GO:0008227	CG5911-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1036.10	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1036.2	Unknown	GO:0009755,GO:0008528,GO:0016021,GO:0048812,GO:0005887,GO:0008188,GO:0042654,GO:0022008,GO:0004997,GO:0007186,GO:0008227	CG5911-PA								PR00237,PR00237		G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1036.3	Unknown		n/a																				
aly1036.4	ER membrane protein complex subunit 6	GO:0097631,GO:0016021,GO:0030176,GO:0072546,GO:0000045	CG11781-PA						PF07019														
aly1036.5	Probable histone-lysine N-methyltransferase Mes-4	GO:0018024,GO:0042054,GO:0018992,GO:0008134,GO:0003712,GO:0005700,GO:0031490,GO:0016458,GO:0008270,GO:0000228,GO:0005721	CG4976-PA				SM00293,SM00293,SM00249,SM00249,SM00249,SM00317,SM00508,SM00570		PF00856,PF00855,PF00855	PS50812,PS50868,PS50280,PS50096,PS50812,PS51215		PS01359	G3DSA:2.170.270.10,G3DSA:2.30.30.160,G3DSA:2.30.30.160,G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF63748,SSF82199,SSF63748,SSF57903,SSF57903		00310+2.1.1.43							
aly1036.6	Unknown		n/a				SM00980		PF05485	PS50950				SSF57716	216~236,86~106								
aly1036.7	Unknown	GO:0003676	n/a				SM00980,SM00692		PF05485	PS50950				SSF57716									
aly1036.8	Octopamine receptor beta-1R	GO:0004930,GO:0010579,GO:0004935,GO:0051482,GO:0007606,GO:0007612,GO:0008227,GO:0007188,GO:0045886,GO:0007189,GO:0005887,GO:0007191,GO:0004989,GO:0007186,GO:0016021,GO:0060158,GO:0001963	CG6919-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly1036.9	Unknown		n/a																				
aly10366.1	Fatty acid synthase	GO:0006633,GO:0047451,GO:0004320,GO:0008144,GO:0008270,GO:0001649,GO:0005737,GO:0016020,GO:0070062,GO:0004313,GO:0005811,GO:0071353,GO:0005739,GO:0030879,GO:0005794,GO:0044822,GO:0004315,GO:0047117,GO:0042587,GO:0005886,GO:0055114,GO:0006084,GO:0042470,GO:0009058,GO:0004312,GO:0016295,GO:0016296,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319	CG3523-PC				SM00829		PF00107				G3DSA:3.40.50.720	SSF50129,SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10366.2	Fatty acid synthase	GO:0006633,GO:0047451,GO:0006631,GO:0016020,GO:0015939,GO:0031325,GO:0008144,GO:0035338,GO:0008270,GO:0004320,GO:0001649,GO:0016491,GO:0005737,GO:0070062,GO:0016295,GO:0005811,GO:0071353,GO:0005739,GO:0006112,GO:0030879,GO:0005794,GO:0006767,GO:0006766,GO:0044822,GO:0004315,GO:0016788,GO:0047117,GO:0042587,GO:0005886,GO:0044255,GO:0055114,GO:0006084,GO:0042470,GO:0005829,GO:0009058,GO:0004312,GO:0004313,GO:0016296,GO:0019432,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319,GO:0044281	CG3524-PB						PF08659				G3DSA:3.40.50.720	SSF51735										
aly10367.1	Unknown	GO:0032313,GO:0005178,GO:0009986,GO:0005097,GO:0033627	CG42612-PC										G3DSA:2.30.29.30	SSF50729									
aly10368.1	Unknown		n/a												111~131								
aly103753.1	Kinesin-like protein KIF3A	GO:0005737,GO:0042384,GO:0035058,GO:0030951,GO:0007605,GO:0007411,GO:0008017,GO:0007018,GO:0008089,GO:0048812,GO:0003777,GO:0005874,GO:0005929,GO:0007288,GO:0005871,GO:0072372,GO:0005524,GO:0007608	CG10642-PA				SM00129		PF00225	PS50067			G3DSA:3.40.850.10	SSF52540									
aly10377.1	Nascent polypeptide-associated complex subunit alpha	GO:0005854,GO:0007317,GO:0005515,GO:0015031,GO:0022008,GO:0048477	CG8759-PB						PF01849	PS51151			G3DSA:1.10.8.10										
aly10377.2	T-complex protein 1 subunit epsilon	GO:0031681,GO:0006457,GO:0042623,GO:0005832,GO:0005815,GO:0007052,GO:0051082,GO:0022008,GO:0005875,GO:0005524	CG8439-PA						PF00118		PR00304,PR00304,PR00304	PS00750,PS00995,PS00751	G3DSA:3.30.260.10,G3DSA:1.10.560.10,G3DSA:3.50.7.10	SSF48592,SSF54849,SSF52029			REACT_17015						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10378.1	T-complex protein 1 subunit epsilon	GO:0031681,GO:0006457,GO:0070062,GO:0042623,GO:0043209,GO:0005813,GO:0005730,GO:0044297,GO:0051082,GO:1901998,GO:0007052,GO:0002199,GO:0007339,GO:0005832,GO:0009615,GO:0022008,GO:0005874,GO:0005875,GO:0005524	CG8439-PA						PF00118		PR00304,PR00304		G3DSA:3.30.260.10	SSF54849									
aly1038.1	Juvenile hormone esterase	GO:0005575,GO:0004453,GO:0008150,GO:0052689	CG4382-PB						PF00135,PF00135,PF00135,PF00135			PS00122,PS00122	G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474,SSF53474,SSF53474	807~810								
aly1038.10	Unknown		n/a																				
aly1038.11	GTPase-activating protein	GO:0005737,GO:0005099,GO:0043547,GO:0007067,GO:0046872,GO:0005096,GO:0007476,GO:0016321,GO:0008595,GO:0032320,GO:0007426,GO:0007165,GO:0005886,GO:0008293,GO:0022008,GO:0007062,GO:0031235,GO:0007265,GO:0045678,GO:0046580	CG6721-PC				SM00323,SM00239,SM00239,SM00233		PF00169,PF00168,PF00168,PF00616	PS50003,PS50004,PS50004,PS50018		PS00509	G3DSA:1.10.494.10,G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:2.30.29.30	SSF48350,SSF49562,SSF50729,SSF49562										
aly1038.12	Histone-lysine N-methyltransferase SETMAR	GO:0018024,GO:0046975,GO:0044774,GO:0008270,GO:0051568,GO:0097676,GO:2001034,GO:0006303,GO:0005634,GO:0034968,GO:0003690,GO:0031297,GO:0003697,GO:0071157,GO:0008283,GO:2000373,GO:0000793,GO:0000014,GO:0042800,GO:0010452,GO:0000737,GO:0005515,GO:0035861,GO:0000729,GO:2001251	CG4565-PB				SM00317,SM00508		PF00856,PF05033	PS50280,PS50868,PS50867			G3DSA:2.170.270.10	SSF82199		00310+2.1.1.43							
aly1038.13	Inter-alpha-trypsin inhibitor heavy chain H4	GO:0005737,GO:0030212,GO:0070062,GO:0004867,GO:0072562,GO:0006953,GO:0005576,GO:0004866,GO:0005886,GO:0010951,GO:0034097	n/a				SM00609		PF08487,PF00092	PS51468,PS50234			G3DSA:3.40.50.410	SSF53300									
aly1038.14	Unknown		n/a																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1038.15	Inter-alpha-trypsin inhibitor heavy chain H4	GO:0005737,GO:0030212,GO:0070062,GO:0004867,GO:0072562,GO:0006953,GO:0005576,GO:0004866,GO:0005886,GO:0010951,GO:0034097	n/a				SM00327,SM00609		PF08487,PF00092	PS50234,PS51468	PR00453,PR00453,PR00453		G3DSA:3.40.50.410	SSF53300									
aly1038.16	Inter-alpha-trypsin inhibitor heavy chain H4	GO:0006953,GO:0030212,GO:0005576,GO:0004867	CG4686-PA				SM00609,SM00327		PF13519,PF04241,PF08487	PS51468,PS50234			G3DSA:3.40.50.410,G3DSA:3.40.50.410	SSF53300,SSF53300,SSF53300	900~920								
aly1038.17	E3 ubiquitin-protein ligase TRIP12	GO:0005654,GO:0006281,GO:0004842,GO:0016874,GO:0006974,GO:0009790,GO:0042752,GO:2000780,GO:0042787,GO:0008270,GO:0022008,GO:0016922,GO:1901315	CG42574-PB				SM00119,SM00678		PF02825,PF00632	PS50237,PS50918			G3DSA:3.30.2160.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF117839,SSF56204,SSF56204,SSF48371,SSF48371					UPA00143				
aly1038.18	Unknown		n/a																				
aly1038.19	Zinc finger protein 879	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG14655-PA				SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60	SSF57667,SSF57667									
aly1038.2	SPRY domain-containing protein 7	GO:0005515	CG7785-PA				SM00449		PF00622					SSF49899,SSF49899									
aly1038.20	Coiled-coil domain-containing protein 39	GO:0005856,GO:0060287,GO:0071910,GO:0070286,GO:0060285,GO:0035469,GO:0030324,GO:0001947,GO:0071907,GO:0005930	CG17387-PA												34~54,133~160,238~300,308~349,203~223									
aly1038.21	Unknown		n/a																				
aly1038.3	Unknown	GO:0030246	CG4115-PA				SM00034			PS50041		PS00615	G3DSA:3.10.100.10	SSF56436									
aly1038.4	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	GO:0005737,GO:0005730,GO:0005819,GO:0003755,GO:0003677	CG11858-PA						PF13616	PS50198			G3DSA:3.10.50.40	SSF54534									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1038.5	Mediator of RNA polymerase II transcription subunit 12	GO:0048749,GO:0045498,GO:0007406,GO:0005634,GO:0036011,GO:0001104,GO:0030177,GO:0006357,GO:0045944,GO:0005515,GO:0006367,GO:0006366,GO:0016592,GO:0022416,GO:0035072	CG8491-PA						PF12145,PF12145,PF09497														
aly1038.6	Unknown		n/a																				
aly1038.7	Twinkle protein, mitochondrial	GO:0034214,GO:0000002,GO:0051260,GO:0005739,GO:0006264,GO:0006390,GO:0006260,GO:0002020,GO:0071333,GO:0003678,GO:0043139,GO:0042645,GO:0006268,GO:0003697,GO:0005524	CG5924-PA				SM00382		PF13481	PS51199			G3DSA:3.40.50.300,G3DSA:3.90.580.10	SSF52540	119~139									
aly1038.8	Pleckstrin homology domain-containing family M member 3	GO:0019992,GO:0035556,GO:0008270,GO:0005622	CG6613-PA				SM00593		PF13901,PF02759	PS50089,PS50826			G3DSA:3.30.40.10	SSF140741									
aly1038.9	Protein cereblon	GO:0004176,GO:0005737,GO:0043161,GO:0005634,GO:0016567,GO:0046872,GO:0031464	n/a						PF03226														
aly10393.1	Protein son of sevenless	GO:0005088,GO:0003677,GO:0046579,GO:0035022,GO:0035023,GO:0005737,GO:2000134,GO:0043547,GO:0045500,GO:0007480,GO:0008595,GO:0008360,GO:0007265,GO:0007264,GO:0031234,GO:0030676,GO:0007015,GO:0007426,GO:0007399,GO:0005829,GO:0016199,GO:0005515,GO:0008293,GO:0046982	CG7793-PA				SM00229,SM00147		PF00617,PF00618	PS51257,PS50212,PS50009		PS00720	G3DSA:1.10.840.10,G3DSA:1.20.870.10	SSF48366,SSF48366										
aly103931.1	Unknown		n/a												48~68,9~43								
aly104.1	Putative phosphatidate phosphatase	GO:0007424,GO:0045177,GO:0019991,GO:0016791,GO:0009880,GO:0016311,GO:0035234,GO:0016021,GO:0016020,GO:0035233,GO:0007602,GO:0007280,GO:0045824,GO:0050829,GO:0005918,GO:0008195,GO:0008354,GO:0042803	CG11426-PA				SM00014		PF01569				G3DSA:1.20.144.10	SSF48317										
aly104.2	Unknown		n/a						PF14932						294~321,100~137								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly104.3	A disintegrin and metalloproteinase with thrombospondin motifs 16	GO:0003073,GO:0004222,GO:0001541,GO:0030713,GO:0008270,GO:0001658,GO:0006508,GO:1902017,GO:0048477,GO:0005578	CG3622-PC						PF01421,PF01562	PS50092,PS50215			G3DSA:3.40.390.10,G3DSA:2.20.100.10	SSF55486,SSF82895									
aly104.4	A disintegrin and metalloproteinase with thrombospondin motifs 17	GO:0004222,GO:0001541,GO:0030713,GO:0008270,GO:0006508,GO:0048477,GO:0005578	CG3622-PC						PF01421	PS50215			G3DSA:3.40.390.10	SSF55486									
aly104.5	Cuticle protein 3	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG6956-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly104.6	Cuticle protein 3	GO:0040003,GO:0005615,GO:0032504,GO:0005214,GO:0008010,GO:0031012,GO:0042302	CG18348-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly104.7	Cuticle protein 3	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG13214-PC						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly104021.1	Putative BEN domain-containing protein B1		n/a						PF10523	PS51457													
aly1041.1	Epidermal retinol dehydrogenase 2	GO:0043616,GO:0004745,GO:0016021,GO:0005789,GO:0008152,GO:0050908,GO:0042574,GO:0042572,GO:0016491	CG15629-PA						PF00106		PR00081,PR00081		G3DSA:3.40.50.720	SSF51735	184~187								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1041.10	Potassium channel AKT3	GO:0048675,GO:0007528,GO:0007016,GO:0005200,GO:0043195,GO:0005249,GO:0042734,GO:0008092,GO:0007605,GO:0007614,GO:0036062,GO:0070050,GO:0031594,GO:0071805,GO:0045887,GO:0000226,GO:0007165,GO:0005887,GO:0005886,GO:0042391,GO:1900074	CG42734-PU				SM00248,SM00248,SM00248,SM00248,SM00248		PF12796	PS50088,PS50088,PS50088,PS50297			G3DSA:1.25.40.20	SSF48403										
aly1041.11	Putative neuropeptide precursor protein	GO:0005737,GO:0005576	n/a																				
aly1041.12	Peptidyl-prolyl cis-trans isomerase-like 4	GO:0000413,GO:0006457,GO:0003676,GO:0071011,GO:1901407,GO:0071013,GO:0044822,GO:0000398,GO:0000166,GO:0003755,GO:0022008,GO:0005634,GO:0003729	CG5808-PA				SM00360		PF00076,PF00160	PS50072,PS50102	PR00153,PR00153,PR00153,PR00153		G3DSA:3.30.70.330,G3DSA:2.40.100.10	SSF54928,SSF50891	205~225								
aly1041.13	Protein lozenge	GO:0035168,GO:0035165,GO:0030154,GO:0035163,GO:0035162,GO:0045467,GO:0046672,GO:0007165,GO:0003677,GO:0035314,GO:0043565,GO:0035211,GO:0000122,GO:0005634,GO:0001709,GO:0042688,GO:0016360,GO:0048477,GO:0005524,GO:0006351,GO:0048749,GO:0007486,GO:0030182,GO:0048592,GO:0009987,GO:0035170,GO:0042675,GO:0042060,GO:0007469,GO:0044212,GO:0045165,GO:0003700,GO:0003705,GO:0006355,GO:0045944,GO:0000981,GO:0030097	CG42267-PC						PF00853	PS51062	PR00967,PR00967,PR00967		G3DSA:2.60.40.720	SSF49417									
aly1041.14	Carboxypeptidase B	GO:0006508,GO:0004181,GO:0005576,GO:0008270	CG3108-PA				SM00631		PF00246		PR00765,PR00765,PR00765,PR00765		G3DSA:3.40.630.10	SSF53187									
aly1041.15	Carboxypeptidase B	GO:0006508,GO:0004181,GO:0005576,GO:0008270	CG3108-PA				SM00631		PF00246		PR00765,PR00765,PR00765,PR00765		G3DSA:3.40.630.10	SSF53187									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1041.16	Carboxypeptidase B	GO:0006508,GO:0004181,GO:0005576,GO:0008270	CG3108-PA				SM00631		PF00246		PR00765,PR00765,PR00765,PR00765	PS00133	G3DSA:3.40.630.10	SSF53187									
aly1041.17	Carboxypeptidase B	GO:0006508,GO:0004181,GO:0005576,GO:0008270	CG3108-PA				SM00631		PF00246		PR00765,PR00765,PR00765,PR00765		G3DSA:3.40.630.10	SSF53187									
aly1041.18	Protein lozenge	GO:0035168,GO:0035165,GO:0030154,GO:0035163,GO:0035162,GO:0045467,GO:0046672,GO:0007165,GO:0003677,GO:0035314,GO:0043565,GO:0035211,GO:0000122,GO:0005634,GO:0001709,GO:0042688,GO:0016360,GO:0048477,GO:0005524,GO:0006351,GO:0048749,GO:0007486,GO:0030182,GO:0048592,GO:0035170,GO:0042675,GO:0042060,GO:0007469,GO:0044212,GO:0045165,GO:0003700,GO:0003705,GO:0006355,GO:0048813,GO:0045944,GO:0000981,GO:0030097	CG34145-PD						PF00853	PS51062	PR00967,PR00967,PR00967,PR00967,PR00967,PR00967,PR00967		G3DSA:2.60.40.720	SSF49417									
aly1041.19	Segmentation protein Runt	GO:0007419,GO:0003677,GO:0007411,GO:0043565,GO:0007366,GO:0007367,GO:0005634,GO:0005524,GO:0006351,GO:0030182,GO:0048592,GO:0045595,GO:0045892,GO:0045893,GO:0007400,GO:0007377,GO:0003700,GO:0007540,GO:0006355,GO:0048813,GO:0006357,GO:0045944,GO:0000981,GO:0030097	CG1849-PA						PF00853	PS51062	PR00967,PR00967,PR00967,PR00967,PR00967,PR00967,PR00967		G3DSA:2.60.40.720	SSF49417									
aly1041.2	Epidermal retinol dehydrogenase 2	GO:0043616,GO:0004745,GO:0016021,GO:0005789,GO:0008152,GO:0050908,GO:0042574,GO:0042572,GO:0016491	CG9265-PA						PF00106				G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1041.20	Protein lozenge	GO:0035168,GO:0035165,GO:0030154,GO:0035163,GO:0035162,GO:0045467,GO:0046672,GO:0007165,GO:0003677,GO:0042981,GO:0035314,GO:0043565,GO:0030182,GO:0000122,GO:0005634,GO:0001709,GO:0042688,GO:0016360,GO:0048477,GO:0005524,GO:0006351,GO:0048749,GO:0007486,GO:0035211,GO:0048592,GO:0035170,GO:0006952,GO:0042675,GO:0042060,GO:0007469,GO:0044212,GO:0045165,GO:0003700,GO:0003705,GO:0006355,GO:0045944,GO:0000981,GO:0030097	CG1689-PA						PF00853	PS51062	PR00967,PR00967,PR00967,PR00967,PR00967,PR00967		G3DSA:2.60.40.720	SSF49417										
aly1041.21	Pre-mRNA-splicing regulator female-lethal(2)D	GO:0048749,GO:0000381,GO:0019099,GO:0005634,GO:0000375,GO:0046331,GO:0007539,GO:0006397,GO:0007530	CG6315-PA						PF17098						112~132,151~171,220~258,70~104									
aly1041.22	Centrosomal protein of 162 kDa	GO:0005879,GO:0042384,GO:0005814	CG42699-PC												328~369,462~482,380~411,248~268,114~148,205~2									
aly1041.23	Carboxypeptidase B	GO:0006508,GO:0004181,GO:0005576,GO:0008270	CG3108-PA				SM00631		PF00246,PF02244		PR00765,PR00765,PR00765,PR00765	PS00132	G3DSA:3.40.630.10,G3DSA:3.30.70.340	SSF54897,SSF53187										
aly1041.24	Unknown		n/a																					
aly1041.25	Pre-mRNA-processing factor 6	GO:0000244,GO:0071001,GO:0050681,GO:0016607,GO:0000381,GO:0005634,GO:0016020,GO:0003713,GO:0005654,GO:0043021,GO:0006403,GO:0071013,GO:0046540,GO:0071011,GO:0044822,GO:0022008,GO:0030532,GO:0000398,GO:0045944,GO:0003723,GO:0005684,GO:0005682	CG6841-PA				SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00028,SM00028,SM00028,SM00028,SM00028		PF06424,PF14559	PS50293,PS50293,PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF81901,SSF48452,SSF48452	639~659,737~757,107~157									
aly1041.26	Unknown		CG15412-PC										G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047,SSF52047										
aly1041.27	Unknown	GO:0045746,GO:0005634,GO:0003714	CG3227-PA				SM01025		PF10523	PS51457														
aly1041.28	Unknown		n/a										G3DSA:3.30.1330.30	SSF55315										
aly1041.29	Probable ribonuclease ZC3H12B	GO:0004519,GO:0046872	CG10889-PA				SM01025		PF11977,PF10523	PS50103,PS51457														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1041.3	17-beta-hydroxysteroid dehydrogenase 13	GO:0046889,GO:0005576,GO:0005811,GO:0008152,GO:0016491	CG9265-PA						PF00106		PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly1041.30	Unknown	GO:0045746,GO:0005634,GO:0003714	CG3227-PA				SM01025		PF10523	PS51457													
aly1041.31	U3 small nucleolar RNA-associated protein 14 homolog B	GO:0016319,GO:0032040,GO:0051321,GO:0005730,GO:0030154,GO:0007283,GO:0006364,GO:0022008,GO:0007275	CG12301-PA						PF04615						219~239,471~498								
aly1041.32	U6 snRNA-associated Sm-like protein LSm3	GO:0030629,GO:0046540,GO:0033962,GO:0030532,GO:0071011,GO:0071013,GO:0000398,GO:0005688,GO:0044822,GO:0003729	CG31184-PA				SM00651		PF01423				G3DSA:2.30.30.100	SSF50182									
aly1041.33	Probable ATP-dependent RNA helicase DDX46	GO:0016607,GO:0000381,GO:0005634,GO:0000398,GO:0005524,GO:0003724,GO:0004004,GO:0003723,GO:0015030,GO:0010501,GO:0010468,GO:0005681,GO:0003729	CG6227-PA				SM00487,SM00490		PF00271,PF00270	PS51194,PS51192,PS51195			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	142~169,230~250,296~316								
aly1041.34	Enhancer of split mbeta protein	GO:0048749,GO:0043565,GO:0007219,GO:0007399,GO:0000122,GO:0003700,GO:0005634,GO:0030154,GO:0045892,GO:0006351,GO:0003677,GO:0046983	CG14548-PA				SM00353,SM00511		PF00010,PF07527	PS50888,PS51054			G3DSA:4.10.280.10	SSF158457,SSF47459									
aly1041.35	Enhancer of split malpha protein	GO:0031625,GO:0001708,GO:0007219,GO:0007423	CG3396-PC						PF15952														
aly1041.4	Integrin beta-nu	GO:0008305,GO:0046982,GO:0016337,GO:0042048,GO:0016021,GO:0007476,GO:0046716,GO:0007160,GO:0045886,GO:0004872,GO:0043277,GO:0007155,GO:0006909,GO:0007157,GO:0050839,GO:0035011,GO:0007229,GO:0033627	CG1762-PA				SM00187		PF08725,PF00362,PF00362,PF00362,PF12661	PS51257	PR01186,PR01186,PR01186,PR01186,PR01186,PR01186,PR01186,PR01186,PR01186,PR01186	PS00243,PS00243,PS00243	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:3.40.50.410,G3DSA:3.40.50.410,G3DSA:3.40.50.410,G3DSA:1.20.5.100	SSF53300,SSF53300,SSF69179			REACT_13552							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1041.5	Phosphatidylinositol 4-phosphate 5-kinase 1	GO:0016308,GO:0005886,GO:0016307,GO:0051015,GO:0003785,GO:0046854,GO:0005524	n/a										G3DSA:2.20.110.10	SSF82185,SSF82185									
aly1041.6	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	GO:0045254,GO:0006086,GO:0005967,GO:0005811,GO:0016746,GO:0008152,GO:0005759,GO:0004742,GO:0006096	CG5261-PB					TIGR01349	PF00198,PF00364	PS50968		PS00189	G3DSA:2.40.50.100,G3DSA:3.30.559.10,G3DSA:4.10.320.10	SSF52777,SSF51230		00620+2.3.1.12,00020+2.3.1.12,00010+2.3.1.12							
aly1041.7	Solute carrier family 41 member 1	GO:0006812,GO:0016021,GO:0008324,GO:0005886	CG33181-PC						PF01769,PF01769				G3DSA:1.10.357.20,G3DSA:1.10.357.20	SSF161093,SSF161093									
aly1041.8	Polypeptide N-acetylgalactosaminyltransferase 5	GO:0005795,GO:0046872,GO:0006486,GO:0016021,GO:0004653,GO:0030246,GO:0000139,GO:0012505,GO:0009312	CG31651-PB				SM00458		PF00652,PF00535	PS50231			G3DSA:2.80.10.50,G3DSA:3.90.550.10	SSF53448,SSF50370									
aly1041.9	Mitogen-activated protein kinase kinase kinase 7	GO:0000187,GO:0016318,GO:0071222,GO:0000186,GO:0006963,GO:0005886,GO:2000378,GO:0006964,GO:0007165,GO:0050829,GO:0043507,GO:0001525,GO:0007256,GO:0007254,GO:0007252,GO:0000165,GO:0048802,GO:0004672,GO:0001841,GO:0046872,GO:0010506,GO:0005524,GO:0043123,GO:0048749,GO:0005737,GO:0006468,GO:0060546,GO:0045087,GO:0006915,GO:2000377,GO:0006952,GO:0046330,GO:0006955,GO:0007179,GO:0097481,GO:0051607,GO:2001234,GO:0007249,GO:0007391,GO:0005575,GO:0006355,GO:0004706,GO:0097110,GO:0006351,GO:0005515,GO:0004709,GO:0004708,GO:1902443	CG18492-PA				SM00220		PF07714	PS50011	PR00109,PR00109,PR00109,PR00109,PR00109	PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1042.1	ATP-binding cassette sub-family G member 4	GO:0043190,GO:0042626,GO:0005215,GO:0016021,GO:0017127,GO:0033344,GO:0016887,GO:0005886,GO:0046982,GO:0055085,GO:0005524,GO:0042803	CG3164-PA						PF00005,PF01061			PS00211	G3DSA:3.40.50.300	SSF52540									
aly1042.10	Striatin-3	GO:0005737,GO:0005794,GO:0007254,GO:0072686,GO:0042332,GO:0000159,GO:0042051,GO:0051726,GO:0003700,GO:0005634,GO:0000122,GO:0007391,GO:0005654,GO:0046330,GO:0045944,GO:0045892,GO:0005515,GO:0005886,GO:0006909	CG7392-PE				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF08232,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50294,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678	G3DSA:2.130.10.10	SSF50978	63~104									
aly1042.11	Esterase FE4	GO:0052689	CG1121-PA						PF00135			PS00941	G3DSA:3.40.50.1820	SSF53474	524~525								
aly1042.12	Unknown		n/a										G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452									
aly1042.13	Unknown		n/a																				
aly1042.14	Juvenile hormone acid O-methyltransfer	GO:0008168,GO:0035049,GO:0006718,GO:0019010	CG17330-PA						PF13489				G3DSA:3.40.50.150	SSF53335									
aly1042.15	Unknown		n/a																				
aly1042.16	Dachshund homolog 1	GO:0016319,GO:0042051,GO:0048147,GO:0060244,GO:0001075,GO:0010629,GO:0003677,GO:0046545,GO:0001078,GO:0010944,GO:0005737,GO:0007479,GO:0030182,GO:0005730,GO:0005634,GO:0005654,GO:0001967,GO:0048749,GO:0030336,GO:0035215,GO:0007483,GO:0005667,GO:0035211,GO:0008283,GO:0048098,GO:2000279,GO:0007585,GO:0045892,GO:0043231,GO:0035263,GO:0043704,GO:0007411,GO:0033262,GO:0006351,GO:0005515	CG4952-PB						PF02437				G3DSA:3.10.260.20	SSF46955	475~495,500~562,645~665									
aly1042.17	Kelch domain-containing protein 3	GO:0005737,GO:0051321	CG12081-PA				SM00612,SM00612,SM00612,SM00612		PF13964,PF07646,PF07646,PF13854				G3DSA:2.120.10.80	SSF117281,SSF50965									
aly1042.18	DDB1- and CUL4-associated factor 13	GO:0032040,GO:0006909,GO:0080008,GO:0005730,GO:0016567,GO:0000462,GO:0022008	CG7275-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF08662,PF04158	PS50082,PS50294,PS50082,PS50082,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978	402~422				UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1042.19	Prolyl 4-hydroxylase subunit alpha-2	GO:0031418,GO:0005783,GO:0004656,GO:0016222,GO:0016702,GO:0005788,GO:0019511,GO:0043412,GO:0018401,GO:0031545,GO:0005506,GO:0055114	CG31022-PA				SM00702		PF03171,PF07719,PF08336	PS51471,PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452	54~74	00330+1.14.11.2							
aly1042.2	Transmembrane protein 62	GO:0016021	n/a						PF00149				G3DSA:3.60.21.10	SSF56300									
aly1042.20	J domain-containing protein	GO:0005575,GO:0006457,GO:0051082	CG2239-PA				SM00271		PF00226	PS50076	PR00625,PR00625,PR00625,PR00625		G3DSA:1.10.287.110	SSF46565									
aly1042.21	Phosphoinositide 3-kinase adapter protein 1	GO:0016020,GO:0007498,GO:0034134,GO:0034154,GO:0001763,GO:0032869,GO:0007509,GO:0008543,GO:0005737,GO:0007369,GO:0050727,GO:0043549,GO:0048477,GO:0008078,GO:0007507,GO:0034122,GO:0031929,GO:0034123,GO:0034162,GO:0014068,GO:0034142,GO:0005886,GO:0036312,GO:0042325,GO:0007424,GO:0007427,GO:0007426,GO:0005829,GO:0007428,GO:0005622	CG31317-PE						PF14545	PS51376			G3DSA:1.25.40.20	SSF48403	846~880								
aly1042.22	Non-lysosomal glucosylceramidase	GO:0004348,GO:0016021,GO:0016139,GO:0008422,GO:0006680,GO:0005886,GO:0008206,GO:0006665	CG33090-PB						PF04685,PF12215					SSF48208,SSF48208,SSF48208		00600+3.2.1.45,00511+3.2.1.45							
aly1042.23	Kinesin-like protein costa	GO:0007228,GO:0045880,GO:0005871,GO:0005874,GO:0005875,GO:0005737,GO:0007476,GO:0030707,GO:0005119,GO:0008134,GO:0005524,GO:0042803,GO:0008017,GO:0045879,GO:0019901,GO:0030162,GO:0012506,GO:0005886,GO:0035301,GO:0042994,GO:0042992,GO:0043433,GO:0007224,GO:0031647,GO:0007018,GO:0003774,GO:0003777,GO:0005515	CG1708-PA				SM00129		PF00225,PF00225	PS50067	PR00380,PR00380		G3DSA:3.40.850.10	SSF52540	608~642,692~712,547~567								
aly1042.24	Unknown		n/a																				
aly1042.25	T-cell activation inhibitor, mitochondrial	GO:0005739	CG13295-PA						PF14688,PF14687						141~161								

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1042.26	Protein decapentaplegic	GO:0008586,GO:0048066,GO:0030509,GO:0048100,GO:0001745,GO:0007516,GO:0007458,GO:0007455,GO:0007450,GO:0045705,GO:0042127,GO:0019827,GO:0007281,GO:0008360,GO:0007179,GO:0007443,GO:0007442,GO:0007440,GO:0007447,GO:0007446,GO:0007444,GO:0007378,GO:0007448,GO:0035263,GO:0060395,GO:0046845,GO:0046843,GO:0005125,GO:0035168,GO:0010629,GO:0010862,GO:0042981,GO:0002168,GO:0008083,GO:0009948,GO:0048477,GO:0035156,GO:0035158,GO:0035309,GO:0007352,GO:0007354,GO:0007425,GO:0007424,GO:0007427,GO:0007423,GO:0009950,GO:0046982,GO:0035147,GO:0042078,GO:0007498,GO:0035224,GO:0035222,GO:0048636,GO:0009790,GO:0010002,GO:0043408,GO:0001708,GO:0001709,GO:0030707,GO:0048619,GO:0042803,GO:0008285,GO:0045595,GO:0008201,GO:0030718,GO:0001715,GO:0005622,GO:0005515,GO:0016015,GO:0048542,GO:0017145,GO:0005518,GO:0061320,GO:0061327,GO:0005160,GO:0007304,GO:0008354,GO:0007479,GO:0005615,GO:0007473,GO:0007476,GO:0030721,GO:0007474,GO:0061353,GO:0035217,GO:0035215,GO:0035214,GO:0046620,GO:0007313,GO:0045476,GO:0036099,GO:0040007,GO:0007507,GO:0007398,GO:0007393,GO:0007391,GO:0005576,GO:0045570,GO:0005768	CG9885-PB				SM00204		PF00688,PF00019	PS51362		PS00250	G3DSA:2.10.90.10	SSF57501										
aly1042.27	39S ribosomal protein L46, mitochondrial	GO:0016787,GO:0005840,GO:0003735,GO:0005743,GO:0005762,GO:0032543	CG13922-PA						PF11788				G3DSA:3.90.79.10	SSF55811										
aly1042.28	60S ribosomal protein L9	GO:0005840,GO:0022625,GO:0019843,GO:0003735,GO:0007052,GO:0000022,GO:0006412,GO:0051298	CG6141-PA			PIRSF002162			PF00347,PF00347			PS00700	G3DSA:3.90.930.12,G3DSA:3.90.930.12	SSF56053,SSF56053										

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1042.29	Disks large 1 tumor suppressor protein	GO:0016333,GO:0016332,GO:0008105,GO:0008104,GO:0016336,GO:0016335,GO:0016334,GO:0007617,GO:0005886,GO:0045197,GO:0045196,GO:0030707,GO:0031594,GO:0045887,GO:0051124,GO:0045202,GO:0004871,GO:0046956,GO:0008049,GO:0043195,GO:0005920,GO:0061176,GO:0005856,GO:0002009,GO:0042332,GO:0000122,GO:0001708,GO:0019991,GO:0045179,GO:0046939,GO:0005198,GO:0097120,GO:0042058,GO:0048471,GO:0007318,GO:0061174,GO:0042127,GO:0008285,GO:0016328,GO:0046425,GO:0005154,GO:0051294,GO:0016327,GO:0004385,GO:0035255,GO:0045175,GO:0045211,GO:0001738,GO:0060581,GO:0045475,GO:0008593,GO:0007268,GO:0007155,GO:0007010,GO:0016020,GO:0016323,GO:0005918,GO:0045167,GO:0008283,GO:0000132,GO:0007399,GO:0042734,GO:0051726,GO:0030710,GO:0030714,GO:0007391,GO:0005515,GO:0014069,GO:0043113,GO:0005938	CG1725-PM				SM00072,SM00228,SM00228,SM00326,SM00569		PF00595,PF00595,PF00018,PF00625,PF09058	PS50106,PS50052,PS51022,PS50002,PS50106,PS50106		PS00856	G3DSA:1.10.287.470,G3DSA:3.30.63.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:2.30.42.10,G3DSA:2.30.30.40,G3DSA:2.30.30.40,G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50044,SSF50044,SSF50156,SSF50156,SSF101288,SSF52540		00230+2.7.4.8		PWY-7221					
aly1042.3	Unknown		n/a																				
aly1042.30	Calcium/calmodulin-dependent protein kinase type 1	GO:0005737,GO:0006468,GO:0004683,GO:0005829,GO:0032793,GO:0040040,GO:0046777,GO:0004674,GO:0048812,GO:0045944,GO:0005516,GO:0045664,GO:0046872,GO:0005634,GO:0005524	CG1495-PB				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly1042.31	Protein sly1 homolog	GO:0005737,GO:0006892,GO:0006890,GO:0006909,GO:0016192,GO:0005801,GO:0006904,GO:0006886,GO:0016020,GO:0009636,GO:0005798,GO:0006605,GO:0060628,GO:0019905,GO:0005886,GO:0000149,GO:0048190,GO:0022008,GO:0001666,GO:0031201,GO:0000902	CG3539-PG			PIRSF005715			PF00995				G3DSA:3.40.50.1910,G3DSA:3.40.50.2060,G3DSA:1.25.40.60,G3DSA:3.90.830.10	SSF56815									

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1042.32	Unknown	GO:0005975,GO:0016810,GO:0005576,GO:0008061,GO:0006030,GO:0022008	CG32499-PA				SM00494		PF01607	PS50940			G3DSA:3.20.20.370,G3DSA:2.170.140.10	SSF88713,SSF57625									
aly1042.33	Serine palmitoyltransferase 1	GO:0017059,GO:0045197,GO:0004758,GO:0009058,GO:0030170,GO:0006665	CG4016-PC						PF00155				G3DSA:3.40.640.10	SSF53383									
aly1042.34	Unknown		n/a																				
aly1042.4	Alpha-glucosidase	GO:0032450,GO:0003824,GO:0005975,GO:0004558,GO:0043169	CG30360-PC				SM00642		PF00128				G3DSA:3.20.20.80	SSF51445									
aly1042.5	Protein expanded	GO:0008101,GO:0007165,GO:0007298,GO:0001745,GO:0042981,GO:0035331,GO:0005856,GO:0009966,GO:0035330,GO:0040008,GO:0016324,GO:0042127,GO:0008285,GO:0032456,GO:0046620,GO:0046621,GO:0007050,GO:0045595,GO:0045892,GO:0035329,GO:0001751,GO:0042327,GO:0007444,GO:0036375,GO:0005915,GO:0006351,GO:0005515,GO:0045571,GO:0007096	CG4114-PA				SM00295		PF00373,PF09380	PS50057			G3DSA:1.20.80.10,G3DSA:2.30.29.30	SSF50729,SSF47031									
aly1042.6	Carnitine O-palmitoyltransferase 2, mitochondrial	GO:0004095,GO:0006810,GO:0016746,GO:0006635,GO:0005743	CG2107-PA						PF00755			PS00440		SSF52777,SSF52777,SSF52777									
aly1042.7	Protein retinal degeneration B	GO:0071482,GO:0015914,GO:0016029,GO:0016021,GO:0008525,GO:0008526,GO:0005509,GO:0046872,GO:0007608,GO:0006810,GO:0007601,GO:0007603,GO:0007602,GO:0046488,GO:0005887,GO:0005886,GO:0016059,GO:0035091,GO:0070588,GO:0005622,GO:0016056,GO:0005388,GO:0045494	CG11111-PJ				SM00775		PF02121,PF02862	PS51043	PR00391,PR00391,PR00391,PR00391,PR00391		G3DSA:3.40.50.1000,G3DSA:3.30.530.20	SSF55961,SSF56784									
aly1042.8	Integral membrane protein GPR180	GO:0016021,GO:0007186,GO:0019236	CG9304-PA						PF10192														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1042.9	Phosphatidylinositol 3-kinase regulatory subunit gamma	GO:0042127,GO:0006468,GO:0045927,GO:0005942,GO:0005943,GO:0046620,GO:0008286,GO:0045793,GO:0019900,GO:0008361,GO:0046834,GO:0046854,GO:2001275,GO:0035014	CG2699-PB				SM00252,SM00252		PF00017,PF00017,PF16454	PS50001,PS50001	PR00678,PR00678,PR00678,PR00678,PR00678,PR00401,PR00401,PR00401,PR00401		G3DSA:3.30.505.10,G3DSA:3.30.505.10	SSF55550,SSF55550	155~175,227~247								
aly10422.1	Unknown		n/a																				
aly10423.1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	GO:0016020,GO:0006486,GO:0016021,GO:0043686,GO:0035220,GO:0008250,GO:0022416,GO:0004576,GO:0004579,GO:0018279	CG1518-PA																				
aly10451.1	Unknown		n/a												51~71								
aly1046.1	LIM domain-binding protein 2	GO:0001085,GO:0048749,GO:0006909,GO:0030274,GO:0007399,GO:0006357,GO:0008134,GO:0005634,GO:0070983,GO:0007476,GO:0003712,GO:0007563,GO:0022416,GO:0045893,GO:0006351,GO:0005515,GO:0007411,GO:0007350,GO:0010468,GO:0008407	CG3924-PB						PF01803														
aly1046.10	Unknown		n/a																				
aly1046.11	DNA-directed RNA polymerases I, II, and III subunit RPABC3	GO:0005736,GO:0005666,GO:0007095,GO:0005634,GO:0003677,GO:0005654,GO:0006360,GO:0005665,GO:0006366,GO:0003899,GO:0006383	CG11246-PA			PIRSF000779	SM00658		PF03870				G3DSA:2.40.50.140	SSF50249										
aly1046.12	H/ACA ribonucleoprotein complex subunit 4	GO:0031429,GO:0005730,GO:0004730,GO:0000495,GO:0005634,GO:0042254,GO:0035220,GO:0031120,GO:0007281,GO:0031118,GO:0009982,GO:0003723,GO:0009267,GO:1990481,GO:0022008,GO:0001522,GO:0006364	CG3333-PF				SM00359	TIGR00425,TIGR00451	PF01509,PF01472,PF08068,PF16198	PS50890			G3DSA:2.30.130.10	SSF88697,SSF55120	476~496								
aly1046.13	Zinc finger protein 26	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872	CG15436-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1046.14	Group 3 secretory phospholipase A2	GO:0006644,GO:0060271,GO:0005814,GO:0016042,GO:0005576,GO:0005509,GO:0005886,GO:0004623	CG1583-PB						PF05826				G3DSA:1.20.90.10	SSF48619		00564+3.1.1.4,00590+3.1.1.4,00592+3.1.1.4,00591+3.1.1.4,00565+3.1.1.4		PWY-7409,PWY-7417,PWY-6803,PWY-7416					
aly1046.2	Translocon-associated protein subunit delta	GO:0005786,GO:0005784,GO:0005783,GO:0070062,GO:0016021,GO:0005811,GO:0006621,GO:0005789,GO:0005048	CG9035-PA						PF05404														
aly1046.3	Cytochrome c oxidase assembly factor 4 homolog,	GO:0005758,GO:0003674,GO:0005739,GO:0033108	CG44194-PA																				
aly1046.4	Methyltransferase-like protein 17, mitochondrial	GO:0005840,GO:0005634,GO:0005739,GO:0005654,GO:0008168,GO:0005507,GO:0006412	CG13126-PA						PF09243				G3DSA:3.40.50.150	SSF53335									
aly1046.5	Unknown	GO:0016787,GO:0046872,GO:0003676	CG6839-PA				SM00892		PF01223				G3DSA:3.40.570.10	SSF54060									
aly1046.6	Probable tyrosyl-DNA phosphodiesterase	GO:0005737,GO:0006281,GO:0005634,GO:0008081,GO:0045197,GO:0017005,GO:0004527,GO:0007417	CG8825-PA						PF06087				G3DSA:3.30.870.10	SSF56024									
aly1046.7	Protein VPRBP	GO:0005737,GO:0000122,GO:1990245,GO:1990244,GO:0035212,GO:0030183,GO:0005634,GO:0033151,GO:0005575,GO:0016567,GO:0003674,GO:0006351,GO:0005515,GO:0016032,GO:0005730,GO:0005524	CG10080-PA				SM00667			PS50896			G3DSA:2.130.10.10	SSF50978									
aly1046.8	Protein single-minded	GO:0035225,GO:0007418,GO:0007419,GO:0001077,GO:0007165,GO:0004871,GO:0007411,GO:0007417,GO:0005737,GO:0043565,GO:0005634,GO:0006366,GO:0000982,GO:0007628,GO:0007409,GO:0000978,GO:0040011,GO:0007420,GO:0007399,GO:0007398,GO:0003700,GO:0006355,GO:0045944,GO:0005667,GO:0046983,GO:0046982	CG7771-PA				SM00353,SM00091,SM00091		PF00989	PS50112,PS50888,PS50112	PR00785,PR00785,PR00785,PR00785		G3DSA:4.10.280.10,G3DSA:3.30.450.20,G3DSA:3.30.450.20	SSF47459,SSF55785,SSF55785									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1046.9	Unknown		n/a																				
aly1047.1	Fanconi anemia group J protein homolog	GO:0005737,GO:0051539,GO:0006281,GO:0004003,GO:0031965,GO:0006289,GO:0005654,GO:0006357,GO:0003677,GO:0046872,GO:0005524	CG4078-PA				SM00488,SM00491		PF06733,PF13307	PS51193			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540										
aly1047.2	Optomotor-blind protein	GO:0007472,GO:0000122,GO:0003700,GO:0005634,GO:0003677,GO:0007476,GO:0048066,GO:0006355,GO:0048100,GO:0006351,GO:0005515,GO:0035265,GO:0001745	CG3578-PF				SM00425		PF00907	PS50252	PR00937,PR00937,PR00937,PR00937,PR00937,PR00937	PS01283,PS01264	G3DSA:2.60.40.820	SSF49417										
aly1047.3	Adenosine deaminase CECR1	GO:0042386,GO:0005615,GO:0043617,GO:0004000,GO:0008283,GO:0008201,GO:0043394,GO:0008270,GO:0031685,GO:0043103,GO:0046103,GO:0006109,GO:0005829,GO:0006154,GO:0008083	CG5992-PA					TIGR01431	PF00962,PF08451				G3DSA:3.20.20.140,G3DSA:3.20.20.140	SSF51556,SSF51556		00230+3.5.4.4		PWY-6609,PWY-7179,PWY-7179-1,PWY-6611					
aly1047.4	Adenosine deaminase CECR1	GO:0042386,GO:0005615,GO:0043617,GO:0004000,GO:0008283,GO:0008201,GO:0043394,GO:0008270,GO:0031685,GO:0007275,GO:0043103,GO:0046103,GO:0042803,GO:0006109,GO:0005829,GO:0006154,GO:0008083	CG5992-PA					TIGR01431	PF00962,PF08451				G3DSA:3.20.20.140,G3DSA:3.20.20.140	SSF51556,SSF51556		00230+3.5.4.4		PWY-6609,PWY-7179,PWY-7179-1,PWY-6611					
aly1047.5	Adenosine deaminase CECR1	GO:0042386,GO:0005615,GO:0043617,GO:0004000,GO:0008283,GO:0008201,GO:0043394,GO:0008270,GO:0031685,GO:0043103,GO:0046103,GO:0006109,GO:0005829,GO:0006154,GO:0008083	CG5992-PA					TIGR01431	PF00962,PF08451				G3DSA:3.20.20.140,G3DSA:3.20.20.140	SSF51556,SSF51556		00230+3.5.4.4		PWY-6609,PWY-7179,PWY-7179-1,PWY-6611					
aly1047.6	Trafficking protein particle complex subunit 3	GO:0005737,GO:0006891,GO:0033227,GO:0006888,GO:0016192,GO:0005829,GO:0017112,GO:0000139,GO:0022008,GO:0030008,GO:0005783	CG3911-PA			PIRSF018293			PF04051				G3DSA:3.30.1380.20	SSF111126	26~46								
aly104730.1	Prolactin regulatory element-binding protein	GO:0000902,GO:0009306,GO:0005634,GO:0006366,GO:0005789,GO:0016192,GO:0006355,GO:0001077,GO:0045944,GO:0003677,GO:0015031,GO:0016021,GO:0005783	CG9175-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10481.1	Cathepsin K	GO:0048102,GO:0008234,GO:0005615,GO:0036021,GO:0030198,GO:0002224,GO:0006508,GO:0022617,GO:0001968,GO:0005576,GO:0035071,GO:0045087,GO:1903955,GO:0043394,GO:0030163,GO:0045453,GO:0051603,GO:0001957,GO:0030574,GO:0045169,GO:0005764,GO:0004197,GO:0005518,GO:1903146	CG6692-PC						PF00112				G3DSA:3.90.70.10	SSF54001										
aly10484.1	Peroxisomal N(1)-acetyl-spermine/spermidine oxidase	GO:0006598,GO:0052899,GO:0005782,GO:0046208,GO:0009447,GO:0009446,GO:0046203,GO:1901307,GO:0046592,GO:0052901,GO:0005102,GO:0052903,GO:0052904,GO:0052902,GO:0055114,GO:0016491	CG7737-PB						PF01593		PR00757,PR00757		G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905										
aly10484.2	Unknown		CG14223-PA						PF15038														
aly10484.3	Survival motor neuron protein	GO:0007409,GO:0032797,GO:0030240,GO:0031594,GO:0030018,GO:0000245,GO:0005737,GO:0000387,GO:0005634,GO:0031674,GO:0005654,GO:0022618,GO:0051393,GO:0035154,GO:0071254,GO:0007528,GO:0010975,GO:0034719,GO:0005829,GO:0097504,GO:0007019,GO:0003723,GO:0015030,GO:0005681	CG16725-PA				SM00333		PF06003	PS50304			G3DSA:2.30.30.140	SSF63748										
aly10484.4	Myelin expression factor 2	GO:0005737,GO:0006351,GO:0003729,GO:0009952,GO:0030529,GO:0000122,GO:0005634,GO:0000166,GO:0008595,GO:0008298,GO:0003730,GO:0003676,GO:0003723,GO:0000978,GO:0007067,GO:0007277,GO:0001078,GO:0035282,GO:0045451	CG9373-PA				SM00360,SM00360		PF00076	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10484.5	Histone H4 transcription factor	GO:0042393,GO:0000082,GO:0000083,GO:0019899,GO:0010629,GO:0010628,GO:0003676,GO:0003677,GO:0045445,GO:0001078,GO:0001701,GO:0005634,GO:0003713,GO:0005654,GO:0046872,GO:0010468,GO:0006281,GO:0045184,GO:0045892,GO:0045893,GO:0044212,GO:0000077,GO:0003700,GO:0006355,GO:0006351,GO:0015030,GO:0000978,GO:0003682	CG17829-PA																				
aly10484.6	Unknown		n/a																				
aly105069.1	Unknown	GO:0005737,GO:0016239,GO:0050688,GO:0048477,GO:0016236,GO:0035096,GO:0003824,GO:0009267,GO:0008340,GO:0010506	CG5489-PA						PF16420														
aly1051.1	Unknown	GO:0005575,GO:0003674,GO:0008150	CG43394-PC																				
aly1051.2	Unknown		n/a																				
aly1051.3	ATP-dependent RNA helicase abstrakt	GO:0010501,GO:0007399,GO:0008026,GO:0071011,GO:0005634,GO:0006915,GO:0000398,GO:0004386,GO:0004004,GO:0030010,GO:0005524,GO:0003723,GO:0009653,GO:0071013,GO:0003676,GO:0008270	CG14637-PA				SM00487		PF00270,PF00271	PS51195,PS51192,PS51194			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	106~126								
aly1051.4	ATP-dependent RNA helicase abstrakt	GO:0030010,GO:0010501,GO:0008026,GO:0007399,GO:0071011,GO:0005634,GO:0006915,GO:0004004,GO:0000398,GO:0004386,GO:0008270,GO:0003676,GO:0009653,GO:0071013,GO:0005524,GO:0003723	CG14637-PA						PF00098				G3DSA:4.10.60.10	SSF57756									
aly1051.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1051.6	Zinc finger protein 616	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG31632-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60	SSF57667,SSF57667									
aly1051.7	Unknown	GO:0003676	n/a				SM00980		PF05485	PS50950				SSF57716									
aly1052.1	Unknown	GO:0043565,GO:0010259,GO:0007623,GO:0007622,GO:0006351,GO:0007424,GO:0005634,GO:0009987,GO:0008407,GO:0007275,GO:0006355,GO:0045823,GO:0045475,GO:0046982,GO:0001078,GO:0035317,GO:0042803	CG14029-PA										G3DSA:1.20.5.170		212~232,7~27								
aly1052.10	Unknown		n/a																				
aly1052.2	Protein THEM6	GO:0005576	CG4660-PA						PF13279				G3DSA:3.10.129.10	SSF54637									
aly1052.3	Unknown	GO:0003677	CG8359-PA				SM00595		PF10545	PS51031,PS51029													
aly1052.4	Unknown		CG7692-PA												1534~1554,3546~3566,1215~1235								
aly1052.5	Rho GTPase-activating protein 190	GO:0016319,GO:0043547,GO:0045792,GO:0050770,GO:0005096,GO:0005622,GO:0005575,GO:0005100,GO:0007266,GO:0005525,GO:0007415,GO:0030215	CG32555-PF				SM00324,SM00173		PF16512,PF00620	PS51676,PS51676,PS50238			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.555.10	SSF48350,SSF52540,SSF52540			REACT_11044						
aly1052.6	Unknown		CG15186-PF										G3DSA:1.20.5.170		51~85								
aly1052.7	Unknown	GO:0003677	CG4404-PA				SM00595		PF10545	PS51029													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1052.8	Transcription factor Adf-1	GO:0040011,GO:0006366,GO:0050773,GO:0007616,GO:0005634,GO:0005705,GO:0007613,GO:0007611,GO:0048813,GO:0001077,GO:0045944,GO:0045893,GO:0005667,GO:0003677,GO:0008345,GO:0003712,GO:0007416,GO:0008355	CG10949-PA				SM00595,SM00595		PF10545,PF10545,PF02944	PS51031,PS51029,PS51029														
aly1052.9	Nuclear factor interleukin-3-regulated protein	GO:0005737,GO:0043565,GO:0006366,GO:0010259,GO:0007623,GO:0007622,GO:0006351,GO:0007424,GO:0003700,GO:0005634,GO:0009987,GO:0008407,GO:0007275,GO:0006355,GO:0045823,GO:0045475,GO:0006955,GO:0046982,GO:0001078,GO:0035317,GO:0042803	CG14029-PA																				
aly105526.1	TBC1 domain family member 20	GO:0044829,GO:0007030,GO:0070309,GO:0005783,GO:0032313,GO:0031965,GO:0019068,GO:0005096,GO:0005097,GO:0005789,GO:0034389,GO:0030173,GO:0072520,GO:1902953,GO:0001675,GO:0046726,GO:0090110	CG17883-PA						PF00566	PS50086				SSF47923									
aly10578.1	Nicotinamide/nicotinic acid mononucleotide adenylyltransferase 1	GO:0097062,GO:0000309,GO:0004515,GO:0005634,GO:0009435,GO:0045494,GO:0005524	CG13645-PA						PF01467				G3DSA:3.40.50.620	SSF52374,SSF52374									
aly1060.1	Zinc finger Ran-binding domain-containing protein 2	GO:0008380,GO:0005634,GO:0006397,GO:0008270,GO:0003723	CG3732-PA				SM00547,SM00547		PF00641,PF00641	PS50199,PS50199		PS01358,PS01358	G3DSA:4.10.1060.10,G3DSA:4.10.1060.10	SSF90209,SSF90209									
aly1060.10	Unknown	GO:0050829,GO:0005737,GO:0005634,GO:0007476,GO:0002218	CG32464-PV																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1060.2	Prenylated Rab acceptor protein 1	GO:0005794,GO:0008021,GO:0016021,GO:0017137,GO:0005886,GO:0030054	CG1418-PA						PF03208														
aly1060.3	Transcription factor E2F7	GO:0060718,GO:0008284,GO:0001047,GO:0035206,GO:0003677,GO:0000082,GO:0000083,GO:0001077,GO:0007307,GO:0043565,GO:2000134,GO:0019730,GO:0000122,GO:0005634,GO:0003714,GO:0007476,GO:0001946,GO:0032466,GO:0002040,GO:0070365,GO:0000981,GO:0048666,GO:0008285,GO:0045850,GO:0005515,GO:0030330,GO:0001012,GO:0008134,GO:0009987,GO:0042023,GO:0045893,GO:0045476,GO:0040007,GO:0071930,GO:0051726,GO:0003700,GO:0007444,GO:0006355,GO:0048813,GO:0010628,GO:0045944,GO:0006351,GO:0005667,GO:0060537,GO:0035189,GO:0032877	CG6376-PD						PF02319,PF02319				G3DSA:1.10.10.10,G3DSA:1.10.10.10	SSF46785,SSF46785									
aly1060.4	Unknown	GO:0005845,GO:0046331,GO:0032259,GO:0003723	CG13807-PA						PF15320														
aly1060.5	Nuclear receptor coactivator 7	GO:0005737,GO:0002218,GO:0005634,GO:0007476,GO:0006355,GO:0006351,GO:0050829	CG32464-PV				SM00584,SM00257		PF07534,PF01476				G3DSA:3.10.350.10	SSF54106									
aly1060.6	Ankyrin repeat domain-containing protein 13C	GO:0005783,GO:0048471,GO:0006621,GO:0005789,GO:0010869,GO:0005102,GO:2000209,GO:0022008	CG5742-PC				SM00248,SM00248,SM00248		PF12796,PF11904	PS50088,PS50297			G3DSA:1.25.40.20	SSF48403									
aly1060.7	Unknown		n/a																				
aly1060.8	Unknown		n/a																				
aly1060.9	Unknown	GO:0050829,GO:0005737,GO:0005634,GO:0007476,GO:0002218	CG32464-PV																				
aly106036.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1063.1	Sex peptide receptor	GO:0045434,GO:0008528,GO:0004930,GO:0016021,GO:0005886,GO:0048042,GO:0008188,GO:0007186	CG13229-PA						PF10324,PF10324	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1063.2	Tyrosine-protein kinase Src42A	GO:0016319,GO:0007616,GO:0034332,GO:0043277,GO:0008335,GO:0030036,GO:0007611,GO:0008064,GO:0007301,GO:0006099,GO:0045886,GO:0030717,GO:0042059,GO:0007169,GO:0007411,GO:0008355,GO:0005737,GO:0007254,GO:0007435,GO:0045172,GO:0007476,GO:0007349,GO:0030723,GO:0004715,GO:0004713,GO:0005886,GO:0016477,GO:0048477,GO:0005524,GO:0048749,GO:0006468,GO:0051017,GO:0030708,GO:0036058,GO:0018108,GO:0008302,GO:0090136,GO:0030046,GO:0036335,GO:0007424,GO:0007300,GO:0007293,GO:0007395,GO:0007391,GO:0042742,GO:0046529,GO:0045860,GO:0005912	CG7524-PK				SM00326		PF00018	PS50002	PR01887,PR01887,PR01887,PR00452,PR00452,PR00452		G3DSA:2.30.30.40	SSF50044										
aly1063.3	Unknown		n/a																				
aly1063.4	Tyrosine-protein kinase Src42A	GO:0034332,GO:0005886,GO:0042059,GO:0006099,GO:0045886,GO:0042742,GO:0007154,GO:0007169,GO:0005737,GO:0007254,GO:0007435,GO:0007476,GO:0004715,GO:0004713,GO:0016477,GO:0046529,GO:0048749,GO:0006468,GO:0051017,GO:0018108,GO:0043277,GO:0090136,GO:0036335,GO:0007424,GO:0007395,GO:0007411,GO:0007391,GO:0005524,GO:0005912	CG44128-PB						PF00017	PS50001	PR00401,PR00401,PR00401		G3DSA:3.30.505.10	SSF55550										
aly10630.1	Protein vestigial	GO:0008022,GO:0044719,GO:0008587,GO:0035220,GO:0003677,GO:0001745,GO:0007049,GO:0007346,GO:0007472,GO:0007473,GO:0005634,GO:0016204,GO:0007476,GO:0007451,GO:0006260,GO:0042127,GO:0048190,GO:0007482,GO:0007480,GO:0007525,GO:0003705,GO:0045944,GO:0006351,GO:0005515	CG3830-PA																					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10630.2	Unknown	GO:0000502	CG13319-PA																				
aly10630.3	Endoplasmin	GO:0006457,GO:0005783,GO:0061031,GO:0005788,GO:0031247,GO:0007494,GO:0034663,GO:0005925,GO:0001666,GO:0005615,GO:0005789,GO:0005634,GO:0005811,GO:0051082,GO:0043066,GO:0005886,GO:0071318,GO:0050750,GO:0005524,GO:0006950,GO:0030433,GO:0031012,GO:0048471,GO:0070062,GO:0042470,GO:0043666,GO:0005829,GO:0030496,GO:0046790,GO:0003723	CG5520-PA	MF_00505		PIRSF002583			PF00183,PF02518		PR00775,PR00775,PR00775,PR00775,PR00775,PR00775,PR00775	PS00298	G3DSA:3.30.565.10,G3DSA:3.30.565.10	SSF110942,SSF54211,SSF55874									
aly10630.4	Solute carrier family 35 member E1 homolog	GO:0015297,GO:0005783,GO:0016021,GO:0016020,GO:0008524,GO:0005575,GO:0008150,GO:0098656,GO:0034219	CG14621-PA						PF03151														
aly10630.5	Palmitoyltransferase ZDHHC18	GO:0042127,GO:0007389,GO:0005783,GO:0007480,GO:0016409,GO:0016021,GO:0034613,GO:0045179,GO:0008270,GO:0005794,GO:0048104,GO:0019706,GO:0001737,GO:0018345	CG42318-PJ						PF01529	PS50216													
aly10630.6	Unknown		CG34391-PD										G3DSA:2.60.40.10										
aly10630.7	Unknown		n/a						PF15868														
aly10630.8	Connector enhancer of kinase suppressor of ras 2	GO:0005737,GO:0005794,GO:0045177,GO:0007426,GO:0070062,GO:0045211,GO:0009966,GO:0043025,GO:0007476,GO:0008586,GO:0019899,GO:0043005,GO:0008595,GO:0005913,GO:0007165,GO:0005515,GO:0005886,GO:0008293,GO:0007265,GO:0001751,GO:0097481	CG6556-PA							PS51290,PS50105			G3DSA:2.30.29.30,G3DSA:1.10.150.50,G3DSA:2.30.42.10	SSF50729,SSF47769,SSF50156	863~883								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10630.9	Protein vestigial	GO:0008022,GO:0044719,GO:0008587,GO:0035220,GO:0003677,GO:0001745,GO:0007049,GO:0007346,GO:0007472,GO:0007473,GO:0005634,GO:0016204,GO:0007476,GO:0007451,GO:0006260,GO:0042127,GO:0048190,GO:0007482,GO:0007480,GO:0007525,GO:0003705,GO:0006355,GO:0045944,GO:0006351,GO:0005515	CG3830-PA						PF07545														
aly106523.1	Unknown		n/a																				
aly10672.1	Complexin	GO:0048786,GO:0043195,GO:0005615,GO:0032504,GO:0051124,GO:0016079,GO:0005829,GO:0016020,GO:0050804,GO:0031594,GO:0046928,GO:0003674,GO:0007274,GO:0005326	CG32490-PAB						PF05835				G3DSA:1.20.5.580	SSF58038	31~76								
aly10672.10	Protein Skeletor, isoforms B/C	GO:0005737,GO:0006997,GO:0005819,GO:0051321,GO:0004500,GO:0005634,GO:0005730,GO:0006584,GO:0005700,GO:0055114,GO:0007067,GO:0005874,GO:0051225,GO:0051301	CG34355-PE				SM00664,SM00686,SM00686		PF03351,PF10517,PF10517	PS51549,PS50836,PS51549													
aly10672.11	Unknown		n/a																				
aly10672.12	Unknown		n/a																				
aly10672.2	Heparanase	GO:0005811,GO:0005975,GO:0030200,GO:0030305,GO:0005634,GO:0016020,GO:0016798,GO:0005765,GO:0005576,GO:0007155	CG14309-PA																				
aly10672.3	Nuclear hormone receptor HR96	GO:0006351,GO:0070328,GO:0043401,GO:0003700,GO:0005634,GO:0003707,GO:0006355,GO:0000977,GO:0042594,GO:0003677,GO:0042632,GO:0070873,GO:0030522,GO:0004879,GO:0008270	CG11783-PA				SM00399,SM00430		PF00105,PF00104	PS51030	PR00047,PR00047,PR00047,PR00047,PR00398,PR00398,PR00398,PR00398,PR00398	PS00031	G3DSA:1.10.565.10,G3DSA:1.10.565.10,G3DSA:1.10.565.10,G3DSA:3.30.50.10	SSF57716,SSF48508			REACT_71							
aly10672.4	Unknown	GO:0005737,GO:0005794,GO:0008283,GO:0005634,GO:0005802,GO:0030177,GO:0003674,GO:0007269,GO:0048477,GO:0005769,GO:0048488	CG42250-PC																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10672.5	Telomere length regulation protein TEL2 homolog	GO:0005737,GO:0005794,GO:0016020,GO:0008283,GO:0005634,GO:0005802,GO:0030177,GO:0003674,GO:0007269,GO:0048477,GO:0005769,GO:0048488	CG31285-PA						PF10193														
aly10672.6	Clathrin interactor 1	GO:0005737,GO:0005794,GO:0016020,GO:0006897,GO:0043231,GO:0008283,GO:0005634,GO:0005802,GO:0008289,GO:0005654,GO:0030177,GO:0003674,GO:0007269,GO:0030276,GO:0048471,GO:0048477,GO:0005769,GO:0048488,GO:0030136	CG42250-PC				SM00273		PF01417	PS50942			G3DSA:1.25.40.90	SSF48464										
aly10672.7	TBC1 domain family member 7	GO:0036064,GO:0032313,GO:0005096,GO:0090630,GO:0005097,GO:0017137,GO:0016023,GO:1902018,GO:0031398,GO:0031410,GO:0032007,GO:0070848	CG6182-PA						PF00566	PS50086				SSF47923,SSF47923,SSF47923	205~225									
aly10672.8	Dynein assembly factor 1, axonemal	GO:0060271,GO:0045502,GO:0044458,GO:0005575,GO:0005515,GO:0007268,GO:0005930	CG31623-PA				SM00365,SM00365,SM00365,SM00365			PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52075	471~498,502~522,286~313,1048~1078,124~144,558~578									
aly10672.9	Protein Star	GO:0016318,GO:0005783,GO:0048149,GO:0007498,GO:0038004,GO:0035225,GO:0042058,GO:0045467,GO:0009790,GO:0042461,GO:0042051,GO:0000042,GO:0016021,GO:0016020,GO:0007476,GO:0048477,GO:0061331,GO:0005794,GO:0007601,GO:0007173,GO:0005886,GO:0046667,GO:0001751,GO:0048865,GO:0097038,GO:0007421,GO:0007422,GO:0000139,GO:0005789,GO:0046845	CG4385-PB																				
aly10679.1	Unknown		n/a																				
aly1068.1	Unknown		n/a				SM00034,SM00034		PF00059,PF00059	PS50041,PS50041			G3DSA:3.10.100.10,G3DSA:3.10.100.10	SSF56436,SSF56436									
aly1068.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1068.3	Unknown		n/a																				
aly1068.4	CTD small phosphatase-like protein 2	GO:0016791,GO:0006470,GO:0005634,GO:0004721,GO:0046827,GO:0030514	CG5830-PB				SM00577	TIGR02251	PF03031	PS50969			G3DSA:3.40.50.1000	SSF56784									
aly1068.5	Uncharacterized protein CG4449	GO:0005575,GO:0008150,GO:0003674	CG4449-PA						PF11976				G3DSA:3.10.20.90,G3DSA:3.10.20.90	SSF54236	16~36								
aly1068.6	Unknown	GO:0005975,GO:0005615,GO:0005576,GO:0008061,GO:0004568,GO:0006030,GO:0006032	CG9307-PA				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly1068.7	Unknown	GO:0006030,GO:0005576,GO:0008061,GO:0016490	CG10725-PA				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly10694.1	SEC23-interacting protein	GO:0070971,GO:0001675,GO:0043231,GO:0005801,GO:0008970,GO:0007286,GO:0097038,GO:0007338,GO:0012507,GO:0048471,GO:0046872,GO:0044822	CG8552-PA							PS50918					919~949								
aly107.1	Unknown		n/a																				
aly107.10	Neuropeptides capa receptor	GO:0004930,GO:0007589,GO:0007186,GO:0016021,GO:0051928,GO:0007218,GO:0016323,GO:0071465,GO:0005887,GO:0008188,GO:0001607	CG14575-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR01565,PR01565,PR01565	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly107.11	Histone acetyltransferase KAT2A	GO:0021537,GO:1990090,GO:0031647,GO:0035066,GO:0003713,GO:0022037,GO:0031667,GO:0035264,GO:0007412,GO:0010485,GO:0010484,GO:0044154,GO:0000124,GO:0007517,GO:0001701,GO:0005615,GO:0000123,GO:0071929,GO:0005634,GO:0055007,GO:0004402,GO:0048813,GO:0043997,GO:0030914,GO:0033276,GO:0005671,GO:1903955,GO:0014070,GO:0016573,GO:0001843,GO:0031346,GO:0042826,GO:0016578,GO:0006351,GO:0048312,GO:1903146,GO:0043966,GO:0043967,GO:0008134,GO:0000790,GO:0072686,GO:0001756,GO:0008283,GO:0008080,GO:0006338,GO:0035948,GO:0043983,GO:0071356,GO:0005703,GO:0005700,GO:0006355,GO:0016407,GO:0030901,GO:0007399,GO:0003682,GO:2000679	CG4107-PA				SM00297		PF00439,PF06466	PS50014	PR00503,PR00503,PR00503,PR00503	PS00633	G3DSA:1.20.920.10,G3DSA:3.40.630.30	SSF47370			REACT_71						
aly107.12	Protein goliath	GO:0001707,GO:0016567,GO:0007498,GO:0061630,GO:0005634,GO:0006355,GO:0008270,GO:0005515,GO:0003677,GO:0005768,GO:0016021,GO:0006351	CG2679-PD				SM00184		PF13639,PF02225	PS50089,PS51257			G3DSA:3.30.40.10,G3DSA:3.50.30.30	SSF57850,SSF52025									
aly107.13	Unknown		n/a																				
aly107.14	Cytoskeleton-associated protein 5	GO:0000086,GO:0035371,GO:0005488,GO:0007411,GO:0007067,GO:0000922,GO:0005875,GO:0051301,GO:0007344,GO:0000022,GO:0007029,GO:0005813,GO:0090063,GO:0016020,GO:0007143,GO:0048477,GO:0051297,GO:0043234,GO:0015631,GO:0000278,GO:0016325,GO:0008017,GO:0031122,GO:0007051,GO:0007264,GO:0045450,GO:0006996,GO:0050658,GO:0007017,GO:0030951,GO:0005829,GO:0005515	CG5000-PD						PF12348,PF12348	PS50077			G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371									
aly107.2	Alpha-(1,3)-fucosyltransferase C	GO:0036065,GO:0006486,GO:0016021,GO:0016020,GO:0008417,GO:0005886,GO:0032580,GO:0046920	CG40305-PB						PF17039,PF00852					SSF53756					UPA00378				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly107.3	Unknown		n/a																				
aly107.4	Alpha-(1,3)-fucosyltransferase C	GO:0036065,GO:0006486,GO:0016021,GO:0016020,GO:0008417,GO:0005886,GO:0032580,GO:0046920	CG40305-PB						PF17039,PF00852					SSF53756					UPA00378				
aly107.5	T-complex protein 11-like protein 1	GO:0005874	CG16721-PB						PF05794														
aly107.6	RNA polymerase II-associated factor 1 homolog	GO:0001711,GO:0006351,GO:0019894,GO:0071222,GO:0000122,GO:0016055,GO:0031442,GO:0045638,GO:0045944,GO:0035327,GO:0016570,GO:0016593,GO:0006368,GO:0022008,GO:0000993,GO:0032968,GO:0006378,GO:0045893	CG2503-PA						PF03985														
aly107.7	Nucleosome assembly protein 1-like 1	GO:0005737,GO:0042470,GO:0042393,GO:0005634,GO:0016020,GO:0044822,GO:0006635,GO:0016590,GO:0006334	CG5330-PA						PF00956					SSF143113									
aly107.8	Stromal interaction molecule homolog	GO:0016021,GO:0006611,GO:0070588,GO:0005789,GO:0005737,GO:0015279,GO:0032237,GO:0005634,GO:0007476,GO:0005509,GO:0048763,GO:0022416,GO:0012505,GO:0005886,GO:0007155,GO:0005049,GO:0002115,GO:0005643,GO:0051924,GO:0008536,GO:0051533,GO:0005513,GO:0005515,GO:0006886	CG9126-PA				SM00454		PF07647,PF16533	PS50105			G3DSA:1.10.150.50	SSF47769	212~260,469~489,272~292,359~379,323~343								
aly107.9	cAMP-responsive element-binding protein-like 2	GO:0043565,GO:0003700,GO:0005634,GO:0030154,GO:0006355,GO:0045600,GO:0045893,GO:0046326,GO:0046889,GO:0046983,GO:0006351	CG18619-PA						PF07716				G3DSA:1.20.5.170	SSF57959	56~76								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly107139.1	Unknown		CG14445-PC											SSF54928									
aly10722.1	Unknown		n/a																				
aly107289.1	Cell division cycle protein 16 homolog	GO:0045842,GO:0051439,GO:0090302,GO:0051437,GO:0051436,GO:0030071,GO:0051301,GO:0005737,GO:0005819,GO:0070979,GO:0005813,GO:0005654,GO:0007088,GO:0000278,GO:0007067,GO:0008283,GO:0031145,GO:0022008,GO:0004842,GO:0005829,GO:0007094,GO:0005680	CG6759-PA										G3DSA:1.25.40.10	SSF48452									
aly1073.1	Unknown		n/a																				
aly1073.10	Unknown		n/a																				
aly1073.11	Geranylgeranyl pyrophosphate synthase	GO:0004161,GO:0006720,GO:0005829,GO:0033384,GO:0035050,GO:0045337,GO:0008299,GO:0004311,GO:0006695,GO:0033386,GO:0004337,GO:0022008,GO:0046872,GO:0008354,GO:0044281	CG8593-PA						PF00348			PS00444,PS00723	G3DSA:1.10.600.10	SSF48576									
aly1073.12	Geranylgeranyl pyrophosphate synthase	GO:0005737,GO:0004161,GO:0006720,GO:0033384,GO:0035050,GO:0045337,GO:0008299,GO:0004311,GO:0033386,GO:0004337,GO:0022008,GO:0046872,GO:0008354	CG8593-PA						PF00348				G3DSA:1.10.600.10	SSF48576									
aly1073.13	Geranylgeranyl pyrophosphate synthase	GO:0005737,GO:0004161,GO:0006720,GO:0033384,GO:0035050,GO:0045337,GO:0008299,GO:0004311,GO:0033386,GO:0004337,GO:0022008,GO:0046872,GO:0008354	CG8593-PA						PF00348				G3DSA:1.10.600.10	SSF48576									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1073.14	Geranylgeranyl pyrophosphate synthase	GO:0005737,GO:0004161,GO:0006720,GO:0033384,GO:0035050,GO:0045337,GO:0008299,GO:0004311,GO:0033386,GO:0004337,GO:0022008,GO:0046872,GO:0008354	CG8593-PA						PF00348				G3DSA:1.10.600.10	SSF48576									
aly1073.15	Pyruvate kinase	GO:0030955,GO:0000287,GO:0043186,GO:0016310,GO:0005829,GO:0005811,GO:0007525,GO:0007520,GO:0004743,GO:0006096,GO:0005524	CG7070-PA				SM00368,SM00368	TIGR01064	PF03250,PF00224,PF02887		PR01050,PR01050,PR01050,PR01050,PR01050,PR01050,PR01050	PS00110	G3DSA:2.40.33.10,G3DSA:3.20.20.60,G3DSA:3.20.20.60,G3DSA:3.40.1380.20,G3DSA:3.80.10.10	SSF52935,SSF52047,SSF50800,SSF51621,SSF51621		00230+2.7.1.40,00010+2.7.1.40,00620+2.7.1.40	REACT_474	PWY-1042,PWY-2221,PWY-6901,PWY-7218,PWY-7383,PWY-6886,PWY-5723,PWY-6142,PWY-5484,PWY-7003	UPA00109				
aly1073.16	Ubiquitin carboxyl-terminal hydrolase 1	GO:0006282,GO:0006281,GO:0009411,GO:0005634,GO:0004843,GO:0006511,GO:0035520,GO:0016579,GO:0036459	CG15817-PE						PF00443	PS50235				SSF54001,SSF54001,SSF54001	283~303								
aly1073.17	Unknown		n/a										G3DSA:3.30.40.10	SSF57903	178~198								
aly1073.18	Geranylgeranyl pyrophosphate synthase	GO:0005737,GO:0004161,GO:0006720,GO:0033384,GO:0035050,GO:0045337,GO:0008299,GO:0004311,GO:0033386,GO:0004337,GO:0022008,GO:0046872,GO:0008354	CG8593-PA						PF00348,PF00348				G3DSA:1.10.600.10,G3DSA:1.10.600.10	SSF48576,SSF48576									
aly1073.19	Unknown	GO:0000276,GO:0015992,GO:0005811,GO:0015986,GO:0008553,GO:0015078	CG3321-PA						PF05680														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1073.2	Methionine aminopeptidase 1	GO:0004177,GO:0022626,GO:0070084,GO:0070006,GO:0006508,GO:0046872,GO:0008235	CG13630-PA	MF_01974				TIGR00500	PF15801,PF00557		PR00599,PR00599,PR00599,PR00599	PS00680	G3DSA:3.90.230.10	SSF55920									
aly1073.3	Unknown		n/a																				
aly1073.4	Unknown		CG14257-PB																				
aly1073.5	Lipase member I	GO:0006629,GO:0016020,GO:0052689,GO:0016042,GO:0005575,GO:0003824,GO:0005576,GO:0008150,GO:0005886,GO:0003674,GO:0004620,GO:0008201,GO:0005615	CG18258-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly1073.6	Unknown		n/a						PF16077					SSF57501									
aly1073.7	Protein spaetzle	GO:0005125,GO:0019732,GO:0008592,GO:0005121,GO:0021556,GO:0006967,GO:0006965,GO:0000578,GO:0008045,GO:0007411,GO:0010941,GO:0031637,GO:0008083,GO:0042803,GO:0007310,GO:0045087,GO:0031334,GO:0050832,GO:0050830,GO:0007311,GO:0006955,GO:0005615,GO:0043234,GO:0006952,GO:0009953,GO:0007399,GO:0009950,GO:0009620,GO:0031640,GO:0005576,GO:0016015,GO:0008063	CG9972-PA						PF16077					SSF57501									
aly1073.8	Protein CutA homolog	GO:0010038	CG11590-PA						PF03091				G3DSA:3.30.70.830	SSF54913									
aly1073.9	Calcium-activated potassium channel slowpoke	GO:0007623,GO:0043005,GO:0045433,GO:0006813,GO:0008582,GO:0016020,GO:0042493,GO:0008076,GO:0071805,GO:0048512,GO:0060072,GO:0005515,GO:0005249,GO:0005886,GO:0043025,GO:0015269,GO:1900074	CG10693-PT						PF00520,PF03493		PR01449,PR01449,PR01449,PR01449,PR01449,PR01449,PR00169,PR00169,PR00169,PR00169,PR00169		G3DSA:1.10.287.70,G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735,SSF81324									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10736.1	Unknown		n/a																				
aly10736.2	Unknown		n/a																				
aly10736.3	Unknown		n/a																				
aly1074.1	Unknown		n/a																				
aly1074.2	Coronin-7	GO:0015629,GO:0030426,GO:0030036,GO:0031594,GO:0007411,GO:0031532,GO:0003779,GO:0005794,GO:0008017,GO:0051015,GO:0005881,GO:0005884,GO:0030041,GO:0030674,GO:0006895,GO:0005829,GO:0005802,GO:0000139,GO:0016023,GO:0005515,GO:0097113,GO:0015031	CG4532-PG				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF16300,PF16300,PF00400,PF00400,PF08953,PF08953	PS50294,PS50082,PS50294,PS50082,PS50082,PS50082		PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978	519~539								
aly1074.3	Ras-related protein Rab-30	GO:0008258,GO:0045202,GO:0005737,GO:0031985,GO:0031982,GO:0031410,GO:0006886,GO:0016020,GO:0046529,GO:0005525,GO:0005794,GO:0003924,GO:0032482,GO:0008152,GO:0007264,GO:0007030,GO:0034389,GO:0016192,GO:0005801,GO:0005802,GO:0007391,GO:0007390,GO:0005515,GO:0015031,GO:0005768	CG9100-PA				SM00173,SM00175,SM00174,SM00176	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly1074.4	Speckle-type POZ protein-like	GO:0043161,GO:0031648,GO:0042067,GO:0048592,GO:0007349,GO:0045879,GO:0043065,GO:0016567,GO:0046330,GO:0046331,GO:0030162,GO:0005515,GO:0042308,GO:0031397,GO:0031463,GO:0005634,GO:0042803	CG12537-PF				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695									
aly1074.5	Probable RNA binding protein EIF1AD	GO:0005575,GO:0005634,GO:0006413,GO:0003743	CG31957-PA				SM00652		PF01176	PS50832			G3DSA:2.40.50.140	SSF50249									
aly1074.6	DNA polymerase subunit gamma-1, mitochondrial	GO:0003887,GO:0005739,GO:0006264,GO:0005760,GO:0007562,GO:0003677,GO:0008340,GO:0008296,GO:0071897,GO:0006261	CG8987-PA				SM00482		PF00476,PF01217,PF00928	PS51072	PR00314,PR00314,PR00314,PR00314,PR00314,PR00314,PR00314	PS00447,PS00990,PS00991	G3DSA:3.30.70.370,G3DSA:3.30.70.370,G3DSA:3.30.70.370,G3DSA:2.60.40.1170,G3DSA:3.30.450.60,G3DSA:1.10.150.20	SSF56672,SSF56672,SSF56672,SSF53098,SSF64356,SSF49447		00240+2.7.7.7,00230+2.7.7.7							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1074.7	Peptidyl-prolyl cis-trans isomerase D	GO:0006457,GO:0031072,GO:0042981,GO:0005737,GO:0043065,GO:0000413,GO:0042277,GO:0000122,GO:0030544,GO:0005634,GO:0045070,GO:0005654,GO:0005528,GO:0003755,GO:0051879,GO:0006461,GO:0030331,GO:0071492,GO:0008134,GO:0006915,GO:0061077,GO:0034389,GO:0050714,GO:0005730,GO:0015031	CG8336-PB				SM00028,SM00028		PF00160,PF07719,PF00515	PS50293,PS50072	PR00153,PR00153,PR00153,PR00153,PR00153		G3DSA:2.40.100.10,G3DSA:1.25.40.10	SSF50891,SSF48452									
aly107405.1	Unknown		n/a																				
aly107550.1	Unknown	GO:0003676	n/a						PF05485	PS50950				SSF57716									
aly107760.1	Unknown		n/a																				
aly10783.1	Unknown		n/a																				
aly10783.2	Unknown		n/a						PF05380														
aly10783.3	Unknown	GO:0003676	n/a										G3DSA:3.30.420.10										
aly1079.1	ATP-binding cassette sub-family G member 4	GO:0043190,GO:0042626,GO:0006909,GO:0005215,GO:0016021,GO:0017127,GO:0033344,GO:0016887,GO:0005886,GO:0046982,GO:0055085,GO:0005524,GO:0042803	CG5853-PA				SM00382		PF01061,PF00005	PS50893		PS00211	G3DSA:3.40.50.300	SSF52540									
aly1079.10	Unknown		n/a																				
aly1079.11	Unknown		n/a																				
aly1079.12	Aldehyde dehydrogenase X, mitochondrial	GO:0005975,GO:0004029,GO:0016620,GO:0005739,GO:0043231,GO:0005654,GO:0006068,GO:0008152,GO:0005759,GO:0006090,GO:0055114,GO:0016491	CG31075-PB						PF00171			PS00687,PS00070	G3DSA:3.40.309.10,G3DSA:3.40.605.10	SSF53720									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1079.13	Lipase member H	GO:0004806,GO:0006629,GO:0016020,GO:0052689,GO:0016042,GO:0005576	CG6431-PC						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly1079.14	Aldehyde dehydrogenase X, mitochondrial	GO:0004029,GO:0016620,GO:0005739,GO:0043231,GO:0005654,GO:0006068,GO:0008152,GO:0005759,GO:0006090,GO:0055114,GO:0016491	CG31075-PB						PF00171			PS00687,PS00070	G3DSA:3.40.309.10,G3DSA:3.40.605.10	SSF53720									
aly1079.15	Lipase member H-A	GO:0004806,GO:0006629,GO:0016020,GO:0052689,GO:0016042,GO:0005576	CG6431-PC						PF00151		PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly1079.16	Mitochondrial sodium/hydrogen exchanger 9B2	GO:0005743,GO:0006812,GO:0016021,GO:0015299,GO:0003096,GO:0006814,GO:0034220,GO:0005903,GO:0015385,GO:0055085	CG10806-PA						PF00999														
aly1079.17	Protein fuzzy homolog	GO:0005737,GO:0005856,GO:0008589,GO:0042384,GO:0048704,GO:0007163,GO:0015031,GO:0010172,GO:0001843,GO:0001737,GO:0001736	CG13396-PA																				
aly1079.18	Polycomb protein Sfmbt	GO:0035064,GO:0007446,GO:0006342,GO:0005634,GO:0010629,GO:0008270,GO:0005515,GO:0003677,GO:0003682,GO:0048477,GO:0016568,GO:0006351	CG16975-PC				SM00561,SM00561,SM00561,SM00561		PF02820,PF02820,PF02820,PF02820,PF00536	PS51079,PS51079,PS51079,PS51079,PS51024			G3DSA:2.30.30.160,G3DSA:2.30.30.160,G3DSA:2.30.30.160,G3DSA:2.30.30.160,G3DSA:1.10.150.50	SSF63748,SSF63748,SSF47769,SSF63748,SSF63748									
aly1079.19	Protein argonaute-2	GO:0033227,GO:0030423,GO:0030422,GO:0035087,GO:0048102,GO:0070868,GO:0009047,GO:0005737,GO:0007367,GO:0004521,GO:0007349,GO:0016246,GO:0046872,GO:0070578,GO:0016032,GO:0035071,GO:0045071,GO:0090502,GO:0051607,GO:0007279,GO:0035195,GO:0005829,GO:0035197,GO:0035190,GO:0005515,GO:0016442,GO:0006413,GO:0003743	CG7439-PC						PF02171,PF16486,PF08699,PF16488	PS50821,PS50822			G3DSA:2.170.260.10,G3DSA:3.40.50.2300	SSF53098,SSF101690			REACT_12472						

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1079.2	ATP-binding cassette sub-family G member 1	GO:0009897,GO:0034375,GO:0034374,GO:0055037,GO:0017127,GO:0030301,GO:0034041,GO:0055099,GO:0042987,GO:1901998,GO:0055091,GO:0005548,GO:0042626,GO:0033993,GO:0016021,GO:0005739,GO:0005654,GO:0034436,GO:0034437,GO:0010745,GO:0010875,GO:0005524,GO:0033700,GO:0005794,GO:0006641,GO:0005215,GO:0042803,GO:0043531,GO:0005886,GO:0010872,GO:0042632,GO:0043691,GO:0010033,GO:0008203,GO:0043190,GO:0019534,GO:0043231,GO:0032367,GO:0006355,GO:0033344,GO:0045542,GO:0046982,GO:0005768,GO:0010888	CG17646-PB				SM00382		PF01061,PF00005	PS50893		PS00211	G3DSA:3.40.50.300	SSF52540										
aly1079.20	ABC transporter G family member 42	GO:0043190,GO:0042626,GO:0042048,GO:0005215,GO:0016021,GO:0006810,GO:0016887,GO:0005524	CG9664-PB						PF00005				G3DSA:3.40.50.300	SSF52540									
aly1079.3	Opioid-binding protein/cell adhesion molecule homolog	GO:0007155,GO:0005886,GO:0031225	CG15630-PA				SM00409,SM00409,SM00409,SM00060,SM00408,SM00408		PF07679,PF07679	PS50835,PS50835,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF48726,SSF48726									
aly1079.4	Hemicentin-1	GO:0005604,GO:0070062,GO:0050896,GO:0007601,GO:0005509,GO:0005515,GO:0030054,GO:0005938	CG15630-PA				SM00409,SM00409,SM00409,SM00408,SM00408		PF07679,PF00047	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF49265,SSF48726									
aly1079.5	Lipase member I	GO:0005615,GO:0016020,GO:0052689,GO:0016042,GO:0005575,GO:0005576,GO:0005886,GO:0004620,GO:0016298,GO:0008201	CG4582-PA						PF00151		PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1079.6	Phospholipase A1 member A	GO:0002080,GO:0070062,GO:0008970,GO:0016042,GO:0005575,GO:0016298	CG6296-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly1079.7	Androgen-dependent TFPI-regulating protein	GO:0016021,GO:0005886	CG11601-PA						PF04750														
aly1079.8	Inactive pancreatic lipase-related protein 1	GO:0005576,GO:0004806,GO:0006629,GO:0005509	CG17292-PA						PF00151,PF00151		PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly1079.9	Unknown		n/a												53~53								
aly108.1	CUGBP Elav-like family member 3	GO:0042078,GO:0031536,GO:2000738,GO:0003676,GO:0002121,GO:0048026,GO:0005737,GO:0043186,GO:0005634,GO:0030727,GO:0007476,GO:0000166,GO:0003730,GO:0048477,GO:0046011,GO:0007281,GO:0007286,GO:0000381,GO:0036099,GO:0007319,GO:0003723,GO:0005515,GO:0017148,GO:0006378,GO:0006397,GO:0003729	CG31762-PB						PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly108.2	GRIP and coiled-coil domain-containing protein 1	GO:0005737,GO:0005794,GO:0048193,GO:0000042,GO:0017137,GO:0000138,GO:0000139,GO:0030306,GO:0005886,GO:0042803	CG10703-PA				SM00755		PF01465	PS50913			G3DSA:1.10.220.60		523~543,240~274,211~231,454~474,6~54,176~203,357~424,95~126								
aly108.3	Protein elav	GO:0005737,GO:0007281,GO:0007399,GO:0031441,GO:0005634,GO:0051252,GO:0000166,GO:0008266,GO:0009790,GO:0003723,GO:0000900,GO:0015030,GO:0008049,GO:0007417,GO:0007319,GO:0003729	CG4396-PC				SM00360,SM00360,SM00360	TIGR01661	PF00076,PF00076,PF14259	PS50102,PS50102,PS50102	PR00961,PR00961,PR00961,PR00961,PR00961		G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928									
aly108.4	Unknown		n/a												92~112								
aly108.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly108.6	Unknown		n/a																				
aly108.7	Unknown		n/a																				
aly1080.1	Transient receptor potential cation channel subfamily A member 1	GO:0050960,GO:0005261,GO:0050965,GO:0005262,GO:0050968,GO:0034605,GO:0015276,GO:0034703,GO:0046957,GO:0040040,GO:0001580,GO:0016021,GO:0010378,GO:0007638,GO:0022843,GO:0033038,GO:0050850,GO:0006812,GO:0006816,GO:0007602,GO:0005886,GO:0009408,GO:0055085,GO:0097604,GO:0043052,GO:0005515,GO:0098655	CG5751-PG				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796,PF12796,PF12796,PF13857,PF00520	PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50297			G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403,SSF48403	1133~1153								
aly1080.10	Disco-interacting protein 2	GO:0005515,GO:0005634,GO:0008134,GO:0003824,GO:0008152,GO:0007275	CG7020-PA						PF00501,PF00501,PF06464				G3DSA:3.40.50.980,G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.40.50.980	SSF56801,SSF56801,SSF56801,SSF56801,SSF56801	140~160								
aly1080.11	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 2	GO:0005737,GO:0005794,GO:0007480,GO:0032312,GO:0005096,GO:0005547,GO:0032320,GO:0008060,GO:0007165,GO:0005100,GO:0046872	CG4937-PC				SM00233,SM00233,SM00324		PF00169,PF00620	PS50238,PS50003,PS50003			G3DSA:2.30.29.30,G3DSA:2.30.29.30,G3DSA:1.10.555.10	SSF50729,SSF50729,SSF48350			REACT_11044						
aly1080.12	Dynein heavy chain 5, axonemal	GO:0036157,GO:0030317,GO:0008152,GO:0042623,GO:0007605,GO:0005874,GO:0007368,GO:0036158,GO:0007018,GO:0070986,GO:0005858,GO:0003774,GO:0005930,GO:0005524,GO:0016887,GO:0003341,GO:0030286,GO:0021670,GO:0005875,GO:0003777	CG9492-PG				SM00382,SM00382,SM00382		PF12775,PF08393,PF08385,PF12774,PF12777,PF12781,PF03028,PF12780,PF07728				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540	1372~1392,267~287,3127~3154,3347~3395,4541~4542,3180~3214,13~40								
aly1080.13	ADP,ATP carrier protein	GO:0051124,GO:0046716,GO:0005739,GO:0001508,GO:0048489,GO:0016021,GO:0005811,GO:0022857,GO:0009612,GO:0051560,GO:0048477,GO:0010507,GO:0015866,GO:0015867,GO:0007629,GO:2001171,GO:0007268,GO:0006839,GO:0008340,GO:0034599,GO:0055085,GO:0040011,GO:0051480,GO:0005829,GO:0070050,GO:0005743,GO:0005740,GO:0005471	CG16944-PC						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920	PR00926,PR00926,PR00926,PR00926,PR00926,PR00926,PR00926,PR00927,PR00927,PR00927,PR00927,PR00927,PR00927		G3DSA:1.50.40.10	SSF103506									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1080.14	ATP-binding cassette sub-family F member 2	GO:0043190,GO:0042626,GO:0006810,GO:0005215,GO:0016020,GO:0005740,GO:0016887,GO:0005524	CG9281-PD				SM00382,SM00382		PF00005,PF00005,PF12848	PS50893,PS50893			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	37~57,159~179								
aly1080.15	Probable calcium-binding mitochondrial carrier CBG00135	GO:0005778,GO:0016021,GO:0006810,GO:0022857,GO:0005743,GO:0005740,GO:0005509,GO:0055085	CG32103-PB				SM00054,SM00054,SM00054		PF00153,PF00153,PF00153,PF13499	PS50920,PS50222,PS50222,PS50222,PS50920,PS50222,PS50920	PR00926,PR00926,PR00926,PR00926,PR00926,PR00926,PR00928,PR00928,PR00928	PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.50.40.10	SSF103506,SSF47473									
aly1080.16	Protein tailless	GO:0016319,GO:0001748,GO:0055057,GO:0008270,GO:0043401,GO:0003677,GO:0001746,GO:0002121,GO:0004879,GO:0007362,GO:0043565,GO:0030522,GO:0009948,GO:0005634,GO:0007369,GO:0014019,GO:0048749,GO:0023061,GO:0035271,GO:0045165,GO:0051726,GO:0003700,GO:0003705,GO:0003707,GO:0006355,GO:0045944,GO:0006351,GO:0008293,GO:0001708	CG1378-PA				SM00430,SM00399		PF00104,PF00105	PS51030	PR00047,PR00047,PR00047,PR00047,PR00398,PR00398,PR00398,PR00398	PS00031	G3DSA:1.10.565.10,G3DSA:1.10.565.10,G3DSA:3.30.50.10	SSF57716,SSF48508,SSF48508			REACT_71						
aly1080.17	Ras-related and estrogen-regulated growth inhibitor	GO:0008285,GO:0030308,GO:0009725,GO:0005829,GO:0016020,GO:0003924,GO:0005575,GO:0008150,GO:0006184,GO:0007264,GO:0005634,GO:0005525	CG8519-PA				SM00173,SM00175,SM00174	TIGR00231	PF00071	PS51421	PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly1080.18	Protein GPR107	GO:0005794,GO:0016021	CG12121-PA						PF06814														
aly1080.19	Probable splicing factor 3B subunit 5	GO:0071011,GO:0005686,GO:0005634,GO:0007052,GO:0000398	CG11985-PA			PIRSF037010			PF07189														
aly1080.2	Unknown		CG13310-PA							PS01180			G3DSA:2.60.120.290	SSF49854									
aly1080.20	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1080.21	Abhydrolase domain-containing protein 16A	GO:0016787,GO:0016021	CG1309-PA						PF12695				G3DSA:3.40.50.1820	SSF53474									
aly1080.22	AarF domain-containing protein kinase 4	GO:0072015,GO:0032836,GO:0016772,GO:0005829,GO:0005886,GO:0006122,GO:0005739,GO:0031966,GO:0004674,GO:0004672,GO:0016021	CG32649-PA						PF03109					SSF56112,SSF56112	118~138								
aly1080.23	F-BAR and double SH3 domains protein 2	GO:0005070,GO:0005737,GO:0030833,GO:0008582,GO:0055037,GO:0005543,GO:0045886,GO:0005515,GO:0007274	CG43479-PI				SM00055,SM00326,SM00326		PF00018,PF00018,PF00611	PS51741,PS50002,PS50002			G3DSA:2.30.30.40,G3DSA:2.30.30.40	SSF103657,SSF50044,SSF50044	393~413,201~221								
aly1080.24	PHD finger protein rhinoceros	GO:0042051,GO:0005634,GO:0042059,GO:0006355,GO:0008270,GO:0003677	CG7036-PB				SM00249,SM00249		PF10513,PF13832,PF13831	PS50016		PS01359	G3DSA:3.30.40.10	SSF57903	2530~2550,2659~2660,2505~2525								
aly1080.25	Rho GTPase-activating protein 68F	GO:0005737,GO:0007370,GO:0043547,GO:0007480,GO:0051497,GO:0005096,GO:0005622,GO:0005575,GO:0045887,GO:0005100,GO:0007266,GO:0043087	CG6811-PA				SM00324,SM00516		PF00620,PF13716	PS50191,PS50238			G3DSA:3.40.525.10,G3DSA:1.10.555.10	SSF52087,SSF48350			REACT_11044						
aly1080.26	Peptidyl-prolyl cis-trans isomerase-like 1	GO:0000413,GO:0006457,GO:0070062,GO:0071011,GO:0071013,GO:0000398,GO:0048042,GO:0003755	CG13892-PA			PIRSF001467			PF00160	PS50072	PR00153,PR00153,PR00153,PR00153,PR00153	PS00170	G3DSA:2.40.100.10	SSF50891									
aly1080.27	Nuclear pore complex protein Nup153	GO:0031490,GO:0008270,GO:0051028,GO:0005487,GO:0034399,GO:0072686,GO:0005719,GO:0006325,GO:0005813,GO:0005634,GO:0005635,GO:0044613,GO:0007184,GO:0017056,GO:0051298,GO:0006606,GO:0031965,GO:0006607,GO:0022008,GO:0006338,GO:0005643,GO:0006999,GO:0045944,GO:0006351,GO:0034401	CG4453-PD				SM00547,SM00547,SM00547,SM00547		PF00641,PF00641	PS50199,PS50199,PS50199,PS50199		PS01358,PS01358,PS01358,PS01358,PS01358		SSF90209,SSF90209										
aly1080.28	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1080.29	Unknown		n/a																				
aly1080.3	Band 7 protein AAEL010189	GO:0003674,GO:0016021,GO:0016020,GO:0008150	CG42540-PG				SM00244		PF01145		PR00721,PR00721,PR00721,PR00721,PR00721,PR00721,PR00721,P	PS01270		SSF117892									
aly1080.30	Unknown		n/a																				
aly1080.31	Unknown		n/a																				
aly1080.32	Protein suppressor of hairy wing	GO:0031936,GO:0043565,GO:0005634,GO:0005700,GO:0006355,GO:0045892,GO:0006351,GO:0005515,GO:0003677,GO:0000785,GO:0046872,GO:0043035	CG8573-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12874,PF12874,PF05605	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028		SSF57667,SSF57667										
aly1080.33	Dynein heavy chain 5, axonemal	GO:0036157,GO:0042384,GO:0008152,GO:0042623,GO:0007605,GO:0005874,GO:0007368,GO:0036158,GO:0007018,GO:0070986,GO:0005858,GO:0003774,GO:0005930,GO:0030317,GO:0005524,GO:0016887,GO:0003341,GO:0030286,GO:0021670,GO:0005875,GO:0003777	CG9492-PG						PF08393														
aly1080.34	Unknown		n/a																				
aly1080.4	Coadhesin (Fragment)	GO:0016021	CG5989-PA				SM00282,SM00282,SM00209,SM00209,SM00209		PF07766,PF00090,PF00090,PF00090,PF00090	PS50092,PS50025,PS50092,PS50092,PS50092	PR01705,PR01705,PR01705		G3DSA:2.60.120.200,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.60.120.200	SSF49899,SSF82895,SSF82895,SSF82895,SSF82895,SSF49899									
aly1080.5	PQ-loop repeat-containing protein 3	GO:0006488,GO:0016021,GO:0005783	CG1265-PB						PF04193														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1080.6	Melatonin receptor type 1A	GO:0007617,GO:0007612,GO:0007613,GO:0004952,GO:0046676,GO:0042594,GO:0090328,GO:0040040,GO:0001588,GO:0008502,GO:0004930,GO:0007212,GO:0016021,GO:0007186,GO:0007187,GO:0007623,GO:0071329,GO:0008306,GO:0005887,GO:0005886,GO:0042562,GO:0043235,GO:0009744,GO:0007568,GO:0043025,GO:0043052,GO:0030828,GO:0097159,GO:0007191,GO:0043010	CG9652-PE						PF00001	PS50262	PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1080.7	Unknown		n/a																				
aly1080.8	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1	GO:0005737,GO:0007423,GO:0016020,GO:0007476,GO:0030246,GO:0005576,GO:0005509,GO:0007155	CG1500-PA				SM00607,SM00034,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032		PF00084,PF00084,PF00084,PF00084,PF00084,PF00084,PF00084,PF00084,PF00084,PF00084,PF00084,PF00059	PS50923,PS50923,PS50923,PS50923,PS50923,PS50923,PS50041,PS50923,PS50923,PS50923,PS50923,PS50923		PS00615	G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.60.120.260,G3DSA:3.10.100.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10	SSF57535,SSF49785,SSF57535,SSF57535,SSF57535,SSF57535,SSF57535,SSF57535,SSF57535,SSF57535,SSF57535,SSF56436,SSF57535									
aly1080.9	Protein phosphatase 1 regulatory subunit 12B	GO:0048675,GO:0000086,GO:0019208,GO:0017022,GO:0017023,GO:0008047,GO:0008544,GO:0035317,GO:0043085,GO:0045177,GO:0030725,GO:0045179,GO:0005654,GO:0048477,GO:0017018,GO:0000278,GO:0006937,GO:0045314,GO:0007264,GO:0005829,GO:0007560,GO:0007391,GO:0005515,GO:0043296,GO:0007165	CG32156-PO				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF15898,PF12796,PF12796	PS50088,PS50088,PS50088,PS50297,PS50088	PR01415,PR01415		G3DSA:1.25.40.20	SSF48403	711~731,744~788								
aly10804.1	Unknown		n/a						PF03564						141~148								
aly10804.2	Unknown		n/a										G3DSA:3.30.40.10	SSF46579	131~151								
aly10804.3	Unknown		n/a												2~22								
aly108174.1	Unknown		n/a																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10825.1	Mycosubtilin synthase subunit C	GO:0005737,GO:0048082,GO:0048022,GO:0007623,GO:0016788,GO:0006583,GO:0043042,GO:0048066,GO:0048067,GO:0042417,GO:0016740,GO:0007593,GO:0042440,GO:0045475,GO:0017000,GO:0001692,GO:0003833	CG3331-PA						PF13193,PF00550,PF00501	PS50075		PS00455	G3DSA:3.40.50.980,G3DSA:1.10.1200.10,G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:3.30.300.30	SSF56801,SSF47336										
aly10825.10	Unknown		n/a																				
aly10825.2	Epsilon-sarcoglycan	GO:0005856,GO:0005794,GO:0042383,GO:0016021,GO:0016020,GO:0030425,GO:0016012,GO:0008307,GO:0005509,GO:0005886,GO:0032590	CG7851-PC				SM00736		PF05510				G3DSA:2.60.40.10											
aly10825.3	Type I inositol 1,4,5-trisphosphate 5-phosphatase	GO:0052658,GO:0070062,GO:0016311,GO:0016020,GO:0046030,GO:0005575,GO:0046856,GO:0046855,GO:0004445,GO:0052659	CG42283-PF				SM00128		PF03372				G3DSA:3.60.10.10,G3DSA:3.60.10.10,G3DSA:3.60.10.10	SSF56219,SSF56219,SSF56219										
aly10825.4	Ubiquitin-like domain-containing CTD phosphatase 1	GO:0005634,GO:0004721	CG6697-PA				SM00577,SM00213	TIGR02245	PF00240,PF03031	PS50969,PS50053			G3DSA:3.40.50.1000,G3DSA:3.10.20.90	SSF54236,SSF56784										
aly10825.5	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445										
aly10825.6	Unknown		n/a																				
aly10825.7	DC-STAMP domain-containing protein 2	GO:0016021	CG6845-PC						PF07782														
aly10825.8	DC-STAMP domain-containing protein 2	GO:0016021	CG6845-PC																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10825.9	Rho-related BTB domain-containing protein 1	GO:0005575,GO:0051056,GO:0005829,GO:0003924,GO:0005622,GO:0035011,GO:0005886,GO:0007264,GO:0005525	CG5701-PB				SM00175,SM00174,SM00173	TIGR00231	PF00071	PS51420	PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly10830.1	UDP-glucuronosyltransferase 1-4	GO:0016758,GO:0015020,GO:0016021,GO:0008152,GO:0005789	CG18578-PA						PF00201				G3DSA:3.40.50.2000	SSF53756									
aly10830.2	Unknown	GO:0015020,GO:0002121,GO:0008152	CG17323-PA											SSF53756									
aly10830.3	UDP-glucuronosyltransferase 1-3	GO:0043231,GO:0052696,GO:0031100,GO:0016021,GO:0052697,GO:0009813,GO:0005789,GO:0032870,GO:0008152,GO:0015020,GO:0002121	CG17323-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									
aly10830.4	UDP-glucuronosyltransferase 2A1	GO:0007608,GO:0050896,GO:0008152,GO:0005886,GO:0015020,GO:0016021,GO:0002121	CG17323-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									
aly10830.5	Unknown		n/a																				
aly10837.1	RNA-directed DNA polymerase from mobile element jockey	GO:0003964	n/a						PF00078														

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1084.1	Tenascin-X	GO:0006631,GO:0006909,GO:0030036,GO:0007160,GO:0042742,GO:0032963,GO:0043506,GO:0016337,GO:0070062,GO:0043206,GO:0016021,GO:0005178,GO:0006641,GO:0009986,GO:0006910,GO:0048251,GO:0046331,GO:0007155,GO:0008201,GO:0005615,GO:0005044,GO:0005578,GO:0005622,GO:0030199,GO:0005515,GO:0042834	CG6124-PC				SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181							SSF57184,SSF57184										
aly1084.10	Phospholipase B1, membrane associated	GO:0006909,GO:0006629,GO:0016324,GO:0016021,GO:0016042,GO:0004622,GO:0004623,GO:0004620	CG7365-PA						PF00657				G3DSA:3.40.50.1110	SSF52266,SSF52266,SSF52266									
aly1084.11	Tubulin alpha-1C chain	GO:0045298,GO:0051258,GO:0005200,GO:0051298,GO:0005634,GO:0009987,GO:0003924,GO:0031982,GO:0005881,GO:0007052,GO:0007017,GO:0007094,GO:0006184,GO:0005874,GO:0005525	CG9476-PA				SM00864,SM00865		PF00091,PF03953		PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161	PS00227	G3DSA:3.30.1330.20,G3DSA:3.40.50.1440,G3DSA:1.10.287.600	SSF55307,SSF52490									
aly1084.12	Palmitoyltransferase ZDHHC6	GO:0007030,GO:0018345,GO:0016021,GO:0005789,GO:0008270,GO:0005515,GO:0019706,GO:0005783	CG5196-PA							PS50216			G3DSA:2.30.30.40	SSF50044									

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1084.13	Moesin/ezrin/radixin homolog 1	GO:0008104,GO:0016336,GO:0015629,GO:0005886,GO:0045197,GO:0030036,GO:0019898,GO:0035003,GO:0007091,GO:0051653,GO:0042052,GO:0005737,GO:0002009,GO:0035088,GO:0005819,GO:0000902,GO:0005634,GO:0005546,GO:0003779,GO:0033109,GO:0042462,GO:0005938,GO:0030029,GO:0042048,GO:0072499,GO:0032154,GO:1990023,GO:0005856,GO:0007315,GO:0007314,GO:0005912,GO:0032956,GO:0007010,GO:0045313,GO:0007318,GO:0000912,GO:0000132,GO:0009952,GO:0008092,GO:0016057,GO:0045433,GO:0007052,GO:0045169,GO:0005515,GO:0007368,GO:0005884	CG10701-PB			PIRSF002305	SM00295		PF00769,PF00373,PF09379,PF09380	PS50057	PR00661,PR00661,PR00661,PR00661,PR00661,PR00661,PR00661,PR00661,PR00935,PR00935,PR00935	PS00660,PS00661	G3DSA:3.10.20.90,G3DSA:1.20.80.10,G3DSA:2.30.29.30,G3DSA:1.20.5.450	SSF48678,SSF47031,SSF54236,SSF50729	369~476,320~350,528~555									
aly1084.14	Zinc finger protein 2	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG31365-PA				SM00868,SM00355,SM00355		PF07776	PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667	165~192								
aly1084.15	Unknown	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0004984	CG14156-PA						PF02949														
aly1084.16	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	GO:0003860,GO:0006574,GO:0005739,GO:0008152	CG5044-PB						PF16113				G3DSA:3.90.226.10	SSF52096,SSF52096									
aly1084.17	Peptide deformylase, mitochondrial	GO:0008284,GO:0043686,GO:0018206,GO:0005739,GO:0031365,GO:0042586,GO:0005506,GO:0006412	CG31278-PA	MF_00163		PIRSF004749			PF01327		PR01576,PR01576,PR01576,PR01576		G3DSA:3.90.45.10	SSF56420									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1084.18	Cytoplasmic dynein 1 intermediate chain	GO:0034501,GO:0005765,GO:0005874,GO:0045503,GO:0031965,GO:0007349,GO:0008088,GO:0003774,GO:0007051,GO:0007291,GO:0000226,GO:0005868,GO:0001754,GO:0051642,GO:0005875,GO:0003777,GO:0016482	CG18000-PJ				SM00320,SM00320,SM00320,SM00320,SM00320		PF11540				G3DSA:2.130.10.10	SSF50978	269~289,64~110								
aly1084.19	Neurexin-4	GO:0008104,GO:0045216,GO:0019991,GO:0007163,GO:0003015,GO:0016021,GO:0048786,GO:0097105,GO:0060857,GO:0035151,GO:0016081,GO:0016080,GO:0008039,GO:0008366,GO:0005887,GO:0005886,GO:0005919,GO:0005918,GO:0008065,GO:0072553,GO:0007391,GO:0004888,GO:0061343,GO:0021682	CG6827-PA				SM00231,SM00282		PF02210,PF00754	PS50022,PS50025		PS01286,PS01285	G3DSA:2.60.120.200,G3DSA:2.60.120.260,G3DSA:2.60.120.260,G3DSA:2.60.120.200	SSF49899,SSF49899,SSF49785,SSF49785										
aly1084.2	von Willebrand factor D and EGF domain-containing protein	GO:0006909,GO:0005044,GO:0016021,GO:0006910,GO:0046331,GO:0042742,GO:0005515,GO:0009986,GO:0042834,GO:0005576	CG6124-PC				SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181																
aly1084.20	L-aminoadipate-semialdehyde dehydrogenase phosphopantetheinyl transferase	GO:0005737,GO:0006633,GO:0000287,GO:0008897,GO:0018215,GO:0009059	CG32099-PA						PF01648				G3DSA:3.90.470.20,G3DSA:3.90.470.20	SSF56214,SSF56214		00770+2.7.8.7		PWY-6012-1,PWY-6012					
aly1084.3	Unknown		CG17364-PC										G3DSA:2.170.300.10		312~332								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1084.4	Heat shock 70 kDa protein cognate 4	GO:0051087,GO:0006457,GO:0051082,GO:0016887,GO:0007411,GO:0007413,GO:0005875,GO:0030018,GO:0005737,GO:0001700,GO:0005634,GO:0005811,GO:0005739,GO:0016246,GO:0005524,GO:0071011,GO:0071013,GO:0007269,GO:0016192,GO:0007399,GO:0005726,GO:0000398,GO:0005743,GO:0035967	CG4264-PE						PF00012				G3DSA:2.60.34.10	SSF100920									
aly1084.5	Transmembrane protein 161B	GO:0016021	CG7638-PA						PF10268														
aly1084.6	V-type proton ATPase 116 kDa subunit a isoform 1	GO:0008021,GO:0042470,GO:0009881,GO:0015991,GO:0016021,GO:0030659,GO:0015078,GO:0048388,GO:0000220,GO:0009416,GO:0005516,GO:0046961,GO:0051452,GO:0005769,GO:0045202	CG1709-PC			PIRSF001293			PF01496						51~71,95~129									
aly1084.7	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6-B	GO:0003727,GO:0033746,GO:0018395,GO:0005730,GO:0070078,GO:0070079,GO:0033749,GO:0030154,GO:0005634,GO:0070815,GO:0005654,GO:0006355,GO:0006351,GO:0048024,GO:0046872,GO:0002040,GO:0008380,GO:0006397	CG14331-PC						PF13621				G3DSA:2.60.120.650	SSF51197									
aly1084.8	Protoporphyrinogen oxidase	GO:0004729,GO:0031304,GO:0006783,GO:0006782,GO:0005743,GO:0055114	CG5796-PA					TIGR00562	PF01593				G3DSA:1.10.3110.10,G3DSA:3.90.660.20	SSF54373,SSF51905,SSF51905		00860+1.3.3.4		PWY-5531,PWY-7159	UPA00251				
aly1084.9	Dynactin subunit 4	GO:0005737,GO:0047485,GO:0019886,GO:0005813,GO:0005829,GO:0007018,GO:0005869,GO:0005868,GO:0022008,GO:0007097,GO:0005634	CG12042-PA						PF05502,PF05502														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1085.1	Unknown	GO:0007157,GO:0005576,GO:0003674	CG10152-PB				SM00409		PF13895,PF08205	PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726									
aly1085.10	Unknown		n/a																				
aly1085.11	Unknown		CG3386-PA				SM00595		PF10545	PS51029													
aly1085.2	Vacuolar protein sorting associated protein 4A	GO:0006909,GO:0045197,GO:0017048,GO:0016887,GO:0043162,GO:0007049,GO:0006886,GO:0000046,GO:0045746,GO:0051301,GO:0032466,GO:0031902,GO:0005524,GO:0016787,GO:0044130,GO:0030036,GO:0016197,GO:0007033,GO:0009838,GO:0030496,GO:0015031,GO:0005768,GO:0005769	CG6842-PA				SM00382,SM00745		PF09336,PF04212,PF00004			PS00674	G3DSA:3.40.50.300,G3DSA:1.10.8.60,G3DSA:1.10.8.60,G3DSA:1.20.58.280	SSF116846,SSF52540										
aly1085.3	Putative peptidyl-tRNA hydrolase PTRHD1	GO:0006470,GO:0004725,GO:0004045,GO:0070062	CG14903-PA						PF01981				G3DSA:3.40.1490.10	SSF102462				PWY-6308					
aly1085.4	U6 snRNA-associated Sm-like protein LSm8	GO:0030532,GO:0071011,GO:0044822,GO:0000398,GO:0005688,GO:0008380,GO:0005681,GO:0006397	CG2021-PA				SM00651		PF01423				G3DSA:2.30.30.100	SSF50182									
aly1085.5	Solute carrier family 25 member 40	GO:0016021,GO:0006810,GO:0005740,GO:0005743,GO:0022857,GO:0055085	CG14209-PB						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920,PS51257			G3DSA:1.50.40.10	SSF103506									
aly1085.6	NADP-dependent malic enzyme	GO:0005737,GO:0046872,GO:0004473,GO:0051287,GO:0004471,GO:0008948,GO:0005739,GO:0006090,GO:0006108,GO:0055114	CG5889-PC			PIRSF000106	SM00919		PF03949,PF00390		PR00072,PR00072,PR00072,PR00072,PR00072,PR00072,PR00072	PS00331	G3DSA:3.40.50.720,G3DSA:3.40.50.10380	SSF53223,SSF51735		00620+1.1.1.38							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1085.7	NADP-dependent malic enzyme	GO:0005737,GO:0046872,GO:0004473,GO:0051287,GO:0004471,GO:0008948,GO:0005739,GO:0006090,GO:0006108,GO:0055114	CG5889-PC			PIRSF000106	SM00919		PF00390,PF03949		PR00072,PR00072,PR00072,PR00072,PR00072,PR00072	PS00331	G3DSA:3.40.50.720,G3DSA:3.40.50.10380	SSF51735,SSF53223		00620+1.1.1.38							
aly1085.8	Unknown		n/a						PF00431				G3DSA:2.60.120.290	SSF49854									
aly1085.9	Myosin regulatory light chain, smooth muscle	GO:0016459,GO:0016460,GO:0005509	CG33098-PB				SM00054		PF13405	PS50222,PS50222		PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473	1~21								
aly10853.1	Unknown		n/a																				
aly108549.1	Unknown		n/a																				
aly10875.1	DnaJ homolog subfamily C member 1	GO:0016020,GO:0006457,GO:0005783,GO:0016021,GO:0051087,GO:0031965,GO:0005788,GO:0005789,GO:0043022,GO:0005886,GO:0003677,GO:0006417,GO:0050708,GO:0003682,GO:0005634	CG7556-PA							PS50090			G3DSA:1.10.10.60	SSF46689									
aly108811.1	ATP-binding cassette sub-family C member 11	GO:0042626,GO:0015865,GO:0070062,GO:0008514,GO:0016021,GO:0015216,GO:0015711,GO:0015238,GO:0008559,GO:0005887,GO:0005886,GO:0055085,GO:0005524	CG11898-PB										G3DSA:3.40.50.300	SSF52540									
aly108838.1	Unknown		n/a																				
aly1089.1	Transmembrane and TPR repeat-containing protein 1	GO:0016021,GO:0017122,GO:0008150,GO:0005739,GO:0016262	CG5038-PA				SM00028,SM00028,SM00028		PF13414,PF13181,PF08409	PS50005,PS50293,PS50005			G3DSA:1.25.40.10	SSF48452									
aly1089.10	Unknown		n/a																				
aly1089.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1089.3	Unknown		n/a						PF16009														
aly1089.4	Unknown	GO:0008080	CG10659-PA										G3DSA:3.40.630.30,G3DSA:3.40.630.30	SSF55729									
aly1089.5	Unknown		n/a																				
aly1089.6	Unknown		n/a																				
aly1089.7	Unknown		n/a																				
aly1089.8	Protein ARV1	GO:0005794,GO:0016125,GO:0006695,GO:0032366,GO:0016021,GO:0097036,GO:0030301,GO:0005575,GO:0003674,GO:0044281,GO:0008150,GO:0008206,GO:0005789,GO:0090181,GO:0006665,GO:0032541	CG32442-PA						PF04161														
aly1089.9	Unknown		n/a																				
aly10892.1	Unknown		n/a																				
aly109.1	Unknown		n/a										G3DSA:3.60.10.10	SSF56219									
aly10900.1	Serine/threonine kinase SAD1	GO:0006468,GO:0046872,GO:0006487,GO:0007416,GO:0034613,GO:0018105,GO:0008088,GO:0030424,GO:0007528,GO:0004674,GO:0050321,GO:0007163,GO:0030054,GO:0030516,GO:0050808,GO:0007411,GO:0030425,GO:0005622,GO:0048489,GO:0005524,GO:0045202	CG6114-PA																				
aly1091.1	Unknown	GO:0005737,GO:0010629,GO:0042826,GO:0005634	CG11160-PA																				
aly1091.10	Unknown		n/a												63~83,268~295,319~347,130~154,175~237,245~265								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1091.11	Transposable element Tc1 transposase	GO:0004803,GO:0006313,GO:0004519,GO:0005634,GO:0015074,GO:0003677	n/a						PF01498														
aly1091.12	Protein transport protein Sec31B	GO:0005795,GO:0008021,GO:0045089,GO:0005783,GO:0090114,GO:0005789,GO:0030127,GO:0015031,GO:0016192,GO:0005515,GO:0012507,GO:0050829,GO:0008380,GO:0030120,GO:0005198,GO:0030134,GO:0005681,GO:0070971	CG8266-PD				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400	PS50082,PS50294,PS50082			G3DSA:2.130.10.10	SSF50978	1102~1122,1158~1158									
aly1091.13	Calexcitin-2	GO:0016529,GO:0003924,GO:0005509	CG14904-PA				SM00054,SM00054		PF13833,PF13202	PS50222,PS50222,PS50222		PS00018,PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									
aly1091.14	Calexcitin-2	GO:0016529,GO:0003924,GO:0005509	CG14904-PA				SM00054,SM00054		PF13833,PF13202	PS50222,PS50222,PS50222		PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									
aly1091.15	Unknown		n/a																				
aly1091.16	Unknown		n/a																				
aly1091.2	Protein msta, isoform A	GO:0005737,GO:0008168,GO:0010629,GO:0042826	CG8503-PA				SM00317		PF01753,PF00856	PS50865		PS01360	G3DSA:2.170.270.10,G3DSA:2.170.270.10	SSF82199,SSF82199									
aly1091.3	Toll-like receptor 13	GO:0005737,GO:0002755,GO:0045087,GO:0009615,GO:0016021,GO:0048935,GO:0019843,GO:0006952,GO:0042803,GO:0004888,GO:0043408,GO:0007165,GO:0006954,GO:0005886,GO:0034178,GO:0002227,GO:0005768,GO:0060049,GO:0010008	CG6890-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00255		PF01582,PF13855,PF13855	PS50104			G3DSA:3.80.10.10,G3DSA:3.40.50.10140,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52047,SSF52200									
aly1091.4	Unknown	GO:0016021,GO:0048935,GO:0006952,GO:0004888,GO:0007165,GO:0005886,GO:0002227,GO:0060049	CG6890-PA						PF13855				G3DSA:3.80.10.10,G3DSA:3.40.50.10140	SSF52200,SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1091.5	Unknown	GO:0008063,GO:0005576,GO:0005121	CG14928-PB						PF16077					SSF57501									
aly1091.6	Protein phosphatase inhibitor 2	GO:0009966,GO:0004864,GO:0043666,GO:0005977	CG6380-PA						PF04979						135~158								
aly1091.7	Unknown	GO:0048598,GO:0007020,GO:0007605,GO:0005813,GO:0051297,GO:0005814,GO:0001539	CG33957-PF												677~697,815~835,555~575,924~944,713~733,395~422								
aly1091.8	Unknown	GO:0048598,GO:0007020,GO:0007605,GO:0005813,GO:0051297,GO:0005814,GO:0001539	CG33957-PF												28~94,130~161,98~118								
aly1091.9	Laminin subunit alpha-2	GO:0030155,GO:0022011,GO:0007411,GO:0007020,GO:0007517,GO:0070062,GO:0005813,GO:0005814,GO:0005198,GO:0005576,GO:0048598,GO:0030334,GO:0042383,GO:0007605,GO:0051297,GO:0032224,GO:0001539,GO:0045995,GO:0007155,GO:0005605,GO:0005604,GO:0043197,GO:0030198	CG33957-PF											SSF57997	120~175,603~696,821~848,377~474,482~550,554~588,68~102,772~816								
aly10928.1	Motile sperm domain-containing protein 2	GO:0005575,GO:0022008,GO:0016020,GO:0016021,GO:0005198	CG33523-PF				SM00516		PF00635,PF00650	PS50191,PS50202			G3DSA:2.60.40.360,G3DSA:3.40.525.10	SSF49354,SSF46938,SSF52087	357~384								
aly10928.2	Motile sperm domain-containing protein 2	GO:0016021,GO:0016020	n/a										G3DSA:2.60.40.360	SSF49354									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly10928.3	RNA exonuclease 4	GO:0004527,GO:0044822,GO:0005634,GO:0003676,GO:0005730	CG6833-PA				SM00479		PF00929				G3DSA:3.30.420.10	SSF53098									
aly10928.4	UDP-N-acetylhexosamine pyrophosphorylase	GO:0001838,GO:0007424,GO:0007417,GO:0035151,GO:0005654,GO:0007391,GO:0005737,GO:0005575,GO:0008362,GO:0030198,GO:0003977,GO:0008152,GO:0005886,GO:0006048,GO:0007413,GO:0006035,GO:0040003,GO:0042802,GO:0070569	CG9535-PA						PF01704				G3DSA:3.90.550.10	SSF53448									
aly10928.5	Histidine triad nucleotide-binding protein	GO:0005737,GO:0016787,GO:0005634,GO:0000166,GO:0005575,GO:0003824,GO:0003674,GO:0008150	CG34015-PA						PF11969	PS51084	PR00332,PR00332		G3DSA:3.30.428.10	SSF54197									
aly10949.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG1213-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly10949.2	Facilitated trehalose transporter Tret1-2 homolog	GO:0022891,GO:0005355,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG1213-PA						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171		G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						
aly10949.3	Unknown		n/a																				
aly10961.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1097.1	Venom dipeptidyl peptidase 4	GO:0004177,GO:0016020,GO:0008239,GO:0005576,GO:0006508,GO:0008236	CG42280-PG						PF00326,PF00930				G3DSA:2.140.10.30,G3DSA:3.40.50.1820	SSF82171,SSF53474									
aly1097.10	Lipase member H	GO:0006629,GO:0016020,GO:0052689,GO:0016042,GO:0005575,GO:0003824,GO:0005576,GO:0008150,GO:0003674	CG18258-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly1097.11	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha	GO:0006887,GO:0006909,GO:0036092,GO:0060326,GO:0006644,GO:0006468,GO:0048268,GO:0044281,GO:0035004,GO:0035005,GO:0030136,GO:0046934,GO:0016020,GO:0070062,GO:0005942,GO:0005634,GO:0005543,GO:0046854,GO:0006661,GO:0010008,GO:0048008,GO:0005524,GO:0014829,GO:0005794,GO:0008286,GO:0016303,GO:0045087,GO:0017137,GO:0006974,GO:0007173,GO:0006954,GO:0005886,GO:0014065,GO:0048015,GO:0030168,GO:0031982,GO:0006897,GO:0035091,GO:0005829,GO:0030866,GO:0005737,GO:0002250,GO:0005515,GO:0071583	CG11621-PC				SM00145,SM00239,SM00144,SM00312,SM00142,SM00146		PF00792,PF00454,PF00168,PF00613,PF00794,PF00787	PS50290,PS50195,PS51545,PS51547,PS51546,PS50004		PS00916,PS00915	G3DSA:2.60.40.150,G3DSA:3.30.1520.10,G3DSA:1.25.40.70,G3DSA:3.30.1010.10,G3DSA:2.60.40.150,G3DSA:3.10.20.90,G3DSA:1.10.1070.11	SSF54236,SSF49562,SSF64268,SSF56112,SSF48371,SSF49562	821~841,1111~131								
aly1097.12	Unknown		n/a																				
aly1097.13	Unknown		CG44836-PE																				
aly1097.14	Ubiquitin-protein ligase E3A	GO:0007616,GO:0060736,GO:0070936,GO:0061630,GO:0005737,GO:0001541,GO:0030521,GO:0004842,GO:0005634,GO:0003713,GO:2000058,GO:0006511,GO:0042787,GO:0031398,GO:0046872,GO:0007623,GO:0035037,GO:0042752,GO:0005938,GO:0000502,GO:0016874,GO:0040011,GO:0005829,GO:0016567,GO:0048813,GO:0051865,GO:0045944,GO:0048935,GO:0014068	CG6190-PA				SM00119		PF00632,PF16558	PS50237			G3DSA:3.30.2160.10	SSF56204					UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1097.15	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta	GO:0016319,GO:0005856,GO:0050896,GO:0030659,GO:0047555,GO:0031410,GO:0005634,GO:0007601,GO:0005095,GO:0004114,GO:0042995,GO:0005829	CG9296-PA						PF05351				G3DSA:2.70.50.40	SSF81296									
aly1097.16	Protein sprouty	GO:0016318,GO:0021782,GO:0042059,GO:0001763,GO:0007169,GO:0001745,GO:0007275,GO:0007430,GO:0009966,GO:0016020,GO:0030707,GO:0060446,GO:0035155,GO:0048747,GO:0008595,GO:0007173,GO:0046580,GO:0005886,GO:0045314,GO:0040037,GO:0007424,GO:0007426,GO:0009968,GO:0007429,GO:0005622,GO:0008293	CG1921-PC						PF05210	PS51227													
aly1097.17	Unknown		n/a																				
aly1097.18	Eukaryotic translation initiation factor 5B	GO:0005737,GO:0044267,GO:0006446,GO:0005829,GO:0003924,GO:0006412,GO:0010467,GO:0005515,GO:0017151,GO:0003743,GO:0006413,GO:0044822,GO:0005525	CG10840-PB					TIGR00231	PF11987,PF00009,PF03144	PS51722	PR00315,PR00315,PR00315,PR00315		G3DSA:3.40.50.300,G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:3.40.50.10050	SSF52540,SSF52156,SSF50447	167~187,243~278,349~412,571~591								
aly1097.19	ATP-dependent RNA helicase SUV3 homolog, mitochondrial	GO:0032508,GO:0004004,GO:0005759,GO:0003676,GO:0003677,GO:0003678,GO:0005634,GO:0005524	CG9791-PC				SM00490		PF00271,PF12513	PS51194			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540									
aly1097.2	Unknown		n/a						PF15055														
aly1097.20	Unknown		n/a				SM00409,SM00409						G3DSA:2.60.40.10	SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1097.21	Transcriptional adapter 1	GO:0000124,GO:0005634,GO:0003713,GO:0006355,GO:0070461,GO:0006351,GO:0016573,GO:0006366	CG31866-PA						PF12767														
aly1097.22	Cytochrome P450 4d2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG3466-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385		G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly1097.23	Acetylcholinesterase	GO:0060179,GO:0042135,GO:0007476,GO:0052689,GO:0005576,GO:0045202,GO:0005886,GO:0003990,GO:0030054,GO:0031225	CG9858-PA						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly1097.24	Unknown		n/a												126~193								
aly1097.3	Unknown		n/a																				
aly1097.4	Unknown	GO:0008021,GO:0005215,GO:0016021,GO:0016020,GO:0005544,GO:0007269,GO:0016079	CG42333-PD																				
aly1097.5	Synaptotagmin 1	GO:0008021,GO:0030672,GO:0007269,GO:0005215,GO:0016021,GO:0016020,GO:0005544,GO:0042584,GO:0005515,GO:0016079,GO:0046872,GO:0030054	CG42333-PD				SM00239,SM00239		PF00168,PF00168	PS50004,PS50004	PR00360,PR00360,PR00360,PR00399,PR00399,PR00399,PR00399		G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1097.6	Unknown		n/a						PF10650	PS50103					650~691								
aly1097.7	TBC domain-containing protein kinase-like protein	GO:0006468,GO:0032313,GO:0007030,GO:0005097,GO:0004672,GO:0005524	CG4041-PB				SM00164,SM00450		PF00069,PF00566,PF00581	PS50206,PS50011,PS50086			G3DSA:1.10.8.270,G3DSA:3.40.250.10,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF47923,SSF47923,SSF56112,SSF52821									
aly1097.8	Cyclic AMP response element-binding protein A	GO:0043565,GO:0007435,GO:0009953,GO:0006351,GO:0007431,GO:0003700,GO:0005634,GO:0003677,GO:0005700,GO:0001158,GO:0008363,GO:0006355,GO:0045944,GO:0045893,GO:0006366,GO:0035293,GO:0042803	CG7450-PA				SM00338		PF00170	PS50217		PS00036	G3DSA:1.20.5.170	SSF57959	315~363								
aly1097.9	Heparan-alpha-glucosaminide N-acetyltransferase	GO:0051259,GO:0030203,GO:0016021,GO:0005765,GO:0016746,GO:0044281,GO:0007041,GO:0005975,GO:0015019,GO:0006027	CG6903-PA						PF07786							00531+2.3.1.78							
aly10978.1	Trypsin-7	GO:0007586,GO:0004252,GO:0004175,GO:0005576,GO:0006508	CG31954-PA				SM00020		PF00089	PS50240			G3DSA:2.40.10.10	SSF50494	198~232								
aly109873.1	Unknown		n/a												2~22								
aly1102.1	Unknown		n/a						PF14227														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1106.1	Homeobox protein HMX1	GO:0043565,GO:0001227,GO:0003700,GO:0005634,GO:0006355,GO:0045892,GO:0009977,GO:0003677,GO:0007275,GO:0006351	CG43748-PD				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly1106.2	Peroxisome proliferator-activated receptor gamma coactivator-related protein 1	GO:0005737,GO:0016607,GO:0008286,GO:0000166,GO:0030307,GO:0005634,GO:0005654,GO:0008134,GO:0051091,GO:0030374,GO:0046627,GO:0001104,GO:0006355,GO:0010821,GO:0006351,GO:0003676,GO:0045944,GO:0001894,GO:0097009,GO:0044822,GO:0003729	CG9809-PB				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly1106.3	Unknown		n/a												82~112,141~161								
aly1106.4	Unknown		n/a																				
aly1106.5	Sperm flagellar protein 1	GO:0005856,GO:0031514,GO:0005930	CG12395-PA						PF06294					SSF47576	177~232								
aly1106.6	Retinol dehydrogenase 14	GO:0008106,GO:0016614,GO:0005783,GO:0005634,GO:0016020,GO:0005739,GO:0005765,GO:0008152,GO:0042572,GO:0001649,GO:0016491	CG7675-PB						PF00106		PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly1106.7	Unknown		n/a						PF14661														
aly1106.8	Nucleolar protein 56	GO:0005737,GO:0016020,GO:0031428,GO:0005732,GO:0030532,GO:0000154,GO:0044822,GO:0005730,GO:0005654,GO:0006364,GO:0032040,GO:0003723,GO:0022008,GO:0030515,GO:0070761	CG13849-PA				SM00931		PF01798,PF08156	PS51358				SSF89124	420~451									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1106.9	DNA-directed RNA polymerase I subunit RPA2	GO:0005736,GO:0005634,GO:0003677,GO:0009303,GO:0006360,GO:0006351,GO:0032549,GO:0003899,GO:0022008,GO:0046872	CG4033-PA						PF00562,PF00562,PF04563,PF04560,PF06883,PF04561			PS01166	G3DSA:3.90.1100.10,G3DSA:3.90.1100.10,G3DSA:3.90.1100.10,G3DSA:2.40.270.10,G3DSA:2.40.270.10	SSF64484		00240+2.7.7.6,00230+2.7.7.6	REACT_1788						
aly110669.1	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG10178-PA						PF00201					SSF53756									
aly1107.1	Monocarboxylate transporter 12-B	GO:0005308,GO:0015293,GO:0016021,GO:1902598,GO:0015355,GO:0005887,GO:0055085	CG8468-PC						PF07690,PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1107.10	Probable JmjC domain-containing histone demethylation protein 2C	GO:0051213,GO:0046966,GO:0007596,GO:0005622,GO:0005654,GO:0006355,GO:0006351,GO:0046872,GO:0016568	n/a																				
aly1107.2	Monocarboxylate transporter 12	GO:0005308,GO:0015293,GO:0016021,GO:1902598,GO:0015355,GO:0005887,GO:0055085	CG13907-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1107.3	Unknown	GO:0016021,GO:0050909	n/a						PF08395														
aly1107.4	Protein takeout	GO:0007631,GO:0007623,GO:0005615,GO:0032504,GO:0007617,GO:0005576,GO:0042594,GO:0042595,GO:0008343,GO:0008049,GO:0007622	CG10407-PA				SM00700		PF06585														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1107.5	Serine protease inhibitor dipetalogastin (Fragment)	GO:0005575,GO:0005576,GO:0030162,GO:0008150,GO:0004867,GO:0010951,GO:0003674,GO:0050819	CG34018-PA				SM00280,SM00280,SM00280		PF00050,PF00050,PF00050	PS51465,PS51465,PS51465			G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30	SSF100895,SSF100895,SSF100895									
aly1107.6	Unknown	GO:0005575,GO:0030162,GO:0003674,GO:0008150,GO:0004867	CG34018-PA				SM00280		PF00050	PS51465			G3DSA:3.30.60.30	SSF100895									
aly1107.7	Unknown		n/a							PS51257			G3DSA:3.30.60.30										
aly1107.8	Unknown	GO:0048190	CG8369-PA						PF00050	PS51257			G3DSA:3.30.60.30	SSF100895									
aly1107.9	Lysine-specific demethylase 3B	GO:0072718,GO:0051213,GO:0006325,GO:0005634,GO:0016577,GO:0005654,GO:0006355,GO:0032452,GO:0006351,GO:2001020,GO:0046872,GO:0016209,GO:0016568	CG8165-PA				SM00558		PF02373	PS51184			G3DSA:2.60.120.650	SSF51197,SSF51197									
aly11083.1	Unknown		n/a																				
aly110841.1	Unknown		n/a																				
aly110886.1	Unknown		n/a																				
aly11097.1	Unknown		n/a																				
aly111000.1	Solute carrier family 22 member 21	GO:0015879,GO:0015226,GO:0016021,GO:1902603,GO:0005777,GO:0022857,GO:0031231,GO:0055085,GO:0005524	CG3790-PA						PF00083					SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly11107.1	Unknown		n/a																				
aly1111.1	Segmentation protein cap'n'collar	GO:0060322,GO:0043565,GO:0007350,GO:0008103,GO:0046982,GO:0003700,GO:0005634,GO:0042070,GO:0005703,GO:0007317,GO:0006355,GO:0048813,GO:0008359,GO:0045944,GO:0006351,GO:0007310,GO:0008340,GO:0060465,GO:0006979,GO:0045450,GO:0045451	CG43286-PO				SM00338		PF03131			PS00036	G3DSA:1.10.880.10	SSF47454										
aly1111.2	Cytoplasmic FMR1-interacting protein	GO:0005737,GO:0045177,GO:0006909,GO:0000902,GO:0030031,GO:0050807,GO:0030866,GO:0017048,GO:0008360,GO:0045202,GO:0007411,GO:0001745,GO:0022416,GO:0031209	CG4931-PA						PF05994														
aly111229.1	Unknown		n/a																				
aly11127.1	Serine palmitoyltransferase 2	GO:0030148,GO:0007444,GO:0016021,GO:0009058,GO:0003824,GO:0004758,GO:0030170,GO:0005886,GO:0006665	CG4162-PA										G3DSA:3.90.1150.10										
aly11127.2	Serine palmitoyltransferase 2	GO:0030148,GO:0007444,GO:0016021,GO:0017059,GO:0005739,GO:0004758,GO:0006666,GO:0030170,GO:0005886,GO:0046512,GO:0046513,GO:0046511	CG4162-PA						PF00155			PS00599	G3DSA:3.40.640.10	SSF53383									
aly11127.3	Reticulon-4	GO:0005635,GO:0005783,GO:0030308,GO:0030517,GO:0030176,GO:0002121,GO:0071786,GO:0042981,GO:0005737,GO:0007413,GO:0070062,GO:0005811,GO:2000172,GO:0005622,GO:0005790,GO:0042048,GO:0044822,GO:0006915,GO:0030334,GO:0060317,GO:0012505,GO:0007409,GO:0005886,GO:0048011,GO:0097481,GO:0050771,GO:0050770,GO:0045169,GO:0021801	CG33113-PH						PF02453	PS50845													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1113.1	Baculoviral IAP repeat-containing protein 6	GO:0042127,GO:2001237,GO:0060711,GO:0060712,GO:0007291,GO:0007067,GO:0000922,GO:0051301,GO:0005737,GO:0009966,GO:0016874,GO:0016020,GO:0005815,GO:0043066,GO:0032465,GO:0048477,GO:0016242,GO:0008284,GO:0006915,GO:0012501,GO:0009267,GO:0007286,GO:0010951,GO:0004869,GO:0004842,GO:0061631,GO:0001890,GO:0005802,GO:0030496,GO:0016567,GO:0005768	CG6303-PB						PF12356														
aly1113.10	UPF0692 protein CG33108	GO:0005575,GO:0003674,GO:0008150	CG33108-PA																				
aly1113.11	Phosphofurin acidic cluster sorting protein 1	GO:0000042,GO:0005794,GO:0048471,GO:0034613,GO:0032092	CG5405-PB						PF10254														
aly1113.12	NADH dehydrogenase [ubiqui] iron-sulfur protein 7, mitochondrial	GO:0097060,GO:0006120,GO:0005743,GO:0051539,GO:0032981,GO:0008137,GO:0005739,GO:0000302,GO:0046872,GO:0005747,GO:0043005,GO:0008340,GO:0048038,GO:0043025,GO:0003954,GO:0055114	CG9172-PB	MF_01356				TIGR01957	PF01058			PS01150	G3DSA:3.40.50.700	SSF56770									
aly1113.13	Probable maleylacetoacetate isomerase 2	GO:0005737,GO:0006572,GO:0004364,GO:0006559,GO:0016034,GO:0003824,GO:0006749,GO:0009072	CG9363-PA					TIGR01262	PF00043,PF13417	PS50404,PS50405			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF52833,SSF47616									
aly1113.14	Unknown		n/a						PF15679,PF15679						90~110								
aly1113.15	Protein anoxia up-regulated	GO:0005575,GO:0008150,GO:0003674,GO:0034059	CG45076-PA												305~414,439~508								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1113.16	Nucleolysin TIA-1 isoform p40	GO:0005737,GO:0010494,GO:0000381,GO:0008143,GO:0005634,GO:0006915,GO:0000398,GO:0000166,GO:0017091,GO:0097165,GO:0017148,GO:0003676,GO:0042036,GO:0048024,GO:0005685,GO:0005654,GO:0044822,GO:0003729	CG5422-PD				SM00360,SM00360,SM00360,SM00361,SM00361		PF00076,PF00076,PF00076	PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928										
aly1113.17	Zinc transporter 7	GO:0005794,GO:0006829,GO:0070062,GO:0016023,GO:0006812,GO:0016021,GO:0008324,GO:0032119,GO:0016323,GO:0005385,GO:0048471,GO:0005622,GO:0055085	CG6672-PA					TIGR01297	PF01545				G3DSA:1.20.1510.10,G3DSA:1.20.1510.10	SSF161111,SSF161111									
aly1113.18	Transmembrane emp24 domain-containing protein bai	GO:0005795,GO:0009953,GO:0016192,GO:0048193,GO:0005215,GO:0016021,GO:0006810,GO:0048042,GO:0007311,GO:0000003	CG11785-PA						PF01105	PS50866													
aly1113.19	Steroid hormone receptor ERR2	GO:0043565,GO:0005975,GO:0019827,GO:0003700,GO:0001831,GO:0005634,GO:0001834,GO:0003707,GO:0006355,GO:0008270,GO:0043401,GO:0005496,GO:0001892,GO:0004879,GO:0006351	CG7404-PB				SM00430,SM00399		PF00105,PF00104	PS51030	PR00047,PR00047,PR00047,PR00047,PR00398,PR00398,PR00398,PR00398	PS00031	G3DSA:3.30.50.10,G3DSA:1.10.565.10	SSF48508,SSF57716			REACT_71						
aly1113.2	Baculoviral IAP repeat-containing protein 6	GO:0042127,GO:2001237,GO:0060711,GO:0060712,GO:0007291,GO:0007067,GO:0000922,GO:0051301,GO:0005737,GO:0009966,GO:0016874,GO:0016020,GO:0005815,GO:0043066,GO:0032465,GO:0048477,GO:0016242,GO:0008284,GO:0006915,GO:0012501,GO:0009267,GO:0007286,GO:0010951,GO:0004869,GO:0004842,GO:0061631,GO:0001890,GO:0005802,GO:0030496,GO:0016567,GO:0005768	CG6303-PB				SM00238		PF00653	PS50143			G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:1.10.1170.10	SSF50978,SSF50978,SSF50978,SSF50978,SSF57924	1679~1699									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1113.20	Probable cleavage and polyadenylation specificity factor subunit 2	GO:0016787,GO:0005847,GO:0006398,GO:0003730,GO:0006378,GO:0006379,GO:0022008,GO:0003723	CG1957-PA				SM00849,SM01027		PF13299,PF16661,PF10996				G3DSA:3.60.15.10	SSF56281,SSF56281									
aly1113.21	Unknown		n/a																				
aly1113.22	Unknown		n/a																				
aly1113.23	Protein turtle homolog A	GO:0007399,GO:0016021,GO:0030154,GO:0045202,GO:0005515,GO:0005886,GO:0030054	CG12950-PA				SM00408,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409,SM00409		PF13927,PF13927,PF08205,PF13895,PF07686	PS50835,PS50835,PS50853,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726	830~830								
aly1113.24	Unknown		n/a						PF13837														
aly1113.25	Unknown	GO:0005575,GO:0003674,GO:0034059	CG45077-PA																				
aly1113.3	Protein O-mannosyl-transferase 2	GO:0016203,GO:0007517,GO:0005783,GO:0016021,GO:0016020,GO:0004169,GO:0005789,GO:0045214,GO:0030259,GO:0035269,GO:0007525	CG12311-PB				SM00472		PF16192,PF02815	PS50919			G3DSA:2.80.10.50	SSF82109									
aly1113.4	Protein O-mannosyl-transferase 2	GO:0016203,GO:0007517,GO:0006493,GO:0005783,GO:0016021,GO:0016020,GO:0004169,GO:0005789,GO:0045214,GO:0030259,GO:0035269,GO:0007525,GO:0000030	CG12311-PB						PF02366				G3DSA:2.80.10.50	SSF82109									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1113.5	Putative cysteine proteinase CG12163	GO:0005764,GO:0003674,GO:0098595,GO:0005615,GO:0035071,GO:0051603,GO:0035220,GO:0045169,GO:0005575,GO:0048102,GO:0004197,GO:0008150,GO:0004869,GO:0006508,GO:0022416	CG12163-PA				SM00043,SM00043,SM00043,SM00043,SM00043,SM00043,SM00043,SM00043,SM00848,SM00645		PF08246,PF00112,PF00031,PF00031,PF00031,PF00031,PF00031,PF00031,PF00031	PS51257	PR00705,PR00705,PR00705	PS00639,PS00640,PS00139	G3DSA:3.10.450.10,G3DSA:3.10.450.10,G3DSA:3.10.450.10,G3DSA:3.10.450.10,G3DSA:3.10.450.10,G3DSA:3.10.450.10,G3DSA:3.10.450.10,G3DSA:3.10.450.10,G3DSA:3.90.70.10	SSF54001,SSF54403,SSF54403,SSF54403,SSF54403,SSF54403,SSF54403,SSF54403,SSF54403,SSF54403,SSF54403	1751~1771,1380~1404									
aly1113.6	Unknown	GO:0005575,GO:0003674,GO:0008150	CG11000-PC				SM00233		PF00169	PS50003			G3DSA:2.30.29.30	SSF50729									
aly1113.7	Zinc finger C2HC domain-containing protein 1C	GO:0005575,GO:0003674,GO:0046872,GO:0008150	CG42675-PG						PF13913,PF13913														
aly1113.8	Unknown		n/a																				
aly1113.9	Neutral and basic amino acid transport protein rBAT	GO:0055085,GO:0043169,GO:0006520,GO:0005975,GO:0070062,GO:0060356,GO:0005743,GO:0005774,GO:0015811,GO:0006865,GO:0015171,GO:0003824,GO:0005887,GO:0006811,GO:0015802,GO:0005886,GO:0015174,GO:0015184,GO:0016020,GO:0031526,GO:0003333	CG2791-PD						PF16028,PF00128				G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.90.400.10	SSF51445									
aly111304.1	Unknown		n/a																				
aly111608.1	Juvenile hormone epoxide hydrolase	GO:0008096,GO:0043231,GO:0033961,GO:0016021,GO:0005789,GO:0004301,GO:0019439,GO:0006719	CG15106-PA						PF06441				G3DSA:3.40.50.1820	SSF53474		00980+3.3.2.9							
aly111736.1	Unknown		n/a												46~51								
aly1118.1	AP-3 complex subunit sigma-1	GO:0008565,GO:0008021,GO:0016183,GO:0016192,GO:0046907,GO:0006886,GO:0006810,GO:0006901,GO:0048072,GO:0006727,GO:0006726,GO:0030659,GO:0048490,GO:0007269,GO:0007040,GO:0030123,GO:0016020,GO:0008089,GO:0030135,GO:0005802	CG3029-PA						PF01217			PS00989	G3DSA:3.30.450.60	SSF64356									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1118.2	Zinc transporter foi	GO:0007506,GO:0035147,GO:0016477,GO:0005887,GO:0022008,GO:0009986,GO:0016020,GO:0008406,GO:0016323,GO:0035262,GO:0007280,GO:0030001,GO:0071577,GO:0005886,GO:0005385,GO:0046873,GO:0006829,GO:0055085,GO:0008354,GO:0007417	CG6817-PA						PF02535														
aly1118.3	Aspartate--tRNA ligase, cytoplasmic	GO:0005737,GO:0004815,GO:0040007,GO:0000166,GO:0003676,GO:0006422,GO:0022008,GO:0005875,GO:0005524	CG3821-PB					TIGR00458	PF00152	PS50862	PR01042,PR01042,PR01042,PR01042		G3DSA:3.30.930.10,G3DSA:2.40.50.140	SSF55681,SSF50249	18~38		REACT_71						
aly1118.4	Unknown	GO:0030246	n/a				SM00276,SM00908		PF00337	PS51304			G3DSA:2.60.120.200	SSF49899									
aly1118.5	Unknown		n/a										G3DSA:1.10.150.50	SSF47769									
aly11190.1	Protein CASC1		n/a						PF15927		PR02043,PR02043				29~49								
aly11190.2	Unknown		n/a																				
aly11190.3	Unknown		n/a																				
aly111927.1	Unknown		n/a																				
aly111945.1	Zinc finger SWIM domain containing protein 7	GO:0005634,GO:0008270,GO:0000724	n/a						PF02144	PS50966	PR01245,PR01245												
aly1121.1	Membrane-bound O-acyltransferase domain-containing protein 2	GO:0008654,GO:0016021,GO:0016020,GO:0007009,GO:0007291,GO:0071617,GO:0016746,GO:0030258,GO:0008354	CG18445-PA						PF03062														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1121.2	Unknown		n/a						PF08234						55~110								
aly1121.3	DCN1-like protein 3	GO:0030308,GO:0010332,GO:0043065,GO:0005886,GO:0048471,GO:0010225	CG13322-PA						PF03556	PS51229													
aly1121.4	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	GO:0006479,GO:0008079,GO:0000184,GO:0005829,GO:0003924,GO:0006415,GO:0003747,GO:0044822,GO:0005525	CG6382-PA						PF07145,PF03143,PF00009	PS51722	PR00315,PR00315,PR00315,PR00315,PR00315	PS00301	G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:3.40.50.300	SSF50465,SSF52540,SSF50447									
aly1121.5	E3 ubiquitin-protein ligase RBBP6	GO:0005737,GO:0004842,GO:0001701,GO:0003676,GO:0005730,GO:0048568,GO:0005634,GO:0006915,GO:0035264,GO:0005815,GO:0005654,GO:0016874,GO:0042787,GO:0008270,GO:0035736,GO:0022008,GO:0005694,GO:0044822,GO:0061053	CG3231-PA				SM00343,SM00184		PF00098,PF08783	PS51282,PS50089,PS50158			G3DSA:3.30.40.10,G3DSA:4.10.60.10	SSF57756,SSF57850	966~986,1549~1569,1047~1081,470~490								
aly1121.6	Sodium-dependent nutrient amino acid transporter 1	GO:0017032,GO:0005328,GO:0003333,GO:0016021,GO:0006814,GO:0015804,GO:0005283,GO:1903825,GO:0005887,GO:0006836,GO:0042940,GO:0042943,GO:0015175,GO:0005326	CG1698-PA						PF00209,PF00209	PS50267,PS50267	PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176	PS00754,PS00610		SSF161070,SSF161070									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly11222.1	Signal transducer and activator of transcription 5B	GO:0019221,GO:0007616,GO:0030720,GO:0038161,GO:0048103,GO:0001077,GO:0007165,GO:0019915,GO:0007298,GO:0005654,GO:0050729,GO:0006549,GO:0007455,GO:0042448,GO:0007595,GO:0045954,GO:0030856,GO:0000255,GO:0019827,GO:0006600,GO:0006366,GO:0035172,GO:0035171,GO:0019903,GO:0007526,GO:0019530,GO:0007442,GO:0006573,GO:0007379,GO:0005829,GO:0060397,GO:0045931,GO:0032825,GO:0035167,GO:0035259,GO:0007538,GO:0030178,GO:0007530,GO:0045647,GO:0043029,GO:0019218,GO:0048477,GO:0046543,GO:0046544,GO:0033077,GO:0032819,GO:0006952,GO:0035019,GO:0007350,GO:0017145,GO:0001779,GO:0007425,GO:0007424,GO:0007548,GO:0006105,GO:0006355,GO:0006107,GO:0006357,GO:0006101,GO:0006103,GO:0046983,GO:0000979,GO:0006631,GO:0042078,GO:0071481,GO:0043697,GO:0030155,GO:0045588,GO:0005737,GO:0006959,GO:0005634,GO:0007259,GO:0005509,GO:0097531,GO:0045621,GO:0008284,GO:0032870,GO:0001553,GO:0030718,GO:0071364,GO:0071363,GO:0007565,GO:0030713,GO:0070672,GO:0070670,GO:0002230,GO:0045944,GO:0005515,GO:0030097,GO:0048541,GO:0003682,GO:0071222,GO:0003677,GO:0004871,GO:0032355,GO:0007476,GO:0043066,GO:0070669,GO:0046449,GO:0048749,GO:0046425,GO:0042104,GO:0045086,GO:0008348,GO:0040014,GO:0007399,GO:0003700,GO:0040018,GO:0045579	CG4257-PK						PF02864,PF01017,PF00017	PS50001			G3DSA:2.60.40.630,G3DSA:1.10.238.10,G3DSA:3.30.505.10,G3DSA:1.20.1050.20	SSF55550,SSF49417,SSF47655	9~36,38~58								
aly11226.1	4,5-DOPA dioxygenase extradiol 1	GO:0008198,GO:0008270,GO:0006725,GO:0050297,GO:0016491	n/a			PIRSF006157			PF02900				G3DSA:3.40.830.10	SSF53213									
aly11226.2	Extradiol ring-cleavage dioxygenase	GO:0051213,GO:0006725,GO:0016701,GO:0008198,GO:0008270,GO:0016491	n/a			PIRSF006157			PF02900				G3DSA:3.40.830.10	SSF53213									
aly11226.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly112274.1	Unknown		n/a																				
aly11253.1	Synaptic vesicular amine transporter	GO:0008021,GO:0015842,GO:0015844,GO:0055085,GO:0008504,GO:0005430,GO:0097159,GO:0016021,GO:0035864,GO:0015238,GO:0031594,GO:0030659,GO:0042583,GO:0006836,GO:0015872,GO:0051608	CG33528-PD						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473										
aly112687.1	Unknown		n/a																				
aly1127.1	Unknown		n/a				SM00211		PF00086,PF14291	PS51162,PS51162			G3DSA:4.10.800.10	SSF57610,SSF57610									
aly1127.2	Protein lunapark-B	GO:0046872,GO:0016021,GO:0071782,GO:0071786,GO:0005789	CG8735-PA												11~31								
aly1127.3	Protein lunapark	GO:0042733,GO:0060173,GO:0032330,GO:0046872,GO:0016021,GO:0007596,GO:0005789,GO:0035115,GO:0071786,GO:0071782	CG8735-PA						PF10058														
aly1127.4	Unknown	GO:0003951,GO:0006741,GO:0019674	CG8080-PA																				
aly1127.5	NAD kinase 2, mitochondrial	GO:0019674,GO:0005739,GO:0006741,GO:0003951,GO:0005524,GO:0042803	CG8080-PA																				
aly1127.6	Unknown	GO:0007424,GO:0045177,GO:0040005,GO:0007475,GO:0008362,GO:0003674	CG3541-PB				SM00241		PF00100	PS51034													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly112713.1	Unknown		n/a																				
aly112865.1	Unknown		CG11550-PA										G3DSA:3.40.525.10	SSF52087									
aly112889.1	Nucleolar protein 4-like	GO:0005737,GO:0005654	CG17341-PB																				
aly113.1	Unknown		n/a																				
aly113.10	Pecanex-like protein 1	GO:0007219,GO:0005783,GO:0007029,GO:0016021,GO:0046331,GO:0005887,GO:0005886	CG3443-PE												79~99								
aly113.11	Protein pecanex	GO:0007219,GO:0005783,GO:0007399,GO:0007029,GO:0016021,GO:0046331,GO:0005887,GO:0005886	CG3443-PE						PF05041						794~814								
aly113.12	Mitochondrial 2-oxodicarboxylate carrier	GO:0035071,GO:0005743,GO:0016021,GO:0006810,GO:0022857,GO:0005739,GO:0048102,GO:0005740,GO:0005371	CG5254-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly113.13	Unknown		n/a																				
aly113.14	Ecdysteroid-regulated 16 kDa protein	GO:0032934,GO:0005615,GO:0015918,GO:0030882,GO:0008039,GO:0001530,GO:0005576,GO:0055092,GO:0045456,GO:0070891,GO:0061057,GO:0042834	CG7291-PA				SM00737		PF02221				G3DSA:2.60.40.770	SSF81296									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly113.15	Unknown		n/a																				
aly113.16	Unknown		n/a																				
aly113.17	Methyltransferase-like protein 25	GO:0008168	CG33964-PA						PF09811,PF13679														
aly113.18	Cytochrome b5	GO:0005811,GO:0043231,GO:0035206,GO:0051726,GO:0016021,GO:0016020,GO:0005789,GO:0020037,GO:0046872,GO:0012505,GO:0009055,GO:0045610,GO:0055114,GO:0002168	CG2140-PB						PF00173	PS50255	PR00363,PR00363,PR00363,PR00363	PS00191	G3DSA:3.10.120.10	SSF55856									
aly113.19	Unknown		n/a																				
aly113.2	Unknown	GO:0003677	CG3838-PA				SM00595		PF02944,PF10545	PS51031,PS51029													
aly113.20	Alkaline phosphatase, tissue-nonspecific isozyme	GO:0016791,GO:0004035,GO:0008152,GO:0005886,GO:0046872,GO:0031225	CG16771-PA				SM00098		PF00245		PR00113,PR00113,PR00113,PR00113,PR00113	PS00123	G3DSA:3.40.720.10	SSF53649		00627+3.1.3.1,00790+3.1.3.1		PWY-5491					
aly113.21	Unknown		n/a																				
aly113.22	Indole-3-acetaldehyde oxidase	GO:0004031,GO:0050660,GO:0016614,GO:0008762,GO:0043546,GO:0051536,GO:0051537,GO:0050302,GO:0009851,GO:0009688,GO:0004855,GO:0004854,GO:0005506,GO:0005829,GO:0055114,GO:0009055	CG6045-PA			PIRSF000127	SM01008,SM01092		PF00111,PF01799,PF00941,PF02738,PF01315,PF03450	PS51387		PS00197	G3DSA:1.10.150.120,G3DSA:3.90.1170.50,G3DSA:3.10.20.30,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.390.50,G3DSA:3.30.465.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10	SSF54665,SSF56176,SSF54292,SSF55447,SSF56003,SSF47741										
aly113.23	Unknown		n/a																				
aly113.24	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly113.25	Indole-3-acetaldehyde oxidase	GO:0004031,GO:0050660,GO:0016614,GO:0008762,GO:0051536,GO:0051537,GO:0050302,GO:0009851,GO:0009688,GO:0004855,GO:0043546,GO:0005506,GO:0005829,GO:0055114,GO:0009055	CG18519-PC			PIRSF000127	SM01092,SM01008		PF00111,PF00941,PF01315,PF03450,PF01799,PF02738	PS51387,PS51085		PS00197	G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.390.50,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.465.10,G3DSA:3.10.20.30,G3DSA:1.10.150.120,G3DSA:3.30.365.10,G3DSA:3.90.1170.50	SSF54665,SSF54292,SSF47741,SSF55447,SSF56003,SSF56176										
aly113.26	Symplekin	GO:0005634,GO:0035363,GO:0005848,GO:0006398,GO:0003723,GO:0003677,GO:0006378,GO:0006379,GO:0005923	CG2097-PA						PF11935,PF12295				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371	496~516								
aly113.27	Unknown		n/a																				
aly113.28	Unknown		n/a																				
aly113.29	Unknown		n/a																				
aly113.3	Breast cancer metastasis-suppressor 1-[illegible]	GO:0070822,GO:0005634,GO:0006351,GO:0006355	CG4400-PA												16~39								
aly113.30	Unknown		n/a																				
aly113.31	Unknown		n/a																				
aly113.32	Unknown		n/a																				
aly113.33	Unknown		n/a																				
aly113.4	Unknown		n/a																				
aly113.5	Probable 39S ribosomal protein L49, mitochondrial	GO:0005840,GO:0005622,GO:0003735,GO:0005762,GO:0006412,GO:0006413,GO:0032543,GO:0003743	CG4647-PA						PF05046														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly113.6	Unknown	GO:0005730,GO:0000089,GO:0005634,GO:0007552,GO:0000705,GO:0016321,GO:0005700,GO:0005654,GO:0010629,GO:0000228	CG4399-PE																				
aly113.7	Homeobox protein MOX-2	GO:0005737,GO:0043565,GO:0070997,GO:0001757,GO:0003700,GO:0007519,GO:0005634,GO:0060173,GO:0008015,GO:0006366,GO:0007275,GO:0006355,GO:0001077,GO:0060021,GO:0016607,GO:0003677,GO:0045944,GO:0000978,GO:0001525,GO:0001205,GO:0000980	CG5264-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689										
aly113.8	Kinesin light chain	GO:0005737,GO:0007017,GO:0008152,GO:0051726,GO:0007018,GO:0005515,GO:0005871,GO:0005874,GO:0005875,GO:0003777,GO:0046843	CG5433-PA				SM00028,SM00028,SM00028,SM00028,SM00028		PF13374,PF13424,PF13424	PS50005,PS50005,PS50005,PS50005,PS50293,PS50005,PS50005,PS50293	PR00381,PR00381,PR00381,PR00381,PR00381,PR00381	PS01160,PS01160,PS01160,PS01160	G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452	83~145									
aly113.9	Thioredoxin, mitochondrial	GO:0005737,GO:0006457,GO:0005730,GO:0000103,GO:0045454,GO:0005739,GO:0016671,GO:0034599,GO:0015035,GO:0006662,GO:0055114,GO:0015036	CG3719-PA						PF00085	PS51352		PS00194	G3DSA:3.40.30.10	SSF52833									
aly11306.1	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6467-PA				SM00020		PF00089	PS50240		PS00135	G3DSA:2.40.10.10	SSF50494									
aly1131.1	Alpha-tocopherol transfer protein	GO:0008431,GO:0005770,GO:0006629,GO:0046909,GO:0005215,GO:0005829,GO:0006810,GO:0090212,GO:0005546,GO:0005622,GO:0043325,GO:0042360,GO:0060548,GO:0051452,GO:0009268,GO:0009636,GO:0001892,GO:0007584,GO:0051180	CG12926-PA						PF00650	PS50191	PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087,SSF46938									
aly1131.2	Alpha-tocopherol transfer protein-like	GO:0016020,GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG2663-PA						PF00650	PS50191	PR00180,PR00180		G3DSA:3.40.525.10	SSF52087									
aly113285.1	Unknown		n/a												37~57								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly11338.1	Unknown		n/a																				
aly11338.2	Protein krasavietz	GO:0005737,GO:0048663,GO:0048149,GO:0007616,GO:0043025,GO:0016199,GO:0030424,GO:0030175,GO:0051491,GO:0005515,GO:0017148,GO:0031369,GO:0043022,GO:0048477,GO:0044295	CG2922-PA				SM00515		PF02020	PS51366,PS51363			G3DSA:1.25.40.180	SSF48371									
aly11338.3	Unknown		n/a																				
aly11338.4	Probable 39S ribosomal protein L45, mitochondrial	GO:0003735,GO:0005762,GO:0005739,GO:0006412	CG6949-PA				SM00978		PF04280					SSF54427									
aly11338.5	Regulator of G protein signaling loco	GO:0055059,GO:0010001,GO:0007310,GO:0008105,GO:0007419,GO:0008277,GO:0007303,GO:0003015,GO:0042594,GO:0008069,GO:0007049,GO:0005737,GO:0043547,GO:0005057,GO:0019991,GO:0045179,GO:0016324,GO:0001965,GO:0060857,GO:0007186,GO:0038032,GO:0032291,GO:0005092,GO:0050790,GO:0005096,GO:0050832,GO:0014045,GO:0009786,GO:0005886,GO:0009408,GO:0006979,GO:0000578,GO:0030866	CG5248-PD				SM00315,SM00455		PF02196,PF00615	PS50132,PS50898	PR01301,PR01301		G3DSA:3.10.20.90,G3DSA:4.10.81.20,G3DSA:1.10.167.10	SSF48097,SSF54236									
aly1134.1	Unknown	GO:0005549	n/a				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly1134.2	Unknown	GO:0022008	CG31344-PA						PF09995														
aly1134.3	Reticulon-4 receptor-like 2	GO:0009897,GO:0031103,GO:0005515,GO:0009986,GO:0045121,GO:0042059,GO:0046658,GO:0046331,GO:0004872,GO:0005887,GO:0070062	CG1804-PB				SM00082,SM00409,SM00369,SM00369,SM00369,SM00369		PF07679,PF13855,PF13855	PS50835			G3DSA:2.60.40.10,G3DSA:3.80.10.10	SSF52058,SSF48726									
aly1134.4	Unknown		n/a																				
aly1134.5	Unknown		n/a																				
aly113534.1	Unknown	GO:0016021,GO:0055085,GO:0008513	CG42269-PE																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly11369.1	Multidrug resistance-associated protein 4	GO:0043190,GO:0042626,GO:0016020,GO:0016404,GO:0005215,GO:0016021,GO:0007596,GO:0042060,GO:0016323,GO:0008559,GO:0055114,GO:0016887,GO:0005886,GO:0031088,GO:0030168,GO:0055085,GO:0005524,GO:0002576	CG7627-PA				SM00382		PF00005,PF00664	PS50893,PS50929		PS00211	G3DSA:1.20.1560.10,G3DSA:3.40.50.300	SSF52540,SSF90123,SSF90123									
aly1139.1	Glutamine-rich protein 2	GO:0005575,GO:0003674,GO:0008150	CG10869-PA						PF16043						251~278,110~130								
aly1139.10	MFS-type transporter SLC18B1	GO:0008021,GO:0015842,GO:0015844,GO:0055085,GO:0008504,GO:0005430,GO:0005215,GO:0016021,GO:0015238,GO:0031594,GO:0006836,GO:0015872,GO:0051608	CG33528-PD						PF07690,PF07690	PS50850	PR01035,PR01035,PR01035		G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly1139.11	Ommochrome-binding protein		n/a										G3DSA:2.120.10.30,G3DSA:2.120.10.30	SSF63829									
aly1139.12	Unknown	GO:0005575,GO:0003674,GO:0008150	CG32032-PA																				
aly1139.13	Unknown		n/a																				
aly1139.14	Unknown	GO:0005575,GO:0003674,GO:0008150	CG32032-PA																				
aly1139.15	Unknown	GO:0005575,GO:0003674,GO:0008150	CG32032-PA											SSF50814,SSF50814									
aly1139.16	GTP:AMP phosphotransferase AK3, mitochondrial	GO:0006139,GO:0046039,GO:0019205,GO:0046051,GO:0046041,GO:0005739,GO:0005524,GO:0046899,GO:0005759,GO:0004017,GO:0046033,GO:0006172,GO:0005525	CG6612-PB	MF_03169,MF_00235				TIGR01351	PF00406,PF05191		PR00094,PR00094,PR00094,PR00094,PR00094	PS00113	G3DSA:3.40.50.300	SSF52540,SSF52540,SSF57774		00230+2.7.4.10,00230+2.7.4.3		PWY-7219	UPA00588				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.17	Probable poly(ADP-ribose) glycohydrolase 2	GO:0004649,GO:0005975,GO:0035065,GO:0050832,GO:0006342,GO:0005634,GO:0043844,GO:0030576,GO:0005654,GO:0009408,GO:0051457,GO:0036099,GO:0006909	CG2864-PB						PF05028,PF05028						518~538								
aly1139.18	COP9 signalosome complex subunit 6	GO:0005737,GO:0050821,GO:0046331,GO:0005515,GO:0007095,GO:0008180	CG6932-PA				SM00232		PF01398														
aly1139.19	Phosphatidate cytidylyltransferase, mitochondrial	GO:0032049,GO:0016024,GO:0005575,GO:0031314,GO:0003674,GO:0004605,GO:0008150	CG33331-PA			PIRSF028840			PF09139							00564+2.7.7.41		PWY-5667,PWY-5981	UPA00557				
aly1139.2	Extracellular sulfatase SULF-1 homolog	GO:0005795,GO:0007389,GO:0016201,GO:0030202,GO:0005783,GO:0005615,GO:0009986,GO:0017015,GO:0045879,GO:0042059,GO:0008449,GO:0030111,GO:0045880,GO:0008152,GO:0008045,GO:0046872,GO:0030178,GO:0018741	CG6725-PA						PF00884,PF12548			PS00523	G3DSA:3.40.720.10,G3DSA:3.40.720.10	SSF53649,SSF53649	1194~1230,878~912								
aly1139.20	GPALPP motifs-containing protein 1	GO:0005575,GO:0008150,GO:0003674	CG33332-PA						PF12572						229~256,539~577,46~66								
aly1139.21	Unknown		n/a																				
aly1139.22	Cyclin-C	GO:0001104,GO:0016592,GO:0006367,GO:0034472,GO:0006355,GO:0000079,GO:0000082,GO:0036011,GO:0019901,GO:0016538,GO:0045498,GO:0006357,GO:0006351,GO:0005515,GO:0019908,GO:0007095,GO:0016591,GO:0005634,GO:0022416	CG7281-PA			PIRSF028758	SM00385,SM00385		PF16899,PF00134				G3DSA:1.10.472.10	SSF47954,SSF47954										
aly1139.23	Unknown	GO:0005575,GO:0008150,GO:0003674	CG33306-PA				SM00700		PF06585				G3DSA:3.15.10.10	SSF55394									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.24	Unknown		n/a						PF06585														
aly1139.25	Lethal(2)neighbour of Tid protein	GO:0005783,GO:0016021,GO:0005789,GO:0030176,GO:0016758,GO:0007275	CG4084-PA						PF05208						333~356	00510+2.4.1.258,00513+2.4.1.258			UPA00378				
aly1139.26	E3 ubiquitin-protein ligase hyd	GO:0048749,GO:0008585,GO:0008270,GO:0000209,GO:0005737,GO:0007455,GO:0005634,GO:0042787,GO:0042127,GO:0004842,GO:0034450,GO:0045879,GO:0007281,GO:0007283,GO:0030162,GO:0007289,GO:0016874,GO:0007112,GO:0007446,GO:0007444,GO:0043130,GO:0003723	CG9484-PB				SM00396,SM00119,SM00517		PF11547,PF00658,PF00632	PS50237,PS51157,PS51309			G3DSA:2.130.10.30,G3DSA:2.130.10.30,G3DSA:1.10.1900.10,G3DSA:3.30.2160.10	SSF63570,SSF56204,SSF56204,SSF50985	2817~2817				UPA00143				
aly1139.27	E3 ubiquitin-protein ligase RNF168	GO:0035518,GO:0042393,GO:0045190,GO:0008270,GO:0010212,GO:0006302,GO:0004842,GO:0005634,GO:0043130,GO:0070530,GO:0070535,GO:0070534,GO:0034244,GO:0006974,GO:0016874,GO:0036352,GO:0036351,GO:0035861,GO:0000151,GO:0016567,GO:0006511,GO:0045739,GO:0003682	n/a				SM00184		PF00097	PS50089			G3DSA:3.30.40.10	SSF57850	128~170,2~22								
aly1139.28	TAR DNA-binding protein 43	GO:0035061,GO:0032024,GO:0008344,GO:0010629,GO:0045886,GO:0030264,GO:0003676,GO:0070935,GO:0007274,GO:0007417,GO:0005737,GO:0005634,GO:0000166,GO:0005654,GO:0003730,GO:0071765,GO:0006366,GO:0003690,GO:0008380,GO:0042802,GO:0016607,GO:0044822,GO:0007628,GO:0007528,GO:0043922,GO:0001205,GO:0008345,GO:0048471,GO:0034976,GO:0005726,GO:0051726,GO:0003700,GO:0048812,GO:0003723,GO:0001933,GO:0006397,GO:0003729	CG10327-PB				SM00360,SM00360		PF00076,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928									
aly1139.29	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2	GO:0006048,GO:0005975,GO:0004360,GO:0006541,GO:0030246,GO:0016051	CG12449-PN					TIGR01135	PF01380,PF01380,PF13522	PS51278,PS51464,PS51464			G3DSA:3.60.20.10,G3DSA:3.40.50.10490,G3DSA:3.40.50.10490	SSF53697,SSF56235		00520+2.6.1.16,00250+2.6.1.16	REACT_17015	PWY-6749					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.3	UPF0544 protein C5orf45 homolog		n/a						PF15749														
aly1139.30	Elongation factor 1-alpha	GO:0005737,GO:0005853,GO:0005811,GO:0003924,GO:0006412,GO:0003746,GO:0006414,GO:0022008,GO:0005525	CG1873-PA					TIGR00483	PF03144,PF03143,PF00009	PS51722	PR00315,PR00315,PR00315,PR00315,PR00315	PS00301	G3DSA:3.40.50.300,G3DSA:2.40.30.10,G3DSA:2.40.30.10	SSF52540,SSF50447,SSF50465									
aly1139.31	GRIP and coiled-coil domain-containing protein 2	GO:0070861,GO:0034453,GO:0031023,GO:0071955,GO:0048193,GO:0000042,GO:0034067,GO:0016020,GO:0017137,GO:0000138,GO:0090161,GO:0005654,GO:0030306,GO:0006622,GO:0042147,GO:0005802,GO:0034499,GO:0042802,GO:0042803	CG3532-PB				SM00755		PF01465	PS50913			G3DSA:1.10.220.60		450~505,997~1024,342~432,844~871,664~719,239~259,299~326,193~227,622~656,1100~1155,875~989,1029~1077,577~611,521~562,92~119,134~175,1320~1354,797~824,734~754,36~84									
aly1139.32	Serine/threonine-protein kinase PAK 1	GO:0006887,GO:0033138,GO:0050803,GO:0060244,GO:0032147,GO:0030036,GO:0030424,GO:0045887,GO:0043507,GO:0007411,GO:0030425,GO:0005925,GO:0042981,GO:0046777,GO:0023014,GO:0043408,GO:0005856,GO:0007254,GO:0016601,GO:0031532,GO:0051496,GO:0005634,GO:0019991,GO:0031098,GO:0004674,GO:0007346,GO:0016477,GO:0001726,GO:0005524,GO:0005794,GO:0006468,GO:0016328,GO:0006915,GO:0033148,GO:0042060,GO:0016358,GO:0007528,GO:0008360,GO:0048754,GO:0005911,GO:0005886,GO:0007155,GO:0007266,GO:0097482,GO:0032587,GO:0097481,GO:0043234,GO:0050770,GO:0007391,GO:0005737,GO:0048365,GO:0004702,GO:0043113,GO:0005518,GO:0030426,GO:0001934	CG10295-PF				SM00220,SM00285		PF00786,PF00069	PS50108,PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.90.810.10,G3DSA:3.30.200.20	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.33	Methionine-R-sulfoxide reductase B1	GO:0033743,GO:0007015,GO:0070191,GO:0005829,GO:0018206,GO:0007526,GO:0008407,GO:0005654,GO:0008270,GO:0030041,GO:0007411,GO:0006979,GO:0055114,GO:0030091	CG6584-PE	MF_01400				TIGR00357	PF01641				G3DSA:2.170.150.20	SSF51316									
aly1139.34	Unknown		n/a																				
aly1139.35	Unknown	GO:0005575,GO:0048813,GO:0046331,GO:0003674	CG8765-PA				SM00595		PF10545	PS51029													
aly1139.36	E3 SUMO-protein ligase RanBP2	GO:0006457,GO:0033132,GO:0042405,GO:0051028,GO:0005875,GO:0044615,GO:0005811,GO:0005739,GO:0003755,GO:0007184,GO:0006606,GO:0031965,GO:0006607,GO:0016925,GO:0016874,GO:0090526,GO:0046907,GO:0005643,GO:0008536,GO:0003723,GO:0015031,GO:0008270	CG11856-PB				SM00160,SM00160,SM00160,SM00547,SM00547,SM00547,SM00028		PF00641,PF00515,PF00638,PF00638,PF00638	PS50005,PS50199,PS50199,PS50199,PS50196,PS50293,PS50005,PS50196,PS50196		PS01358,PS01358,PS01358	G3DSA:2.30.29.30,G3DSA:2.30.29.30,G3DSA:2.30.29.30,G3DSA:2.30.29.30,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF50729,SSF90209,SSF50729,SSF48452,SSF50729	886~937,1632~1652									
aly1139.37	Transcription initiation factor TFIID subunit 6	GO:0000124,GO:0007221,GO:0051090,GO:0051123,GO:0006355,GO:0005634,GO:0001075,GO:0006367,GO:0006366,GO:0005669,GO:0022008,GO:0046982	CG32211-PA				SM00803		PF07571,PF02969				G3DSA:1.25.10.10,G3DSA:1.10.20.10	SSF47113									
aly1139.38	Unknown		n/a																				
aly1139.39	Protein Wnt-11b-1	GO:0048675,GO:0060541,GO:0007435,GO:0009952,GO:0007369,GO:0000122,GO:0016204,GO:0016055,GO:0009950,GO:0060070,GO:0005578,GO:0005576,GO:0005110,GO:0005886,GO:0050919,GO:0007411,GO:0005102,GO:0033564,GO:0007275,GO:0005615	CG6407-PA				SM00097		PF00110		PR01349,PR01349,PR01349						REACT_14797						
aly1139.4	Unknown		n/a				SM00355,SM00355					PS00028,PS00028			149~169,35~55								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.40	UDP-glucose:glycoprotein glucosyltransferase	GO:0005737,GO:0005791,GO:0005783,GO:0006486,GO:0005635,GO:0005788,GO:0012505,GO:0003980,GO:0097359	CG6850-PA						PF06427,PF06427,PF06427				G3DSA:3.90.550.10	SSF53448	1062~1082				UPA00378				
aly1139.41	Transport and Golgi organization protein 11	GO:0005783,GO:0009306,GO:0016021,GO:0005777,GO:0005789,GO:0005741,GO:0003674	CG30404-PA						PF05644,PF05644						136~156								
aly1139.42	Pantothenate kinase 4	GO:0005737,GO:0004594,GO:0005524,GO:0015937	CG5828-PA						PF01937					SSF111321									
aly1139.43	Protein ECT2	GO:0005089,GO:0043547,GO:0051056,GO:0070830,GO:0005085,GO:0032147,GO:0048011,GO:0004871,GO:0051225,GO:0043231,GO:0032507,GO:0005737,GO:0071479,GO:0072686,GO:0000902,GO:0005923,GO:0005634,GO:0051260,GO:0000281,GO:0097149,GO:0032314,GO:0043065,GO:0045666,GO:0031965,GO:0032467,GO:0043123,GO:0030676,GO:0008078,GO:0030215,GO:0097190,GO:0070301,GO:0005096,GO:0032154,GO:0071277,GO:0045859,GO:0008360,GO:0005938,GO:0005911,GO:0190198 1,GO:0007155,GO:0030496,GO:0022008,GO:0007264,GO:0000915,GO:0007443,GO:0007110,GO:0045792,GO:0007415,GO:0050770,GO:0007399,GO:0007422,GO:0005829,GO:0090630,GO:0007509,GO:0015031,GO:0000910,GO:0042803,GO:0042307,GO:0007111,GO:0051988	CG8114-PB				SM00292,SM00292,SM00325		PF12738,PF00621	PS50172,PS50172,PS50010		PS00741	G3DSA:1.20.900.10,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190,G3DSA:2.30.29.30	SSF52113,SSF52113,SSF50729,SSF48065			REACT_14797,REACT_11044,REACT_11061							
aly1139.44	Mediator of RNA polymerase II transcription subunit 14	GO:0006367,GO:0005634,GO:0001104,GO:0006357,GO:0006351,GO:0005515,GO:0006366,GO:0016592	CG12031-PC						PF08638														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.45	Glutamate--cysteine ligase	GO:0005515,GO:0004357,GO:0017109,GO:0006974,GO:0006749,GO:0006750,GO:0048471,GO:0005634,GO:0005524	CG2259-PA						PF03074				G3DSA:2.40.50.140	SSF55931,SSF55931		00480+6.3.2.2		PWY-7255,PWY-6840	UPA00142				
aly1139.46	Beta-catenin-like protein 1	GO:0005654,GO:0016020,GO:0005634,GO:0006915,GO:0019899,GO:0005575,GO:0043065,GO:0003674,GO:0000974,GO:0008150,GO:0016445,GO:0005681	CG11964-PA						PF08216				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371	451~471								
aly1139.47	Hydroxyacid oxidase 1	GO:0052852,GO:0001561,GO:0005782,GO:0005777,GO:0052854,GO:0008891,GO:0047969,GO:0046296,GO:0003973,GO:0052853,GO:0034641,GO:0044281,GO:0010181,GO:0005102,GO:0046487,GO:0006979,GO:0055114,GO:0016491	CG18003-PB			PIRSF000138			PF01070	PS51349		PS00557	G3DSA:3.20.20.70	SSF51395									
aly1139.48	Probable ubiquitin carboxyl-terminal hydrolase FAF	GO:0008583,GO:0009790,GO:0006511,GO:0050829,GO:0008354,GO:0005737,GO:0043161,GO:0007349,GO:0045824,GO:0048477,GO:0048749,GO:0061136,GO:0007601,GO:0004843,GO:0006897,GO:0009950,GO:0016579,GO:0035192,GO:0004197,GO:0005515,GO:0045861,GO:0007097	CG1945-PA						PF00443	PS50235		PS00973,PS00972		SSF54001,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371									
aly1139.49	DTW domain-containing protein 1		CG2006-PA						PF03942														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.5	Protein tramtrack, beta isoform	GO:0035147,GO:0048750,GO:0045467,GO:0035001,GO:0031208,GO:0003677,GO:0043388,GO:0007298,GO:0001078,GO:0002121,GO:0031987,GO:0040003,GO:0000122,GO:0005634,GO:0001709,GO:0007476,GO:0030707,GO:0001964,GO:0060446,GO:0042682,GO:0003682,GO:0016476,GO:0046872,GO:0000980,GO:0048666,GO:0035151,GO:0017053,GO:0042675,GO:0008360,GO:0045892,GO:0048053,GO:0007426,GO:0007422,GO:0003700,GO:0048854,GO:0005700,GO:0048813,GO:0006357,GO:0045944,GO:0006351,GO:0005515,GO:0000978,GO:0042803,GO:0046843	CG1856-PE				SM00355,SM00355,SM00225		PF00651	PS50157,PS50097		PS00028	G3DSA:3.30.710.10,G3DSA:3.30.160.60	SSF54695,SSF57667									
aly1139.50	F-box-like/WD repeat-containing protein TBL1XR1	GO:0042393,GO:0035264,GO:0090207,GO:0003677,GO:0035220,GO:0042058,GO:0060613,GO:0060612,GO:0045892,GO:0060070,GO:0005876,GO:0070491,GO:0005654,GO:0007219,GO:0000122,GO:0043161,GO:0005634,GO:0003714,GO:0016042,GO:0016575,GO:0045747,GO:0002021,GO:0010468,GO:0005525,GO:0005515,GO:0017053,GO:0050872,GO:0008013,GO:0000118,GO:0042676,GO:0001106,GO:0042461,GO:0007173,GO:0045893,GO:0044212,GO:0045572,GO:0047485,GO:0051726,GO:0005700,GO:0022416,GO:0045944,GO:0006351,GO:0031065,GO:0030162,GO:0003682,GO:0030814	CG4063-PA				SM00667,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF08513,PF00400,PF00400,PF00400,PF00400,PF00400,PF00400	PS50896,PS50082,PS50082,PS50082,PS50294,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978									
aly1139.51	Gamma-tubulin complex component 3	GO:0005737,GO:0007020,GO:0072686,GO:0005827,GO:0005813,GO:0008017,GO:0016020,GO:0005814,GO:0000922,GO:0008275,GO:0043147,GO:0007052,GO:0007017,GO:0000226,GO:0043015,GO:0022008,GO:0005815,GO:0051011,GO:0051297,GO:0007140,GO:0005875	CG10988-PA						PF04130								REACT_152						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.52	Gamma-tubulin complex component 3	GO:0005200,GO:0000086,GO:0008275,GO:0000226,GO:0005815,GO:0005875,GO:0007140,GO:0005737,GO:0007020,GO:0072686,GO:0005813,GO:0016020,GO:0005814,GO:0000922,GO:0043147,GO:0051011,GO:0000278,GO:0008017,GO:0007052,GO:0005819,GO:0007338,GO:0022008,GO:0007017,GO:0005827,GO:0005829,GO:0005198,GO:0051297,GO:0043015	CG10988-PA						PF04130								REACT_152						
aly1139.53	Unknown		n/a												85~126,205~239,145~193								
aly1139.54	Ras-like GTP-binding protein RhoL	GO:0035099,GO:0005575,GO:0007516,GO:0007498,GO:0005886,GO:0003924,GO:0030707,GO:0005622,GO:0006974,GO:0008360,GO:0005509,GO:0005525,GO:0007155,GO:0007298,GO:0007264,GO:0035011,GO:0022409	CG9366-PB				SM00174,SM00176,SM00173,SM00175	TIGR00231	PF00071	PS51420	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly1139.55	Nuclear cap-binding protein subunit 2	GO:0005846,GO:0071011,GO:0030422,GO:0005634,GO:0045071,GO:0000398,GO:0000166,GO:0006370,GO:0031047,GO:0000339,GO:0045292,GO:0035195,GO:0071013,GO:0005875,GO:0005681,GO:0003729	CG12357-PA						PF13893				G3DSA:3.30.70.330	SSF54928									
aly1139.56	NAD(P) transhydrogenase, mitochondrial	GO:0008021,GO:0050661,GO:0015992,GO:0005887,GO:0046907,GO:0016079,GO:0016021,GO:0005544,GO:0008750,GO:0005743,GO:0072593,GO:0005515,GO:0045454	CG6643-PC				SM01002,SM00239,SM00239,SM00239,SM01003	TIGR00561	PF02233,PF17047,PF12769,PF01262,PF00168,PF00168,PF00168,PF05222	PS50004,PS50004			G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:3.40.50.1220,G3DSA:3.40.50.1770,G3DSA:3.40.50.1770,G3DSA:2.60.40.150	SSF49562,SSF49562,SSF51735,SSF52283,SSF49562,SSF52467		00760+1.6.1.2							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.57	Isocitrate dehydrogenase [NADP], mitochondrial (Fragment)	GO:0000287,GO:0070062,GO:0005743,GO:0051287,GO:0005811,GO:0005777,GO:0005739,GO:0004450,GO:0006099,GO:0001561,GO:0006103,GO:0006102,GO:0006097	CG7176-PC			PIRSF000108		TIGR00127	PF00180			PS00470	G3DSA:3.40.718.10	SSF53659	420~436	00020+1.1.1.42,00720+1.1.1.42,00480+1.1.1.42	REACT_1046	PWY-5913,PWY-7268,PWY-6969,PWY-6728,PWY-6549,PWY-7254,PWY-7124					
aly1139.58	O-glucosyltransferase rumi homolog	GO:0045746,GO:0007030,GO:0007219,GO:0006486,GO:0005788,GO:0046527,GO:0045747,GO:0033577,GO:2000035,GO:0016757,GO:0008593,GO:0005576	CG31152-PA				SM00672		PF05686						37~57								
aly1139.59	Probable serine incorporator	GO:0005789,GO:0016021,GO:0016020,GO:0008654,GO:0005886	CG4672-PF						PF03348														
aly1139.6	Follicle cell protein 3C-1	GO:0005575,GO:0008150,GO:0003674	CG4015-PA																				
aly1139.60	Zinc finger protein 395	GO:0005737,GO:0005634,GO:0007476,GO:0006355,GO:0006351,GO:0003677,GO:0046872	CG34360-PG						PF15997														
aly1139.61	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	GO:0006767,GO:0004485,GO:0005829,GO:0006552,GO:0006768,GO:0005739,GO:0006551,GO:0005743,GO:0034641,GO:0006766,GO:0009083,GO:0005759,GO:0004075,GO:0046872,GO:0009374,GO:0005524,GO:0044281	CG2118-PA				SM00878		PF02786,PF02785,PF00289,PF00364	PS50968,PS50975,PS50979		PS00867,PS00188	G3DSA:3.30.1490.20,G3DSA:2.40.50.100,G3DSA:3.40.50.20,G3DSA:3.30.470.20	SSF51246,SSF56059,SSF51230,SSF52440										
aly1139.62	Flap endonuclease GEN	GO:0000014,GO:0006284,GO:0000738,GO:0006302,GO:0006281,GO:0004518,GO:0004519,GO:0005634,GO:0000737,GO:0004520,GO:0048256,GO:0008310,GO:0008311,GO:0035312,GO:0046872,GO:0003677,GO:0003684	CG10670-PA				SM00485,SM00484		PF00752,PF00867		PR00853,PR00853,PR00853,PR00853,PR00853		G3DSA:3.40.50.1010	SSF47807,SSF47807,SSF88723									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.63	Cyclic nucleotide-gated cation channel alpha-3	GO:0030553,GO:0042391,GO:0006810,GO:1902495,GO:0005249,GO:0071805,GO:0005221,GO:0006812,GO:0005223,GO:0005222,GO:0046549,GO:0015276,GO:0001750,GO:0007601,GO:0019935,GO:0007165,GO:0005887,GO:0055085,GO:0017071	CG42260-PA				SM00100		PF00520,PF00027	PS50042		PS00889,PS00888	G3DSA:1.10.287.70,G3DSA:2.60.120.10,G3DSA:1.10.287.630	SSF51206,SSF81324	657~677								
aly1139.64	Unknown		n/a																				
aly1139.65	Filamin-C	GO:0005737,GO:0042383,GO:0015629,GO:0030029,GO:0008092,GO:0048747,GO:0005886,GO:0009612,GO:0003779,GO:0030506,GO:0005515,GO:0048104,GO:0005925,GO:0030018	CG30092-PN				SM00033,SM00033,SM00033,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557		PF00630,PF00630,PF00630,PF00630,PF00630,PF00630,PF00630,PF00630,PF00630,PF00630,PF00630,PF00630,PF00307,PF00307,PF00307	PS50021,PS50194,PS50021,PS50194,PS50194,PS50194,PS50194,PS50021,PS50194,PS50194,PS50194,PS50194,PS50194,PS50194,PS50194,PS50194,PS50194,PS50194,PS50194,PS50194		PS00019	G3DSA:1.10.418.10,G3DSA:2.60.40.10,G3DSA:1.10.418.10,G3DSA:1.10.418.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF81296,SSF81296,SSF81296,SSF81296,SSF81296,SSF81296,SSF81296,SSF81296,SSF81296,SSF81296,SSF81296,SSF81296,SSF47576,SSF81296,SSF81296,SSF47576,SSF81296,SSF81296,SSF81296	2850~2850								
aly1139.66	Unknown		n/a																				
aly1139.67	Unknown		n/a				SM00700		PF06585														
aly1139.68	Unknown		n/a																				
aly1139.69	Putative ATP-dependent RNA helicase an3	GO:0005737,GO:0000070,GO:0043186,GO:0008026,GO:0048477,GO:0005811,GO:0004004,GO:0005875,GO:0007283,GO:0003723,GO:0003676,GO:0007286,GO:0016246,GO:0004386,GO:0016442,GO:0043025,GO:0010468,GO:0005524,GO:0002168	CG9748-PB				SM00490,SM00487		PF00271,PF00270	PS51194,PS51195,PS51192		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									
aly1139.7	Hydroxyacyl-thioester dehydratase type 2, mitochondrial	GO:0006631,GO:0005739,GO:0016829,GO:0008152,GO:0016491	CG14881-PA						PF01575				G3DSA:3.10.129.10	SSF54637									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.70	Pair-rule protein odd-paired	GO:0007494,GO:0008101,GO:0007365,GO:0003700,GO:0007455,GO:0005634,GO:0006357,GO:0045944,GO:0006366,GO:0007366,GO:0001205,GO:0046872,GO:0008354,GO:0000980	CG1133-PA				SM00355,SM00355,SM00355,SM00355,SM00355		PF00096	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly1139.71	Glycerophosphodiester phosphodiesterase GDPD6	GO:0008889,GO:0006071,GO:0006629,GO:0008081	n/a						PF03009	PS51704			G3DSA:3.20.20.190	SSF51695									
aly1139.72	UDP-glucuronic acid decarboxylase 1	GO:0050662,GO:0006629,GO:0008081,GO:0070062,GO:0016021,GO:0044237,GO:0051262,GO:0033320,GO:0005739,GO:0070403,GO:0008460,GO:0032580,GO:0042803,GO:0048040	CG7979-PA						PF03009,PF16363	PS51704			G3DSA:3.90.25.10,G3DSA:3.40.50.720,G3DSA:3.20.20.190	SSF51735,SSF51695	437~471								
aly1139.73	Beta-1,3-galactosyltransferase 6	GO:0030206,GO:0005797,GO:0035250,GO:0006486,GO:0016021,GO:0016020,GO:0000139,GO:0015012,GO:0008378,GO:0047220,GO:0008499,GO:0006024	CG8734-PA						PF01762										UPA00378				
aly1139.74	Probable multidrug resistance-associated protein lethal(2)03659	GO:0043190,GO:0042626,GO:0005215,GO:0016021,GO:0006810,GO:0007275,GO:0055085,GO:0005524	CG4562-PE				SM00382,SM00382		PF00664,PF00664,PF00005,PF00005	PS50893,PS50929,PS50929,PS50893		PS00211,PS00211	G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF90123,SSF52540,SSF52540,SSF90123									
aly1139.75	Fibroblast growth factor receptor 3	GO:0008284,GO:0005515,GO:0016021,GO:0006915,GO:0001501,GO:0005007,GO:0005886,GO:0005524	n/a				SM00409,SM00409		PF07679,PF13927	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:3.40.50.10140,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF52200									
aly1139.76	IQ domain-containing protein G	GO:0070062,GO:0005515	n/a				SM00015			PS50096													

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.77	Diuretic hormone 45	GO:0005179,GO:0009755,GO:0007218,GO:0005184,GO:0005615,GO:0007589,GO:0008613,GO:0005576,GO:0001664,GO:0007186	CG8348-PA				SM00039		PF00473			PS00511			72~92								
aly1139.78	Unknown		n/a											SSF50494									
aly1139.79	von Willebrand factor A domain-containing	GO:0005634,GO:0034472,GO:0032039	CG4785-PA						PF13519	PS50234			G3DSA:3.40.50.410	SSF53300									
aly1139.8	Armadillo repeat-containing	GO:0005737,GO:0005488,GO:0008152,GO:0016491	CG14881-PA										G3DSA:1.25.10.10	SSF48371									
aly1139.80	Transmembrane and TPR repeat-containing protein 4	GO:0016021,GO:0017122,GO:0008150,GO:0005515,GO:0016262	CG5038-PA				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF13414,PF13424,PF08409,PF13374	PS50293,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005			G3DSA:1.25.40.10	SSF48452									
aly1139.81	Unknown		n/a																				
aly1139.82	DNA topoisomerase 2-binding protein 1-B	GO:0033314,GO:0005737,GO:0006281,GO:0005694,GO:0005634,GO:0005815,GO:0006260,GO:0003677,GO:0007095,GO:0007067,GO:0000922,GO:0048477,GO:0007049	CG11156-PA				SM00355,SM00355,SM00868,SM00868		PF07776	PS50157		PS00028	G3DSA:3.40.50.10190,G3DSA:3.40.50.10190	SSF52113,SSF52113,SSF57716										
aly1139.83	Decapping and exoribonuclease protein	GO:0008409,GO:0071028,GO:0005634,GO:0000287,GO:0050779,GO:0034353,GO:0000166,GO:0090305,GO:0008152,GO:0006402,GO:0003729	CG9125-PA						PF08652														
aly1139.84	Unknown	GO:0006355,GO:0003677	CG9727-PB																				
aly1139.85	DNA-binding protein Rfx5	GO:0000122,GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003677,GO:0000978	CG9727-PB						PF02257	PS51526			G3DSA:1.10.10.10	SSF46785									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.86	Exostosin-3	GO:0030210,GO:0005794,GO:0046872,GO:0007367,GO:0008101,GO:0007224,GO:0016021,GO:0016055,GO:0006044,GO:0042328,GO:0000139,GO:0015012,GO:0001888,GO:0015014,GO:0007275,GO:0008375,GO:0005789,GO:0031227,GO:0006024,GO:0005783	CG15110-PA						PF09258,PF03016				G3DSA:3.90.550.10	SSF53448	70~132								
aly1139.87	Aquaporin AQPAe.a	GO:0005215,GO:0016021,GO:0015267,GO:0005372,GO:0055085	CG7777-PC					TIGR00861	PF00230		PR00783,PR00783,PR00783,PR00783,PR00783,PR00783		G3DSA:1.20.1080.10	SSF81338									
aly1139.88	Zinc finger and BTB domain-containing protein 17	GO:0001702,GO:0044267,GO:0006351,GO:0045786,GO:0030968,GO:0007398,GO:0003700,GO:0005634,GO:0005654,GO:0036498,GO:0042023,GO:1903955,GO:0006260,GO:0008270,GO:0045893,GO:0003677,GO:0007067,GO:0046872,GO:1903146,GO:0060968	CG3941-PA				SM00384,SM00384,SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57716,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	651~671									
aly1139.89	Multiple C2 and transmembrane domain-containing protein 2	GO:0019722,GO:0016021,GO:0016020,GO:0005622,GO:0008150,GO:0005509,GO:0005515	CG33146-PA				SM00239		PF00168	PS50004			G3DSA:2.60.40.150	SSF49562,SSF49562									
aly1139.9	Eukaryotic translation initiation factor 2A	GO:0005737,GO:0006468,GO:0000049,GO:0032933,GO:0005615,GO:0005850,GO:0009967,GO:0042255,GO:0072562,GO:0006417,GO:0043022,GO:0003743	CG7414-PA						PF08662				G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF82171,SSF82171	507~527,532~552								
aly1139.90	Multiple C2 and transmembrane domain-containing protein 1	GO:0019722,GO:0016021,GO:0005622,GO:0008150,GO:0005509,GO:0005515	CG33146-PA				SM00239,SM00239		PF00168,PF00168	PS50004,PS50004			G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.91	Neuronal membrane glycoprotein M6-b	GO:0051612,GO:0051893,GO:0016021,GO:0045121,GO:0015031,GO:0001503,GO:0005886,GO:0046956,GO:0030501,GO:0085029,GO:0001745,GO:0048477,GO:2000009,GO:0032956	CG7540-PF						PF01275														
aly1139.92	Probable Golgi SNAP receptor complex member 2	GO:0005795,GO:0005794,GO:0006891,GO:0006888,GO:0006909,GO:0016192,GO:0007430,GO:0060439,GO:0000149,GO:0006906,GO:0031902,GO:0006623,GO:0000139,GO:0016021,GO:0042147,GO:0012507,GO:0005484,GO:0048280,GO:0005789,GO:0031201,GO:0006896	CG4780-PA			PIRSF028865										85~105								
aly1139.93	Protein tramtrack, beta isoform	GO:0035147,GO:0048750,GO:0045467,GO:0035001,GO:0031208,GO:0003677,GO:0043388,GO:0007298,GO:0001078,GO:0002121,GO:0031987,GO:0040003,GO:0000122,GO:0005634,GO:0001709,GO:0007476,GO:0030707,GO:0001964,GO:0060446,GO:0042682,GO:0003682,GO:0016476,GO:0046872,GO:0000980,GO:0048666,GO:0035151,GO:0017053,GO:0042675,GO:0008360,GO:0045892,GO:0048053,GO:0007426,GO:0007422,GO:0003700,GO:0048854,GO:0005700,GO:0048813,GO:0006357,GO:0045944,GO:0006351,GO:0005515,GO:0000978,GO:0042803,GO:0046843	CG1856-PE				SM00355,SM00355		PF05605	PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667	133~153									
aly1139.94	UDP-glucose:glycoprotein glucosyltransferase	GO:0005737,GO:0005791,GO:0005783,GO:0006486,GO:0005635,GO:0005788,GO:0012505,GO:0003980,GO:0097359	CG6850-PA						PF06427										UPA00378				
aly1139.95	UDP-glucose:glycoprotein glucosyltransferase	GO:0005737,GO:0005791,GO:0005783,GO:0006486,GO:0005635,GO:0005788,GO:0012505,GO:0003980,GO:0097359	CG6850-PA						PF06427										UPA00378				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1139.96	Unknown		n/a																				
aly1139.97	Unknown		n/a																				
aly11398.1	Unknown	GO:0005515	CG14372-PD						PF13927	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726										
aly11398.2	Contactin-2	GO:0048710,GO:0097090,GO:0007612,GO:0030246,GO:0007160,GO:0022010,GO:0000226,GO:0045202,GO:0007411,GO:0007413,GO:0048168,GO:0031225,GO:0043209,GO:0044224,GO:0045665,GO:0021853,GO:0043025,GO:0042802,GO:0060168,GO:0009986,GO:0008076,GO:0007628,GO:0005887,GO:0005886,GO:0007155,GO:0010954,GO:0031623,GO:0045163,GO:0031133,GO:0033268,GO:0071205,GO:0071206	CG14372-PD				SM00408,SM00409		PF07679	PS50835			G3DSA:2.60.40.10	SSF48726										
aly11398.3	Neural cell adhesion molecule 2	GO:0016021,GO:0005886,GO:0007158,GO:0030424	CG14372-PD							PS50853			G3DSA:2.60.40.10	SSF49265									
aly11398.4	Unknown		n/a																				
aly11398.5	Unknown		n/a																				
aly114.1	N-sulphoglucosamine sulphohydrolase	GO:0043202,GO:0005975,GO:0008152,GO:0003824,GO:0006029,GO:0044281,GO:0008484,GO:0016250,GO:0030203,GO:0046872,GO:0006027,GO:0070062	CG14291-PA						PF00884			PS00523,PS00149	G3DSA:3.30.1120.10,G3DSA:3.30.1120.10,G3DSA:3.40.720.10	SSF53649,SSF53649										
aly114.10	Cytosolic endo beta-N-acetylglucosaminidase	GO:0005737,GO:0005829,GO:0017022,GO:0033925	CG5613-PA						PF03644							00511+3.2.1.96							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly114.11	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0046331,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9518-PA			PIRSF000137			PF00732,PF05199			PS00623	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly114.12	Unknown	GO:0016021	CG17600-PD																				
aly114.13	Unknown		n/a																				
aly114.14	Clusterin-associated protein 1	GO:0030992,GO:0005634,GO:0042384,GO:0005813,GO:0005929	CG17599-PA						PF10234														
aly114.15	Peptidyl-tRNA hydrolase ICT1, mitochondrial	GO:0070126,GO:0004045,GO:0005739,GO:0016150,GO:0005762,GO:0006415,GO:0003747	CG6094-PA						PF00472			PS00745	G3DSA:3.30.160.200	SSF110916									
aly114.16	Protein singed	GO:0015629,GO:0030034,GO:0016358,GO:0030036,GO:0007163,GO:0035317,GO:0005737,GO:0008407,GO:0003779,GO:0048800,GO:0043005,GO:0043025,GO:0031941,GO:0051017,GO:0051015,GO:0042060,GO:0035017,GO:0035099,GO:0007015,GO:0030674,GO:0009913,GO:0048477,GO:0048812,GO:0046847	CG32858-PA			PIRSF005682			PF06268,PF06268,PF06268,PF06268				G3DSA:2.80.10.50,G3DSA:2.80.10.50,G3DSA:2.80.10.50,G3DSA:2.80.10.50	SSF50405,SSF50405,SSF50405,SSF50405									
aly114.17	Epsin-2	GO:0009997,GO:0006914,GO:0008289,GO:0045747,GO:0030128,GO:0007269,GO:0008593,GO:0006897,GO:0015032,GO:0030100,GO:0048488	CG8532-PE				SM00273,SM00726,SM00726		PF01417	PS50330,PS50942			G3DSA:1.25.40.90	SSF48464	5~39,131~161								
aly114.18	Nuclear pore complex protein Nup85	GO:0017056,GO:0031080,GO:0031965,GO:0006607,GO:0006406,GO:0015031,GO:0051028,GO:0007184	CG5733-PA						PF07575,PF07575						93~113								
aly114.19	7,8-dihydro-8-oxoguanine triphosphatase	GO:0005737,GO:0016787,GO:0046872,GO:0006195,GO:0070062,GO:0006281,GO:0008413,GO:0031965,GO:0006203,GO:0042262,GO:0047693,GO:0046061,GO:0001669,GO:0005739,GO:0005759,GO:0030515,GO:0036219,GO:0005634,GO:0035539	n/a						PF00293	PS51462	PR01403,PR01403,PR01403,PR01403,PR01403,PR01403,PR01403		G3DSA:3.90.79.10	SSF55811				PWY-6502					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly114.2	Probable phosphomannomutase	GO:0005737,GO:0009298,GO:0019307,GO:0004615,GO:0071456	CG10688-PA					TIGR01484	PF03332				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF56784		00520+5.4.2.8,00051+5.4.2.8	REACT_17015	PWY-7456,PWY-5659,PWY-882,PWY-7586	UPA00126				
aly114.20	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0007498,GO:0006066,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9509-PA			PIRSF000137			PF00732,PF05199			PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly114.21	Unknown		n/a																				
aly114.3	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial	GO:0006631,GO:0016829,GO:0009631,GO:0005739,GO:0017091,GO:0004300,GO:0008152,GO:0005875	CG8778-PA						PF00378			PS00166	G3DSA:3.90.226.10,G3DSA:1.10.12.10	SSF52096									
aly114.4	EKC/KEOPS complex subunit Tprkb	GO:0005737,GO:0019901,GO:0005829,GO:0008033,GO:0005634	n/a						PF08617					SSF143870									
aly114.5	Regulatory-associated protein of mTOR	GO:0001030,GO:0001031,GO:0001032,GO:0031931,GO:0045886,GO:0046676,GO:0007411,GO:0071902,GO:0005737,GO:0016049,GO:0005654,GO:0071889,GO:0001156,GO:0071230,GO:0031929,GO:0006974,GO:0032403,GO:0008361,GO:0019901,GO:0031669,GO:0043231,GO:0005764,GO:0005765,GO:0045945,GO:0032008,GO:0001932,GO:0001934	CG4320-PB						PF14538		PR01547,PR01547,PR01547,PR01547,PR01547,PR01547,PR01547,PR01547,PR01547,PR01547,PR01547,PR01547,PR01547		G3DSA:1.25.10.10	SSF48371									
aly114.6	Vacuolar protein sorting-associated protein 41 homolog	GO:0033227,GO:0051020,GO:0003674,GO:0008270,GO:0007041,GO:0016020,GO:0006886,GO:0005770,GO:0030897,GO:0015630,GO:0048193,GO:0005798,GO:0006727,GO:0006726,GO:0035542,GO:0042144,GO:0008340,GO:0006623,GO:0007033,GO:0007220,GO:0006897,GO:0016192,GO:0046907,GO:0005829,GO:0005765,GO:0033263,GO:0005515,GO:0005769	CG18028-PA				SM00320,SM00299		PF00637	PS50082,PS50236,PS50089,PS50294			G3DSA:2.130.10.10,G3DSA:1.25.40.10	SSF48371,SSF50978									
aly114.7	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly114.8	DNA polymerase nu	GO:0006303,GO:0008026,GO:0006281,GO:0005634,GO:0004386,GO:0003887,GO:0006260,GO:0071897,GO:0003677,GO:0006289,GO:0005524,GO:0006261	CG6019-PA				SM00482		PF00476		PR00868,PR00868,PR00868,PR00868		G3DSA:1.10.150.20,G3DSA:1.20.1060.10,G3DSA:3.30.70.370,G3DSA:3.30.70.370	SSF56672		00240+2.7.7.7,00230+2.7.7.7							
aly114.9	Beta-1,4-N-acetylgalactosaminyltransferase bre-4	GO:0075015,GO:0005794,GO:0005975,GO:0033207,GO:0006486,GO:0009636,GO:0006044,GO:0016021,GO:0009247,GO:0033842,GO:0045747,GO:0008376,GO:0046872	CG14517-PA						PF13733,PF02709		PR02050,PR02050,PR02050,PR02050		G3DSA:3.90.550.10	SSF53448					UPA00378				
aly11403.1	Unknown		n/a																				
aly11426.1	Scavenger receptor class B member 1	GO:0034375,GO:0015914,GO:0043691,GO:0005901,GO:0051000,GO:0070328,GO:0032497,GO:0010867,GO:0070062,GO:0010886,GO:0016020,GO:0043654,GO:0035461,GO:0010899,GO:0008035,GO:0006707,GO:0035071,GO:0015920,GO:0006952,GO:0043534,GO:0005887,GO:0005886,GO:0007155,GO:0042632,GO:0001530,GO:0030169,GO:0048102,GO:0005044,GO:0044406,GO:0034384,GO:0005764,GO:0005765,GO:0033344,GO:0034383,GO:0001875,GO:0070506,GO:0001935	CG2727-PB						PF01130														
aly11426.2	Unknown	GO:0005737,GO:0007016,GO:0005200,GO:0046427,GO:0019730,GO:0008283,GO:0005811,GO:0043066,GO:0003723,GO:0007169,GO:0001751,GO:0051298	CG33106-PC				SM00248,SM00248,SM00248,SM00248		PF12796	PS50297			G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403										
aly11426.3	THAP domain containing protein 1	GO:0043565,GO:0016605,GO:0005634,GO:0007346,GO:0006355,GO:0006351,GO:0001935,GO:0007049,GO:0008270	n/a				SM00355,SM00980,SM00692		PF05485	PS50950,PS50157		PS00028	G3DSA:3.30.160.60	SSF57667,SSF57716									
aly11426.4	Unknown		n/a				SM00614		PF02892	PS50808				SSF57667,SSF53098,SSF53098,SSF53098									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly114376.1	Anaphase-promoting complex subunit 1	GO:0048749,GO:0000278,GO:0070979,GO:0005829,GO:0031145,GO:0005654,GO:0051437,GO:0051439,GO:0090302,GO:0007094,GO:0007067,GO:0051436,GO:0022008,GO:0051301,GO:0005680	CG9198-PA																				
aly114394.1	Ryanodine receptor	GO:0072347,GO:0005219,GO:0006936,GO:0006874,GO:0016021,GO:0070588,GO:0006816,GO:0005789,GO:0033017,GO:0060047,GO:0005509,GO:0035206,GO:0007275,GO:0005875	CG10844-PI																				
aly1146.1	Otopetrin-2	GO:0016021	CG42265-PD						PF03189,PF03189														
aly1146.10	Unknown		n/a																				
aly1146.11	Cytoplasmic dynein 2 heavy chain 1	GO:0008105,GO:0030326,GO:0030031,GO:0005886,GO:0045880,GO:0016887,GO:0030286,GO:0031223,GO:0008049,GO:0005874,GO:0005875,GO:0045177,GO:0072372,GO:0070062,GO:0042623,GO:0007368,GO:0031512,GO:0035721,GO:0003774,GO:0005524,GO:0005794,GO:0021522,GO:0042384,GO:0019886,GO:0007605,GO:0007628,GO:0001539,GO:0005868,GO:0016485,GO:0005930,GO:0006996,GO:0007030,GO:0009953,GO:0045433,GO:0005829,GO:0007018,GO:0097542,GO:0030900,GO:0003777	CG15148-PD						PF12781,PF12781						398~422,171~205,115~163								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1146.12	Laminin subunit beta-1	GO:0048598,GO:0005605,GO:0009887,GO:0005604,GO:0045089,GO:0003143,GO:0034446,GO:0008406,GO:0070831,GO:0009888,GO:0031012,GO:0048513,GO:0012505,GO:0030198,GO:0050829,GO:0055013,GO:0016477,GO:0033627	CG7123-PA				SM00136,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180		PF12774,PF07728,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00055,PF08393	PS50027,PS50027,PS50027,PS51116,PS50027,PS50027,PS51117,PS50027,PS50027,PS50027,PS50027,PS50027,PS50027,PS50027	PR00011,PR00011,PR00011,PR00011	PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF52540,SSF52540,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196	1795~1829,1549~1569,1638~1682,1894~1914,1426~1460,1687~1759,1309~1343								
aly1146.13	Cytoplasmic dynein 2 heavy chain 1	GO:0030030,GO:0030031,GO:0005929,GO:0016887,GO:0031223,GO:0030286,GO:0008049,GO:0005874,GO:0005875,GO:0005737,GO:0042623,GO:0007275,GO:0051959,GO:0035721,GO:0003774,GO:0005524,GO:0007605,GO:0007628,GO:0001539,GO:0005868,GO:0005886,GO:0045433,GO:0007018,GO:0003777	CG15148-PD						PF08393						71~91,584~611								
aly1146.14	Cytoplasmic dynein 2 heavy chain 1	GO:0030030,GO:0030031,GO:0005929,GO:0016887,GO:0031223,GO:0030286,GO:0008049,GO:0005874,GO:0007275,GO:0005737,GO:0042623,GO:0005875,GO:0035721,GO:0003774,GO:0005524,GO:0007605,GO:0007628,GO:0001539,GO:0005868,GO:0005886,GO:0045433,GO:0007018,GO:0003777	CG15148-PD						PF08385														
aly1146.15	Succinate dehydrogenase assembly factor 2-A, mitochondrial	GO:0018293,GO:0006121,GO:0055070,GO:0005739,GO:0005759,GO:0005507	CG14757-PA	MF_03057					PF03937				G3DSA:1.10.150.250	SSF109910									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1146.16	Branched-chain-amino-acid aminotransferase, cytosolic	GO:0005737,GO:0008283,GO:0052654,GO:0052655,GO:0052656,GO:0000082,GO:0005739,GO:0034641,GO:0044281,GO:0004084,GO:0005829,GO:0009083,GO:0009082	CG1673-PA			PIRSF006468		TIGR01123	PF01063			PS00770	G3DSA:3.20.10.10,G3DSA:3.30.470.10	SSF56752		00280+2.6.1.42,00966+2.6.1.42,00770+2.6.1.42,00290+2.6.1.42	REACT_13	PWY-5057,PWY-5108,PWY-5076,PWY-5103,PWY-5101,PWY-5078,PWY-5104					
aly1146.17	Intraflagellar transport protein 88 homolog	GO:0021537,GO:0008589,GO:0008104,GO:0030324,GO:0060173,GO:0050680,GO:0042073,GO:0060021,GO:0002080,GO:0002081,GO:0007290,GO:0030990,GO:0001889,GO:0031512,GO:0003382,GO:0005929,GO:0060259,GO:0008544,GO:0036064,GO:0045177,GO:0007219,GO:0090102,GO:0060914,GO:0005813,GO:0007368,GO:0043568,GO:0001822,GO:0005814,GO:0031513,GO:0061351,GO:0019894,GO:1902017,GO:0045598,GO:0030992,GO:0009887,GO:0042384,GO:0060426,GO:0035058,GO:0060271,GO:0055007,GO:0007605,GO:0042487,GO:0031122,GO:0060122,GO:0072372,GO:0001654,GO:0021513,GO:2000785,GO:0007507,GO:0007288,GO:0005930,GO:0060091,GO:0009952,GO:0042733,GO:0070613,GO:0009953,GO:0007420,GO:0007399,GO:0007224,GO:0005802,GO:0048853,GO:0036334,GO:0097542,GO:0097541,GO:0032391,GO:0097546,GO:0005515,GO:0031016,GO:0060411,GO:0034405	CG12548-PD				SM00028,SM00028,SM00028		PF13414	PS50293,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452									
aly1146.18	Unknown		n/a												159~183								
aly1146.19	Cysteine--tRNA ligase, cytoplasmic	GO:0005737,GO:0000049,GO:0006423,GO:0004817,GO:0005829,GO:0046872,GO:0005524	CG8431-PA	MF_00041				TIGR00435	PF01406		PR00983,PR00983,PR00983,PR00983		G3DSA:3.40.50.620,G3DSA:3.40.50.620	SSF52374,SSF52374	164~191	00970+6.1.1.16	REACT_71						
aly1146.2	Unknown		CG3332-PA						PF03189,PF03189														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1146.20	Protein krueppel	GO:0035206,GO:0035220,GO:0007419,GO:0010629,GO:0007411,GO:0043565,GO:0007517,GO:0000122,GO:0006342,GO:0005634,GO:0007400,GO:0040034,GO:0000981,GO:0048749,GO:0061332,GO:0045892,GO:0007402,GO:0035290,GO:0007443,GO:0046872,GO:0003700,GO:0003705,GO:0007354,GO:0000977,GO:0003682	CG3340-PA				SM00355,SM00355,SM00355,SM00355		PF12874,PF13909,PF13909	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										
aly1146.21	SUN domain-containing protein 3	GO:0034399,GO:0005637,GO:0048471,GO:0007097	CG44154-PA						PF07738	PS51469													
aly1146.22	Eukaryotic translation initiation factor 3 subunit M	GO:0006446,GO:0005794,GO:0007030,GO:0005852,GO:2001233,GO:0009306,GO:0016282,GO:0005829,GO:0048812,GO:0001731,GO:0003824,GO:2001272,GO:0007291,GO:0005515,GO:0033290,GO:0070865,GO:0005875,GO:0003743	CG8309-PA	MF_03012			SM00088		PF01399					SSF48371									
aly1146.23	Elongator complex protein 4	GO:0005737,GO:0008023,GO:0045859,GO:0033588,GO:0006357,GO:0006351,GO:0008607	CG6907-PA						PF05625				G3DSA:3.40.50.300,G3DSA:3.40.50.300										
aly1146.24	Tetraspanin-17	GO:0031749,GO:0016021,GO:0005802,GO:0030425,GO:0030424,GO:0046331,GO:0003674,GO:0005886,GO:0030097,GO:0048471	CG32136-PA						PF00335					SSF48652									
aly1146.25	Unknown		n/a																				
aly1146.26	Neurogenic protein mastermind	GO:0048749,GO:0016607,GO:0007219,GO:0007500,GO:0007399,GO:0007398,GO:0003713,GO:0005634,GO:0005703,GO:0008587,GO:0008407,GO:0005700,GO:0007475,GO:0003007,GO:0045944,GO:0035019,GO:0007476,GO:0008356,GO:0007418,GO:0030718	CG8118-PA						PF09596						509~529		REACT_71						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1146.27	Heat shock protein 75 kDa, mitochondrial	GO:0009386,GO:0019901,GO:1901856,GO:0016020,GO:0006457,GO:0070062,GO:0044822,GO:0005811,GO:1902176,GO:0005739,GO:0005654,GO:0005743,GO:0006950,GO:0051082,GO:0016887,GO:0005759,GO:0005758,GO:0006979,GO:0005524	CG3152-PA	MF_00505		PIRSF002583	SM00387		PF00183,PF02518		PR00775,PR00775,PR00775,PR00775,PR00775,PR00775,PR00775		G3DSA:3.30.565.10	SSF110942,SSF55874,SSF54211									
aly1146.28	Neurotactin	GO:0005737,GO:0016021,GO:0052689,GO:0016323,GO:0007409,GO:0005886,GO:0007155,GO:0007411,GO:0007413,GO:0007417	CG9704-PB						PF00135			PS00941	G3DSA:3.40.50.1820	SSF53474	9~38								
aly1146.29	Splicing factor 3A subunit 2	GO:0071011,GO:0071013,GO:0044822,GO:0000398,GO:0007052,GO:0008270,GO:0003676,GO:0005686,GO:0022008,GO:0008380,GO:0005681,GO:0006397	CG10754-PA				SM01050,SM00451		PF16835,PF12874	PS50171				SSF57667	536~563,576~625,875~902,645~732,504~524,462~496,397~424,747~795,828~869									
aly1146.3	RING-box protein 1A	GO:0008270,GO:0019915,GO:0022008,GO:0043224,GO:0005737,GO:0045116,GO:0080008,GO:0061630,GO:0005634,GO:0019788,GO:0042787,GO:0006508,GO:0008283,GO:0031146,GO:0016322,GO:0031462,GO:0031463,GO:0004842,GO:0031467,GO:0097602,GO:0007224,GO:0030178,GO:0016567,GO:0019005	CG16982-PD						PF12678	PS50089			G3DSA:3.30.40.10	SSF57850					UPA00143				
aly1146.30	40S ribosomal protein S10	GO:0003735,GO:0005840,GO:0022627,GO:0006412,GO:0005875	CG14206-PE						PF03501														
aly1146.31	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 9, mitochondrial	GO:0050662,GO:0008137,GO:0006120,GO:0003824,GO:0005747,GO:0005759,GO:0070469,GO:0003954,GO:0055114	CG6020-PA						PF01370				G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1146.32	Synembryn-A	GO:0005737,GO:0008105,GO:0040001,GO:0007163,GO:0005829,GO:0005085,GO:0055059,GO:0050821,GO:0010004,GO:0001965,GO:0005886,GO:0008356	CG15797-PA						PF10165		PR01802,PR01802,PR01802,PR01802,PR01802,PR01802		G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371									
aly1146.33	Spondin-1	GO:0007155,GO:0005576,GO:0005578,GO:0004867	CG17739-PA				SM00209,SM00209,SM00209,SM00209,SM00131		PF06468,PF00014,PF00090,PF00090,PF00090	PS51020,PS50092,PS50279,PS50092,PS50092	PR00759,PR00759,PR00759	PS00280	G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:4.10.410.10	SSF82895,SSF82895,SSF57362									
aly1146.34	Zinc transporter 1	GO:0005783,GO:0006829,GO:0005737,GO:0001701,GO:0090281,GO:0019855,GO:0016021,GO:0006882,GO:0070574,GO:0006874,GO:0005794,GO:0030315,GO:0006812,GO:0031965,GO:0016323,GO:0046929,GO:0005886,GO:0055085,GO:0005622,GO:0070509,GO:0005385,GO:0071585,GO:0071584	CG5130-PA					TIGR01297	PF01545				G3DSA:1.20.1510.10	SSF161111									
aly1146.35	Unknown		n/a												228~262,482~502,694~714,294~335,522~								
aly1146.36	Unknown		n/a												119~174,1~21,42~73								
aly1146.37	Unknown		n/a												107~141,149~243,356~376,307~341								
aly1146.38	Unknown	GO:0005575,GO:0003674,GO:0008150	CG13164-PA												783~803,677~697,429~491,748~768,549~								
aly1146.39	Coiled-coil domain-containing protein 94	GO:0022008	CG8435-PA						PF04502						143~163,106~132								
aly1146.4	Histone-lysine N-methyltransferase Suv4-20	GO:0005720,GO:0034772,GO:0006342,GO:0005634,GO:0040029,GO:0005700,GO:0034773,GO:0070512,GO:0034770,GO:0016571,GO:0042799,GO:0006351	CG13363-PA				SM00317		PF00856	PS51570,PS50280			G3DSA:2.170.270.10	SSF82199		00310+2.1.1.43							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1146.40	G1/S-specific cyclin-D3	GO:0042098,GO:0030307,GO:0000307,GO:0007165,GO:0004693,GO:0007005,GO:0051301,GO:0005737,GO:0016049,GO:0005634,GO:0016020,GO:0007259,GO:0016538,GO:0007049,GO:0008283,GO:0009987,GO:0019901,GO:0051726,GO:0000079,GO:0045737,GO:0005515,GO:0001934	CG9096-PD						PF00134				G3DSA:1.10.472.10	SSF47954									
aly1146.41	G1/S-specific cyclin-D3	GO:0005737,GO:0016020,GO:0016049,GO:0008283,GO:0030307,GO:0000079,GO:0009987,GO:0051301,GO:0007259,GO:0019901,GO:0016538,GO:0007049,GO:0005515,GO:0005634,GO:0007005	CG9096-PD				SM00385		PF00134,PF02984				G3DSA:1.10.472.10,G3DSA:1.10.472.10	SSF47954,SSF47954	195~215								
aly1146.42	Protein lava lamp	GO:0050775,GO:0005794,GO:0050774,GO:0008017,GO:0007349,GO:0003779,GO:0048812,GO:0005938,GO:0005515,GO:0051683,GO:0000137,GO:0005875,GO:0030507	CG6450-PC												2092~2140,1124~1228,543~570,2375~2395,1930~1978,250~302,1642~1697,2462~2521,2580~2614,661~698,2165~2231,310~347,2282~2344,953~1025,128~148,1717~1744,1292~1364,1592~1626,1250~1284,1438~1458,2412~2439,1379~1399,828~890,2629~2670,1463~1528,595~629,1749~1769,706~775,1996~2054,898~918,371~398,1554~1581,2721~2741,1027~1121,476~503								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1146.43	39S ribosomal protein L28, mitochondrial	GO:0003735,GO:0006412,GO:0005762,GO:0032543	CG3782-PA											SSF143800									
aly1146.44	Probable phosphorylase b kinase regulatory subunit alpha	GO:0006468,GO:0005977,GO:0005964,GO:0005886,GO:0003824,GO:0005516,GO:0004553,GO:0008607	CG7766-PH						PF00723				G3DSA:1.50.10.10	SSF48208			REACT_474						
aly1146.45	Unknown		CG7453-PA																				
aly1146.46	Adenylate cyclase type 9	GO:0005622,GO:0016021,GO:0016849,GO:0004016,GO:0046872,GO:0005886,GO:0007190,GO:0035556,GO:0009190,GO:0006171,GO:0005524	CG9210-PC				SM00044,SM00044		PF00211,PF00211	PS50125,PS50125		PS00452,PS00452	G3DSA:3.30.70.1230,G3DSA:3.30.70.1230	SSF55073,SSF55073										
aly1146.47	Gamma-aminobutyric acid receptor subunit alpha-6	GO:0045211,GO:0005230,GO:0007214,GO:0034707,GO:0006811,GO:0004890,GO:0005254,GO:0016021,GO:0030054	CG8916-PB					TIGR00860	PF02931,PF02932		PR00252,PR00252,PR00252,PR00252,PR01079,PR01079,PR01079,PR01079,PR01079,PR00253,PR00253,PR00253,PR00253	PS00236	G3DSA:1.20.58.390,G3DSA:1.20.58.390,G3DSA:2.70.170.10	SSF63712,SSF90112										
aly1146.48	Gamma-aminobutyric acid receptor subunit beta-like	GO:0016021,GO:0045211,GO:0006811,GO:0016020,GO:0034707,GO:0007165,GO:0006810,GO:0005886,GO:0004890,GO:0005254,GO:0005230,GO:0030054	CG17336-PC					TIGR00860	PF02932,PF02931		PR01160,PR01160,PR01160,PR01160,PR00253,PR00253,PR00253,PR00253,PR00252,PR00252,PR00252,PR00252	PS00236	G3DSA:2.70.170.10,G3DSA:1.20.58.390,G3DSA:1.20.58.390	SSF63712,SSF90112,SSF90112										

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1146.49	Low-density lipoprotein receptor-related protein 4	GO:0050808,GO:0060173,GO:0030425,GO:0031594,GO:0030509,GO:0051124,GO:0097060,GO:0016600,GO:0016021,GO:0030971,GO:0001822,GO:0097105,GO:0097104,GO:0005509,GO:0043025,GO:0090090,GO:0009986,GO:0051290,GO:0060070,GO:0014069,GO:0050771,GO:0044332,GO:0030279,GO:0042733,GO:0009954,GO:0006897,GO:0005041,GO:0071340,GO:1901631,GO:0042813,GO:0048813,GO:0030198,GO:0097110,GO:0017147,GO:0001932,GO:0001942,GO:0042475	CG8909-PA				SM00135,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00179,SM00179,SM00179		PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF14670,PF14670,PF00058,PF00058,PF00058,PF00058,PF00058,PF00058,PF00058,PF00058,PF00058,PF00058	PS51120,PS51120,PS50068,PS51120,PS50068,PS51120,PS50068,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS50068,PS50068,PS51120,PS51120,PS50068,PS51120,PS51120,PS51120,PS50068,PS51120,PS50068,PS51120	PR00261,PR00261,PR00261,PR00261,PR00261,PR00261	PS01209,PS01209,PS01187,PS01209,PS01209,PS01209,PS01209,PS01209,PS01209	G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.1220.10,G3DSA:4.10.400.10,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:2.10.25.10	SSF57424,SSF57424,SSF63825,SSF57424,SSF57196,SSF63825,SSF63825,SSF57424,SSF63825,SSF57196,SSF57424,SSF57424,SSF57424,SSF57196,SSF57424,SSF57196									
aly1146.5	Mitochondrial ornithine transporter 1	GO:1903352,GO:0016021,GO:0000064,GO:0000050,GO:0000066,GO:0006520,GO:0005740,GO:0015171,GO:0005743,GO:0022857,GO:0044281,GO:0034641,GO:0003333	CG1628-PB						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly1146.50	Sorting nexin-25	GO:0038032,GO:0032801,GO:0035091,GO:0060394,GO:0015031,GO:0008340,GO:0030512,GO:0010008	CG1514-PA				SM00315,SM00313		PF08628,PF02194,PF00787,PF00615	PS50132,PS51207,PS50195			G3DSA:1.10.167.10,G3DSA:1.10.196.10,G3DSA:3.30.1520.10	SSF48097,SSF64268	550~570,62~82,346~366								
aly1146.51	Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 1	GO:0055114,GO:0016491	CG10721-PA						PF07992		PR00368,PR00368,PR00368,PR00368		G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51735,SSF51735,SSF51905,SSF51905									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1146.52	Vesicle-associated membrane protein 7	GO:0016020,GO:0006906,GO:0005789,GO:0045202,GO:0034197,GO:0005484,GO:0033133,GO:0031201,GO:0030054,GO:0005737,GO:0045177,GO:0006888,GO:0070062,GO:0016021,GO:0006887,GO:0000046,GO:0035577,GO:0031143,GO:0043001,GO:0097352,GO:0043320,GO:0006886,GO:0048471,GO:0031902,GO:0017156,GO:0005794,GO:0008333,GO:0043005,GO:0030027,GO:0030141,GO:0009986,GO:0030667,GO:0006911,GO:0030658,GO:0045335,GO:0019905,GO:0005886,GO:0031091,GO:0043308,GO:0047496,GO:0043231,GO:0050775,GO:0016192,GO:0030670,GO:0005802,GO:0043312,GO:0048280,GO:0005765,GO:1903595,GO:0000149,GO:0035493,GO:1900483	CG1599-PA						PF13774,PF00957	PS50892,PS50859			G3DSA:3.30.450.50,G3DSA:1.10.3840.10	SSF58038,SSF64356									
aly1146.53	Unknown		n/a																				
aly1146.54	Otopetrin-2	GO:0016021	CG42265-PD						PF03189														
aly1146.55	Otopetrin-3	GO:0016021,GO:0016020	CG11473-PA						PF03189														
aly1146.56	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1146.57	Vesicle-associated membrane protein 7	GO:0006906,GO:0005789,GO:0045202,GO:0034197,GO:0005484,GO:0035577,GO:0030054,GO:0043308,GO:0045177,GO:0006888,GO:0070062,GO:0016021,GO:0006887,GO:0000046,GO:0031201,GO:0031143,GO:0043001,GO:0097352,GO:0043320,GO:0006886,GO:0048471,GO:0031902,GO:0017156,GO:0008333,GO:0043005,GO:0030027,GO:0009986,GO:0006911,GO:0030658,GO:0045335,GO:0019905,GO:0005886,GO:0031091,GO:0047496,GO:0050775,GO:0016192,GO:0030670,GO:0005802,GO:0043312,GO:0048280,GO:0005765,GO:1903595,GO:0000149,GO:0035493,GO:1900483	CG1599-PA						PF13774	PS50859			G3DSA:3.30.450.50	SSF64356										
aly1146.58	Unknown		n/a																				
aly1146.6	Unknown		n/a																				
aly1146.7	S-phase kinase associated protein 1	GO:0045931,GO:0005819,GO:0051298,GO:0042023,GO:0005813,GO:0031647,GO:0016322,GO:0046627,GO:0030261,GO:0010824,GO:0006511,GO:0005875,GO:0019005,GO:0005515,GO:0016567,GO:0007095,GO:0022008,GO:0007067,GO:0031467	CG16983-PE			PIRSF028729	SM00512		PF01466,PF03931				G3DSA:3.30.710.10	SSF54695,SSF81382			REACT_6185		UPA00143				
aly1146.8	Cytochrome b561 domain-containing	GO:0016021,GO:0046872,GO:0055114	CG13077-PA				SM00665		PF03188	PS50939					247~247								
aly1146.9	Unknown		n/a							PS51257													
aly114883.1	Unknown		n/a																				
aly1149.1	Unknown	GO:0042067,GO:0003674,GO:0045179,GO:0035159	CG12758-PF						PF12736														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1149.10	Metastasis suppressor protein 1	GO:0015629,GO:0017124,GO:0030036,GO:0034334,GO:0030139,GO:0030041,GO:0007009,GO:0007165,GO:0007169,GO:0007298,GO:0048261,GO:0010960,GO:0030282,GO:0008354,GO:2001013,GO:0005737,GO:0001726,GO:0001701,GO:0005543,GO:0003779,GO:0042802,GO:0042803,GO:0072102,GO:0061333,GO:0071498,GO:0030035,GO:0072160,GO:0032233,GO:0003785,GO:0007155,GO:0006928,GO:0043234,GO:0007015,GO:0008093,GO:0002230,GO:0005102,GO:0046847,GO:0050680,GO:0005912	CG33558-PF						PF08397	PS51338			G3DSA:1.20.1270.80	SSF103657	92~122,60~87									
aly1149.11	Tektin-4	GO:0005737,GO:0007017,GO:0030030,GO:0008017,GO:0031514,GO:0000226,GO:0005874,GO:0005875	CG4767-PA						PF03148		PR00511,PR00511,PR00511,PR00511				267~322,340~381,80~110									
aly1149.2	Unknown		CG15649-PA																					
aly1149.3	PRKCA-binding protein	GO:0008022,GO:0060292,GO:0021782,GO:0005080,GO:0030425,GO:0015872,GO:0051020,GO:0003674,GO:0045202,GO:0016887,GO:0034316,GO:0001664,GO:0030054,GO:0005737,GO:0097061,GO:0097062,GO:0030971,GO:0045055,GO:0043005,GO:0048471,GO:0046872,GO:0046875,GO:0042802,GO:0005794,GO:0006468,GO:0015844,GO:0060548,GO:0035256,GO:0051015,GO:0045211,GO:0014069,GO:0019904,GO:0005886,GO:0042149,GO:0043113,GO:0043234,GO:0071933,GO:0042734,GO:0043025,GO:0005856,GO:0007205,GO:0010629,GO:0036294,GO:0005102,GO:0002092	CG6167-PE				SM00228,SM01015		PF00595,PF06456	PS50870,PS50106			G3DSA:1.20.1270.60,G3DSA:2.30.42.10	SSF50156,SSF103657										
aly1149.4	Unknown		n/a																					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1149.5	Charged multivesicular body protein 4b	GO:0005829,GO:0007034,GO:0000815,GO:0006914,GO:0032509,GO:0030496,GO:0042059,GO:0031902,GO:0045746,GO:0048813,GO:0048812,GO:0005515,GO:0008593,GO:0015031,GO:0043162,GO:0044130,GO:0005771	CG8055-PA						PF03357						23~43,151~178,69~89									
aly1149.6	Armadillo repeat-containing protein 6 homolog	GO:0005575,GO:0003674,GO:0008150,GO:0005488	CG5721-PA				SM00185,SM00185,SM00185		PF00514				G3DSA:1.25.10.10	SSF48371										
aly1149.7	Structural maintenance of chromosomes protein 5	GO:0000781,GO:0016605,GO:0000070,GO:0000724,GO:0005634,GO:0090398,GO:0030915,GO:0006974,GO:0045842,GO:0000796,GO:0051301,GO:0007067,GO:0034184,GO:0000722,GO:0005524	CG32438-PE						PF02463				G3DSA:3.40.1140.10,G3DSA:3.40.50.300	SSF52540,SSF52540	734~761,769~803,594~614,165~192,200~245,665~717,549~583,102~146,287~321									
aly1149.8	Unknown	GO:0043234,GO:0007015,GO:0046847,GO:0008093,GO:0005543,GO:0017124,GO:0003779,GO:0007165,GO:0007298,GO:0048261,GO:0008354,GO:0042803	CG33558-PF												244~264,484~504									
aly1149.9	Unknown		n/a																					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly115136.1	Runt-related transcription factor 1	GO:1903431,GO:0006366,GO:0035162,GO:0001501,GO:0001889,GO:0003677,GO:0048266,GO:0007417,GO:0005737,GO:0001701,GO:0006355,GO:0009966,GO:0005634,GO:0045766,GO:0005654,GO:0030853,GO:0071336,GO:0005509,GO:0030854,GO:0032729,GO:0045944,GO:0070491,GO:0005524,GO:0042803,GO:0048666,GO:0008285,GO:0032526,GO:0030182,GO:0032743,GO:0008134,GO:0000975,GO:0002667,GO:0045892,GO:0045893,GO:0001047,GO:0060216,GO:0031069,GO:0005604,GO:0043231,GO:0003700,GO:0001228,GO:0071560,GO:0048813,GO:0002318,GO:0000977,GO:0030099,GO:0030097,GO:0046982,GO:0000981	CG34145-PD						PF00853	PS51062	PR00967,PR00967,PR00967,PR00967,PR00967		G3DSA:2.60.40.720	SSF49417										
aly1153.1	Unknown		n/a											SSF56219									
aly1153.2	Unknown		n/a																				
aly1153.3	Unknown		n/a																				
aly1153.4	Unknown		n/a																				
aly115313.1	Unknown	GO:0005355,GO:0015771,GO:0016021,GO:0016020,GO:0008643,GO:0055085	CG30035-PA																				
aly115376.1	Unknown	GO:0003677	n/a						PF05225					SSF46689									
aly115436.1	Unknown		n/a																				
aly1155.1	Arginyl-tRNA-protein transferase 1	GO:0005737,GO:0004057,GO:0016598,GO:0005634,GO:0006511	CG9204-PD			PIRSF037207			PF04376,PF04377					SSF55729									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1155.10	Calmodulin	GO:0051383,GO:0042052,GO:0046716,GO:0031476,GO:0031475,GO:0005875,GO:0005737,GO:0016028,GO:0016062,GO:0016061,GO:0016060,GO:0005814,GO:0000922,GO:0005509,GO:0007099,GO:0032036,GO:0006468,GO:0007605,GO:0072499,GO:0030048,GO:0007052,GO:0005819,GO:2001020,GO:0031489,GO:0070855,GO:0016059,GO:0016056,GO:0030496,GO:0051533,GO:0005513,GO:0046331,GO:0005516,GO:0005515	CG8472-PA							PS50222,PS50222			G3DSA:1.10.238.10	SSF47473										
aly1155.11	FAS-associated factor 2-B	GO:0005783,GO:0005811,GO:0005575,GO:0008150,GO:0005515,GO:0003674	CG10372-PA				SM00594,SM00166		PF00789,PF14555	PS50033			G3DSA:1.10.8.10,G3DSA:3.40.30.10,G3DSA:3.10.20.90	SSF54236,SSF52833	302~337								
aly1155.12	Cytochrome b5 reductase 4	GO:0004128,GO:0005783,GO:0020037,GO:0046872,GO:0055114,GO:0016491	CG11257-PA										G3DSA:3.10.120.10	SSF55856									
aly1155.13	Cytochrome b5 reductase 4	GO:0004128,GO:0005783,GO:0020037,GO:0046872,GO:0055114,GO:0016491	CG11257-PA						PF00175,PF00173,PF00970	PS51384,PS50255	PR00406,PR00406,PR00406,PR00406,PR00406,PR00406	PS00191	G3DSA:2.40.30.10,G3DSA:3.40.50.80,G3DSA:3.10.120.10	SSF55856,SSF52343,SSF63380									
aly1155.14	Fatty-acid amide hydrolase 2	GO:0016787,GO:0016021,GO:0005811,GO:0017064,GO:0016884	CG8839-PD						PF01425				G3DSA:3.90.1300.10	SSF75304		00970+6.3.5.7		PWY-5921					
aly1155.15	Sentrin-specific protease 8	GO:0005737,GO:0019784,GO:0000338,GO:0043065,GO:0006508,GO:0008234	CG8493-PC						PF02902	PS50600			G3DSA:3.30.310.130	SSF54001									
aly1155.16	Cytochrome c	GO:0070469,GO:0046872,GO:0020037,GO:0005739,GO:0005743,GO:0005759,GO:0005758,GO:0045155,GO:0006119,GO:0005506,GO:0055114,GO:0009055	CG17903-PB						PF00034	PS51007	PR00604,PR00604,PR00604,PR00604,PR00604,PR00604		G3DSA:1.10.760.10	SSF46626									
aly1155.17	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1155.18	Thioredoxin domain-containing protein 17	GO:0033209,GO:0070062,GO:0005829,GO:0047134,GO:0006726,GO:0009055,GO:0004601,GO:0015036	CG11024-PA						PF06110	PS50064			G3DSA:3.40.30.10	SSF52833									
aly1155.2	Sialin	GO:0006865,GO:0006820,GO:0030054,GO:0005737,GO:0044267,GO:0015992,GO:0006488,GO:0016021,GO:0016020,GO:0043687,GO:0018279,GO:0015739,GO:0005351,GO:0006811,GO:0005316,GO:0005887,GO:0005886,GO:0055085,GO:0030672,GO:0015136,GO:0005764,GO:0005765	CG9864-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly1155.3	Uncharacterized transporter slc-17.2	GO:0016021,GO:0006814,GO:0055085,GO:0015293,GO:0005316	CG9864-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1155.4	Uncharacterized transporter slc-17.2	GO:0016021,GO:0006814,GO:0055085,GO:0015293,GO:0005316	CG9864-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly1155.5	Rho GTPase-activating protein 20	GO:0007370,GO:0007480,GO:0051497,GO:0005096,GO:0005622,GO:0005575,GO:0045887,GO:0007165,GO:0005100,GO:0007266	CG6811-PA				SM00324		PF00620	PS50238			G3DSA:1.10.555.10,G3DSA:2.30.29.30	SSF50729,SSF48350			REACT_11044						
aly1155.6	Unknown	GO:0005089,GO:0035023	n/a										G3DSA:1.20.900.10,G3DSA:1.20.900.10	SSF48065	640~640								
aly1155.7	Probable trans-2-enoyl-CoA reductase, mitochondrial	GO:0006633,GO:0006631,GO:0005739,GO:0008270,GO:0019166,GO:0005875,GO:0055114	CG16935-PB				SM00829		PF00107,PF08240				G3DSA:3.40.50.720,G3DSA:3.40.50.720,G3DSA:3.90.180.10,G3DSA:3.90.180.10	SSF51735,SSF50129,SSF50129,SSF51735									
aly1155.8	Unknown	GO:0046872	n/a				SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028		SSF57667									
aly1155.9	Uncharacterized protein C17orf53		n/a						PF15072														
aly11571.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1158.1	Tubulin beta chain	GO:0045298,GO:0051258,GO:0007017,GO:0003924,GO:0005737,GO:0007435,GO:0005200,GO:0006184,GO:0005874,GO:0005525	CG9359-PA				SM00864,SM00865		PF00091,PF03953		PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163	PS00228,PS00227	G3DSA:3.30.1330.20,G3DSA:3.40.50.1440,G3DSA:1.10.287.600	SSF52490,SSF55307	408~435		REACT_152						
aly1158.10	Transmembrane and coiled-coil domains protein 2	GO:0005575,GO:0016021,GO:0003674,GO:0007420	CG1021-PH						PF10267						393~438,208~228,359~382								
aly1158.11	Putative dual specificity tyrosine-phosphorylation-regulated kinase 3 homolog	GO:0006468,GO:0005575,GO:0004674,GO:0004712,GO:0004713,GO:0004672,GO:0005524	CG40478-PA				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112	253~273								
aly1158.12	Unknown		n/a																				
aly1158.13	Dual specificity tyrosine-phosphorylation-regulated kinase 2	GO:0005737,GO:0005654,GO:0006468,GO:0000151,GO:0007224,GO:0051534,GO:0005634,GO:0000287,GO:0030145,GO:0018108,GO:0030529,GO:0005575,GO:0004674,GO:0043130,GO:0004712,GO:0004713,GO:0004672,GO:0045725,GO:0005524,GO:0042771	CG40478-PA				SM00220		PF00069	PS50011			G3DSA:1.10.510.10	SSF56112,SSF56112									
aly1158.14	DNA-directed RNA polymerases I, II, and III subunit RPABC5	GO:0005736,GO:0005666,GO:0005634,GO:0006366,GO:0006360,GO:0005665,GO:0006351,GO:0003677,GO:0003899,GO:0006383,GO:0008270	CG13628-PA	MF_00250		PIRSF005653			PF01194			PS01112	G3DSA:1.10.10.60	SSF46924									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1158.15	Unknown		n/a																				
aly1158.16	Unknown	GO:0003676	n/a						PF05485	PS50950				SSF57716									
aly1158.2	Unknown	GO:0031362,GO:0016020,GO:0050839,GO:0008150,GO:0016167	CG43224-PE				SM00907,SM00907,SM00907		PF02351,PF02351					SSF110035,SSF110035,SSF110035									
aly1158.3	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA			PIRSF036514			PF00525,PF00011	PS01031	PR00299,PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly1158.4	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA			PIRSF036514			PF00525,PF00011	PS01031	PR00299,PR00299,PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly1158.5	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA						PF00011	PS01031	PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly1158.6	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA			PIRSF036514			PF00011	PS01031	PR00299,PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764	158~174								
aly1158.7	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0022857,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850	PR00171,PR00171,PR00171	PS00217,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473	218~245		REACT_15518						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1158.8	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA			PIRSF036514			PF00011	PS01031	PR00299,PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly1158.9	Plastin-2	GO:0032432,GO:0033157,GO:0015629,GO:0030175,GO:0051020,GO:0005925,GO:0005737,GO:0071803,GO:0001726,GO:0002102,GO:0002286,GO:0070062,GO:0005615,GO:0009611,GO:0003779,GO:0005509,GO:0016477,GO:0022617,GO:0042802,GO:0001725,GO:0051017,GO:0016321,GO:0051015,GO:0005884,GO:0005886,GO:0032587,GO:0001891,GO:0005829,GO:0010737	CG8649-PD				SM00054,SM00033,SM00033,SM00033,SM00033		PF00307,PF00307,PF00307,PF00307,PF13405	PS50021,PS50021,PS50222,PS50021,PS50021		PS00018,PS00019,PS00020,PS00019	G3DSA:1.10.418.10,G3DSA:1.10.238.10,G3DSA:1.10.418.10,G3DSA:1.10.418.10,G3DSA:1.10.418.10	SSF47473,SSF47473,SSF47576										
aly115890.1	Unknown		n/a																				
aly11591.1	Unknown		n/a												38~72,111~148,77~97								
aly11591.2	Unknown		n/a																				
aly11591.3	Unknown		n/a																				
aly11591.4	Unknown		n/a																				
aly11591.5	Unknown		n/a												52~96								
aly11591.6	Unknown		n/a												57~77								
aly116.1	Trypsin-1	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG18681-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly116.10	Unknown		n/a																				
aly116.11	Huntingtin-interacting protein K	GO:0005737,GO:0005634	CG9922-PA										G3DSA:1.10.8.10										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly116.12	Protein roadkill	GO:0031648,GO:0007367,GO:0042067,GO:0048592,GO:0007349,GO:0045879,GO:0043065,GO:0016567,GO:0046330,GO:0046331,GO:0030162,GO:0005515,GO:0042308,GO:0001654,GO:0005634,GO:0042803	CG12537-PF				SM00225,SM00061		PF00651,PF00917	PS50144,PS50097			G3DSA:3.30.710.10,G3DSA:2.60.210.10	SSF49599,SSF54695									
aly116.13	Origin recognition complex subunit 2	GO:0000792,GO:0005723,GO:0000808,GO:0008283,GO:0006342,GO:0005634,GO:0006270,GO:0030261,GO:0007052,GO:0006260,GO:0005664,GO:0007307,GO:0007076,GO:0022008,GO:0003682,GO:0003677,GO:0006261	CG3041-PA						PF04084														
aly116.14	Unknown		n/a																				
aly116.15	Acidic leucine rich nuclear phosphoprotein 32 family member A	GO:0005737,GO:0007017,GO:0005783,GO:0008017,GO:0005634,GO:0006913,GO:0019212,GO:0048471,GO:0005875	CG5784-PC						PF14580	PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									
aly116.16	Alpha-1,6-mannosyl-glycoprotein 2 beta-N-acetylglucosaminyltransferase	GO:0005795,GO:0008455,GO:0005797,GO:0006487,GO:0016021,GO:0030246,GO:0009312,GO:0008375,GO:0000139,GO:0018279	CG7921-PA						PF05060							00513+2.4.1.143,00510+2.4.1.143		PWY-7426	UPA00378				
aly116.17	Unknown		CG13954-PC																				
aly116.18	Homeobox protein ceh-19	GO:0043565,GO:0003700,GO:0005634,GO:0006355,GO:0003677,GO:0007275	CG34031-PC				SM00389		PF00046	PS50071	PR00031,PR00031,PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly116.19	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly116.2	Unknown	GO:0003677	CG4404-PA				SM00595		PF10545,PF02944	PS51029,PS51031													
aly116.20	Striatin-interacting protein 1	GO:0005737,GO:0022604,GO:0070062,GO:0005634,GO:0030866,GO:0005575,GO:0008150,GO:0003674	CG11526-PB						PF11882,PF07923														
aly116.21	Abl interactor 2	GO:0006909,GO:0030031,GO:0030032,GO:0017124,GO:0030036,GO:0006928,GO:0030175,GO:0031209,GO:0004871,GO:0003677,GO:0005737,GO:0070064,GO:0000902,GO:0016601,GO:0048846,GO:0021955,GO:0048471,GO:0016477,GO:0016203,GO:0005856,GO:2000601,GO:0016032,GO:0031258,GO:0030027,GO:0007528,GO:0019900,GO:0008360,GO:0018108,GO:0007155,GO:0043234,GO:0008154,GO:0007030,GO:0031625,GO:0007010,GO:0008093,GO:0005829,GO:0030866,GO:0032403,GO:0022416,GO:0005515,GO:0045860	CG9749-PD						PF07815														
aly116.22	Abl interactor 2	GO:0006909,GO:0030031,GO:0030032,GO:0017124,GO:0030036,GO:0006928,GO:0030175,GO:0031209,GO:0004871,GO:0003677,GO:0005737,GO:0070064,GO:0000902,GO:0016601,GO:0048846,GO:0021955,GO:0048471,GO:0016477,GO:0016203,GO:0005856,GO:2000601,GO:0016032,GO:0031258,GO:0030027,GO:0007528,GO:0019900,GO:0008360,GO:0018108,GO:0007155,GO:0043234,GO:0008154,GO:0007030,GO:0031625,GO:0007010,GO:0008093,GO:0005829,GO:0030866,GO:0032403,GO:0022416,GO:0005515,GO:0045860	CG9749-PD				SM00326		PF14604	PS50002	PR00452,PR00452,PR00452,PR00452		G3DSA:2.30.30.40	SSF50044									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly116.23	Cell division cycle and apoptosis regulator protein 1	GO:0008284,GO:0030335,GO:0003714,GO:0005641,GO:0006915,GO:0003713,GO:1903507,GO:0043065,GO:0006355,GO:0006351,GO:0001047,GO:0048471,GO:0030374,GO:0044822,GO:0007049	n/a				SM00513		PF14443,PF14444	PS50800		PS00018	G3DSA:1.10.720.30	SSF68906	697~731,808~828,597~617								
aly116.24	Unknown		CG14086-PD						PF16054														
aly116.25	Unknown	GO:0005549,GO:0016020,GO:0007608,GO:0004984	n/a						PF02949														
aly116.26	Putative sodium-dependent multivitamin transporter	GO:0006810,GO:0015293,GO:0008523,GO:0016020,GO:0055085,GO:0006814,GO:0016021	CG10444-PA					TIGR00813	PF00474	PS50283													
aly116.27	Putative sodium-dependent multivitamin transporter	GO:0006810,GO:0015293,GO:0005215,GO:0008523,GO:0016020,GO:0055085,GO:0006814,GO:0016021	CG10444-PA					TIGR00813	PF00474	PS50283													
aly116.28	Centrosomal protein of 290 kDa	GO:0000086,GO:0070201,GO:0007163,GO:0060041,GO:0042384,GO:0005737,GO:0005813,GO:0005634,GO:0016020,GO:0030916,GO:0042462,GO:0032391,GO:0034451,GO:0000278,GO:0060271,GO:0042048,GO:0090316,GO:0045893,GO:0043234,GO:0001750,GO:0006996,GO:0035869,GO:0036038,GO:0005829,GO:0048793,GO:0030902,GO:0015031,GO:0030814,GO:0045494	CG13889-PA												973~993,722~742,770~797,314~334,1254~1274,904~924,1464~1484,198~232,1802~1822,1657~1691,1282~1338,1032~1066,48~82,1754~1774,255~282,110~165,1598~1625,1872~1934,1375~1431,1194~1214,355~406,807~841,1548~1589									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly116.29	Vinexin	GO:0016203,GO:0007015,GO:0031589,GO:0017166,GO:0005925,GO:0006936,GO:0000122,GO:0007605,GO:0050954,GO:0005829,GO:0005856,GO:0005200,GO:0043410,GO:0051495,GO:0051496,GO:0007155,GO:0016477,GO:0005634	CG18408-PX				SM00326,SM00326,SM00326,SM00459		PF00018,PF00018,PF02208,PF14604	PS50002,PS50002,PS50002,PS50831	PR00499,PR00499,PR00499,PR00499		G3DSA:2.30.30.40,G3DSA:2.30.30.40,G3DSA:2.30.30.40	SSF50044,SSF50044,SSF50044	550~570,997~1024,1697~1717,8~35									
aly116.3	Fatty-acid amide hydrolase 2	GO:0016787,GO:0016021,GO:0050567,GO:0016884	CG5191-PB						PF01425				G3DSA:3.90.1300.10	SSF75304		00970+6.3.5.7		PWY-5921					
aly116.30	Unknown		n/a																				
aly116.31	PDZ and LIM domain protein 3	GO:0007015,GO:0015629,GO:0007507,GO:0030239,GO:0008307,GO:0008270,GO:0005515,GO:0030018	CG14168-PG				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156									
aly116.32	Ras-related protein Rab-27A	GO:0008021,GO:0045921,GO:1903435,GO:0006904,GO:0007596,GO:0030425,GO:0010628,GO:0045202,GO:1990182,GO:0050766,GO:0030667,GO:0031982,GO:0006886,GO:0006887,GO:0070382,GO:0009306,GO:1903428,GO:0071985,GO:0036257,GO:0032402,GO:0032585,GO:0005525,GO:0005794,GO:0019882,GO:0030318,GO:0030141,GO:0016324,GO:0003924,GO:0043320,GO:0033093,GO:0006605,GO:0032482,GO:0030431,GO:1903307,GO:0001750,GO:0070062,GO:0042470,GO:0016192,GO:0043316,GO:0005764,GO:0019903,GO:0005515,GO:0031031,GO:0097278,GO:0019904	CG14791-PB				SM00174,SM00176,SM00173,SM00175	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly116.33	Migration and invasion enhancer 1	GO:0005737,GO:0030335,GO:0008430,GO:0070062,GO:0005829,GO:0006915,GO:0051491,GO:0005654,GO:0043066,GO:0045454,GO:0031235	CG15456-PA					TIGR02174	PF10262				G3DSA:3.40.30.10	SSF52833									
aly116.34	Molybdenum cofactor sulfurase	GO:0006777,GO:0043545,GO:0016829,GO:0030151,GO:0005575,GO:0003824,GO:0016740,GO:0008265,GO:0006727,GO:0030170	CG1692-PA	MF_03050					PF03473,PF00266	PS51340			G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383,SSF53383,SSF141673,SSF50800				PWY-5963					
aly116.35	Lipase 3	GO:0048812,GO:0004806,GO:0006629,GO:0016788,GO:0016042	CG31871-PA			PIRSF000862			PF00561				G3DSA:3.40.50.1820	SSF53474									
aly116.36	Unknown		n/a																				
aly116.37	Unknown		n/a																				
aly116.38	Unknown		n/a												770~797,993~1013								
aly116.4	G protein alpha q subunit	GO:0030322,GO:0071244,GO:0046673,GO:0004871,GO:0001664,GO:0060158,GO:0016028,GO:0016060,GO:0005834,GO:0016027,GO:0007188,GO:0002385,GO:0046872,GO:0007186,GO:0005525,GO:0031683,GO:0007608,GO:0007601,GO:0003924,GO:0007629,GO:0007602,GO:0008152,GO:0005886,GO:0006184,GO:0031234,GO:0006897,GO:0016056,GO:0043052,GO:0007202,GO:0016199	CG17759-PJ				SM00275		PF00503		PR00442,PR00442,PR00442,PR00442,PR00318,PR00318,PR00318,PR00318		G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.400.10	SSF52540,SSF52540,SSF47895	5~36		REACT_14797,REACT_15380,REACT_604,REACT_1505						
aly116.5	Guanine nucleotide-binding protein G(q) subunit alpha	GO:0030322,GO:0071244,GO:0046673,GO:0004871,GO:0001664,GO:0060158,GO:0016028,GO:0016060,GO:0005834,GO:0016027,GO:0007188,GO:0002385,GO:0046872,GO:0007186,GO:0005525,GO:0031683,GO:0007608,GO:0003924,GO:0007629,GO:0007602,GO:0005886,GO:0006184,GO:0031234,GO:0006897,GO:0016056,GO:0043052,GO:0007202,GO:0016199	CG17759-PJ				SM00275		PF00503		PR01241,PR01241,PR01241,PR01241,PR00318,PR00318,PR00318,PR00318		G3DSA:3.40.50.300,G3DSA:1.10.400.10,G3DSA:1.10.400.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF47895,SSF47895			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly116.6	Unknown	GO:0009593,GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0004970	CG15324-PA				SM00918						G3DSA:3.40.190.10	SSF53850,SSF53850									
aly116.7	Glutamate receptor ionotropic, NMDA 3B	GO:0005261,GO:0030594,GO:0009593,GO:0045211,GO:0035235,GO:0006812,GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0042165,GO:0034220,GO:0030054,GO:0005886,GO:0017146,GO:0030425,GO:0098655,GO:0004972,GO:0035249,GO:0004970,GO:0016594	CG15324-PA										G3DSA:3.40.190.10,G3DSA:1.10.287.70	SSF53850,SSF53850									
aly116.8	Lachesin	GO:0007155,GO:0007169,GO:0004714,GO:0005886,GO:0031225	CG14010-PD				SM00409,SM00409,SM00408,SM00408		PF07679,PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly116.9	Unknown	GO:0005179,GO:0005576	n/a						PF00049			PS00262	G3DSA:1.10.100.10	SSF56994									
aly11655.1	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005886,GO:0006508	CG6865-PB				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly11655.2	Protein msta, isoform A	GO:0008168,GO:0010629,GO:0042826	CG14590-PA										G3DSA:2.170.270.10	SSF82199	331~355								
aly11655.3	Unknown		n/a																				
aly1166.1	Unknown	GO:0005549	n/a						PF01395				G3DSA:1.10.238.20	SSF47565									
aly1166.2	Unknown	GO:0005549	n/a						PF01395				G3DSA:1.10.238.20	SSF47565									
aly1166.3	Unknown	GO:0005549,GO:0007606,GO:0005576,GO:0008145,GO:0005550	CG1668-PA				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly1166.4	Beta-1,4-glucuronyltransferase 1	GO:0005794,GO:0035269,GO:0016021,GO:0008109,GO:0000139,GO:0002121,GO:0046872,GO:0015020	CG9171-PC						PF13896														

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1166.5	Unknown		n/a																				
aly116684.1	Cullin-1	GO:1990452,GO:0009887,GO:0031625,GO:0008283,GO:0006915,GO:0031146,GO:0016322,GO:0046627,GO:0006513,GO:0006511,GO:0019005,GO:0031461,GO:0032007,GO:0007095,GO:0000152	CG1877-PC						PF00888	PS50069			G3DSA:1.20.1310.10	SSF75632					UPA00143				
aly1168.1	Tigger transposable element-derived protein 2	GO:0005634,GO:0003676,GO:0003677	n/a						PF03184														
aly1168.2	Unknown		n/a																				
aly11685.1	Ommochrome-binding protein		n/a										G3DSA:2.120.10.30	SSF101898									
aly11685.2	Disks large homolog 1	GO:0016333,GO:0016332,GO:0008105,GO:0008104,GO:0016336,GO:0016335,GO:0016334,GO:0007617,GO:0005886,GO:0045197,GO:0045196,GO:0005789,GO:0031594,GO:0045887,GO:0051124,GO:0045202,GO:0046956,GO:0008049,GO:0043195,GO:0005920,GO:0061176,GO:0005856,GO:0002009,GO:0042332,GO:0019991,GO:0045179,GO:0046939,GO:0005198,GO:0097120,GO:0030054,GO:0048471,GO:0042127,GO:0008285,GO:0016328,GO:0005154,GO:0051294,GO:0016327,GO:0004385,GO:0035255,GO:0045175,GO:0045211,GO:0001738,GO:0014069,GO:0045475,GO:0007268,GO:0007010,GO:0016020,GO:0016323,GO:0005918,GO:0045167,GO:0008283,GO:0000132,GO:0007399,GO:0042734,GO:0051726,GO:0030710,GO:0007391,GO:0005515,GO:0043113,GO:0005938	CG1725-PM				SM00228,SM00228,SM00228		PF00595,PF00595,PF00595	PS50106,PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156,SSF50156										
aly11685.3	Unknown		n/a																				
aly11699.1	Unknown		n/a																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly11699.2	Dehydrodolichyl diphosphate syntase complex subunit nus1	GO:0005783,GO:0006486,GO:0009306,GO:0016021,GO:0035220,GO:0005789,GO:0016765,GO:0002040	CG4775-PA										G3DSA:3.40.1180.10	SSF64005									
aly11699.3	40S ribosomal protein S30	GO:0022627,GO:0003735,GO:0007052,GO:0005515,GO:0000022,GO:0006412,GO:0005840	CG15697-PA				SM00213		PF04758,PF00240	PS50053			G3DSA:3.10.20.90	SSF54236									
aly1170.1	Elongation of very long chain fatty acids protein 4	GO:0009922,GO:0005783,GO:0016021,GO:0030497,GO:0005575,GO:0016740,GO:0030176,GO:0019367,GO:0042761	CG5278-PA						PF01151							00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					
aly1170.2	Elongation of very long chain fatty acids protein 7	GO:0009922,GO:0005783,GO:0016021,GO:0030497,GO:0005789,GO:0005575,GO:0016740,GO:0034626,GO:0019367,GO:0042761	CG5278-PA						PF01151							00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					
aly1170.3	Elongation of very long chain fatty acids protein 7	GO:0009922,GO:0005783,GO:0016021,GO:0030497,GO:0005789,GO:0005575,GO:0016740,GO:0034626,GO:0019367,GO:0042761	CG5278-PA						PF01151			PS01188				00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					
aly1170.4	Elongation of very long chain fatty acids protein 7	GO:0009922,GO:0005783,GO:0016021,GO:0030497,GO:0005789,GO:0005575,GO:0016740,GO:0034626,GO:0019367,GO:0042761	CG5278-PA						PF01151			PS01188				00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1170.5	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG4576-PA																				
aly1170.6	Unknown		n/a																				
aly1170.7	Unknown		n/a																				
aly11700.1	Collagen alpha 1(XV) chain	GO:0005201,GO:0030154,GO:0030246,GO:0005788,GO:0031012,GO:0007165,GO:0008045,GO:0001525,GO:0007005,GO:0005581,GO:0005582,GO:0016021,GO:0005198,GO:0005576,GO:0022617,GO:2001046,GO:0014732,GO:0007155,GO:0005615,GO:0070062,GO:0030574,GO:0030198,GO:0071711,GO:0014899	CG42543-PR						PF01391,PF01391,PF01391,PF06482				G3DSA:3.10.100.10	SSF56436										
aly11707.1	Unknown		n/a												157~191								
aly11713.1	Sodium/calcium exchanger 1	GO:0055013,GO:0044557,GO:0098735,GO:0055074,GO:0030501,GO:0044325,GO:0006883,GO:0060048,GO:0030506,GO:0035994,GO:0071436,GO:0002027,GO:0016021,GO:0016020,GO:0006814,GO:1901660,GO:0002026,GO:0071313,GO:0035725,GO:0005509,GO:0046872,GO:0014829,GO:0042383,GO:0060402,GO:0030315,GO:0034614,GO:0006816,GO:0048747,GO:0007602,GO:0003007,GO:0005887,GO:0005886,GO:0007154,GO:0016323,GO:0001892,GO:0055085,GO:0009791,GO:0097369,GO:0008092,GO:0035050,GO:0086038,GO:0005432,GO:0086036,GO:0070588,GO:0005622,GO:0070509,GO:0051481,GO:0005829	CG5685-PG						PF01699		PR01259,PR01259,PR01259,PR01259			SSF141072			REACT_15518							
aly117158.1	Unknown		n/a																				
aly11743.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1175.1	Cullin-2	GO:0031625,GO:0005730,GO:0008582,GO:0000152,GO:0005654,GO:0006511,GO:0042787,GO:0030163,GO:0007295,GO:0031461,GO:0022008,GO:0031462	CG1512-PA				SM00182		PF00888	PS50069			G3DSA:1.20.1310.10,G3DSA:1.20.1310.10,G3DSA:1.20.1310.10,G3DSA:4.10.1030.10,G3DSA:1.20.1310.10	SSF75632,SSF74788	541~561				UPA00143				
aly1175.2	Unknown		n/a																				
aly1175.3	Mitogen-activated protein kinase-binding protein 1	GO:0005515	CG7337-PG				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50294,PS50294,PS50294			G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978									
aly1175.4	Unknown		CG7337-PG												695~729								
aly1177.1	Unknown		n/a																				
aly1177.2	Unknown		n/a																				
aly117804.1	Unknown		n/a																				
aly1184.1	Scavenger receptor class B member 1	GO:0007155,GO:0005901,GO:0016021,GO:0016020	CG40006-PA						PF01130		PR01609,PR01609,PR01609												
aly1184.2	Coatomer subunit gamma	GO:0035147,GO:0007424,GO:0006890,GO:0006909,GO:0016192,GO:0008362,GO:0005794,GO:0009306,GO:0006886,GO:0000281,GO:0035149,GO:0005198,GO:0005801,GO:0048812,GO:0010883,GO:0030198,GO:0007112,GO:0007436,GO:0030126,GO:0035158,GO:0005783	CG1528-PA			PIRSF037093			PF08752,PF16381,PF01602				G3DSA:2.60.40.1480,G3DSA:1.25.10.10,G3DSA:3.30.310.30	SSF55711,SSF48371,SSF49348									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1184.3	Transcriptional repressor protein YY1	GO:0006351,GO:0016363,GO:0030154,GO:0031011,GO:0001158,GO:0031490,GO:0010629,GO:0008270,GO:0003677,GO:0001078,GO:0005737,GO:0043565,GO:0031519,GO:0000724,GO:0006342,GO:0005634,GO:0003714,GO:0003713,GO:0006265,GO:0016458,GO:0034696,GO:0046872,GO:0000980,GO:0044212,GO:0048593,GO:0046332,GO:0000790,GO:0045892,GO:0010225,GO:0051276,GO:0006974,GO:0000400,GO:0006403,GO:0007283,GO:0009952,GO:0003700,GO:0005704,GO:0000122,GO:0005703,GO:0005700,GO:0034644,GO:0006355,GO:0048813,GO:0006357,GO:0045944,GO:0003723,GO:0005667,GO:0003682,GO:0071347	CG17743-PA				SM00355,SM00355		PF00096	PS50157,PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly1184.4	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	GO:0005975,GO:0005730,GO:0051287,GO:0000287,GO:0005739,GO:0005654,GO:0006099,GO:0006734,GO:0006103,GO:0006102,GO:0005759,GO:0045926,GO:0044237,GO:0004449,GO:0005875,GO:0005524,GO:0044281	CG5028-PA						PF00180				G3DSA:3.40.718.10,G3DSA:3.40.718.10	SSF53659										
aly1184.5	Transcription factor SUM-1	GO:0005737,GO:0016202,GO:0007517,GO:0016204,GO:0003700,GO:0005634,GO:0006355,GO:0003677,GO:0046983,GO:0007526	CG10250-PA				SM00353,SM00520		PF00010,PF01586	PS50888			G3DSA:4.10.280.10	SSF47459			REACT_21303						
aly1184.6	43 kDa receptor-associated protein of the synapse homolog	GO:0005856,GO:0007268,GO:0033130,GO:0043495,GO:0045211,GO:0008270,GO:0005886,GO:0030054,GO:0045202	CG1909-PA				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF10579,PF13181,PF13181	PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452	488~488								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1184.7	CUE domain-containing protein 2	GO:0005737,GO:0005654,GO:0031965,GO:0005515	CG9636-PC							PS51140													
aly1184.8	Protein diaphanous	GO:0008104,GO:0030589,GO:0090303,GO:0017048,GO:0007349,GO:0007279,GO:0045448,GO:0003383,GO:0005912,GO:0051225,GO:0005737,GO:0045177,GO:0045010,GO:0030838,GO:0000281,GO:0005546,GO:0003779,GO:0009306,GO:0016476,GO:0043234,GO:0032507,GO:0030029,GO:0007424,GO:0007605,GO:0032154,GO:0035011,GO:0007283,GO:0051489,GO:0005938,GO:0012506,GO:0022008,GO:0005826,GO:0007111,GO:0007110,GO:0007015,GO:0000915,GO:0005856,GO:0031532,GO:0097320,GO:0005515,GO:0000910,GO:0005884	CG1768-PD				SM00498		PF06371,PF06371,PF06345,PF02181,PF02181,PF06367	PS51231,PS51232				SSF101447,SSF48371										
aly1184.9	Unknown		n/a																				
aly118415.1	MOXD1 homolog 1	GO:0004500,GO:0016715,GO:0005575,GO:0005576,GO:0005507,GO:0055114	CG5235-PA						PF03712				G3DSA:2.60.120.310,G3DSA:2.60.120.230	SSF49742,SSF49742									
aly1186.1	Unknown		CG14968-PB						PF00640				G3DSA:2.30.29.30	SSF50729									
aly1186.2	Unknown		n/a												73~96								
aly1186.3	Unknown		n/a												82~102								
aly1186.4	Zinc finger protein 431	GO:0003682,GO:0000122,GO:0005634,GO:0030154,GO:0006355,GO:0006351,GO:0001046,GO:0003677,GO:0046872,GO:0043433	CG1454-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57716										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1186.5	Angiotensin-converting enzyme (Fragment)	GO:0007552,GO:0005615,GO:0008241,GO:0009609,GO:0016020,GO:0004180,GO:0007291,GO:0008270,GO:0007289,GO:0006508,GO:0046872,GO:0016021,GO:0008237,GO:0005576	CG8827-PA						PF01401		PR00791,PR00791,PR00791,PR00791,PR00791,PR00791,PR00791			SSF55486,SSF55486									
aly11875.1	Unknown		n/a						PF13518				G3DSA:1.10.10.10	SSF46689									
aly1188.1	Cathepsin L	GO:0035071,GO:0030154,GO:0045169,GO:0005764,GO:0048102,GO:0004197,GO:0030163,GO:0007275,GO:0006508,GO:0008234	CG6692-PC				SM00645,SM00848		PF08246,PF00112		PR00705,PR00705,PR00705	PS00639,PS00640,PS00139	G3DSA:3.90.70.10	SSF54001									
aly1188.10	Glutamate receptor ionotropic, kainate 2	GO:0060025,GO:0019228,GO:0050806,GO:0030425,GO:0030424,GO:0008066,GO:0043524,GO:0043525,GO:0060080,GO:0046328,GO:0048169,GO:0035249,GO:0004970,GO:0001662,GO:0045202,GO:0032983,GO:0006886,GO:0032839,GO:0015277,GO:0007268,GO:0030054,GO:0042802,GO:0042803,GO:0008328,GO:0035235,GO:0006874,GO:0006811,GO:0005234,GO:0034220,GO:0051402,GO:0030165,GO:0014069,GO:0005887,GO:0005886,GO:0060079,GO:0043204,GO:0031624,GO:0031625,GO:0043195,GO:0042734,GO:0045211,GO:0051967,GO:0048172,GO:0043113,GO:0007165	CG5621-PC				SM00079		PF00497,PF00060		PR00177,PR00177,PR00177		G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:1.10.287.70	SSF53850,SSF53850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1188.11	Platelet glycoprotein Ib alpha chain	GO:0009897,GO:0016020,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0031362,GO:0035007,GO:0008063,GO:0007599,GO:0006955,GO:0007416,GO:0005737,GO:0000902,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0006952,GO:0009986,GO:0016201,GO:0007596,GO:0009880,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005887,GO:0005886,GO:0007155,GO:0007352,GO:0070062,GO:0043234,GO:0007507,GO:0042730,GO:0009950,GO:0009620,GO:0004888,GO:0005515,GO:0030097,GO:0045610,GO:0005769,GO:0007165	CG5490-PC				SM00369,SM00369,SM00369,SM00369		PF13855	PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058										
aly1188.12	Protein toll	GO:0009897,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0035007,GO:0008063,GO:0006955,GO:0007416,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0002229,GO:0006952,GO:0042802,GO:0016201,GO:0009880,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005887,GO:0005886,GO:0007155,GO:0007352,GO:0043234,GO:0007507,GO:0009950,GO:0009620,GO:0004888,GO:0045944,GO:0005515,GO:0030097,GO:0045610,GO:0005769,GO:0007165	CG5490-PC				SM00082,SM00255		PF01582	PS51450,PS50104,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.40.50.10140	SSF52058,SSF52200										
aly1188.13	Unknown		n/a																				
aly1188.2	Zinc finger C4H2 domain-containing protein	GO:0005737,GO:0021522,GO:0007399,GO:0005634,GO:0007528,GO:0045211,GO:0046872,GO:0030054	CG13001-PA						PF10146						47~67								
aly1188.3	PHD and RING finger domain-containing protein 1	GO:0070063,GO:0005634,GO:0016020,GO:0008270,GO:0005515,GO:0006366,GO:0000381,GO:0006397	CG2926-PA				SM00184		PF13639	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1188.4	Lysosomal aspartic protease	GO:0035071,GO:0006915,GO:0005764,GO:0048102,GO:0005576,GO:0004190,GO:0045476,GO:0050829,GO:0006508,GO:0005875	CG1548-PA						PF00026,PF07966	PS51257	PR00792,PR00792,PR00792,PR00792	PS00141	G3DSA:2.40.70.10,G3DSA:2.40.70.10	SSF50630									
aly1188.5	Unknown		n/a																				
aly1188.6	Unknown		n/a																				
aly1188.7	Unknown		n/a																				
aly1188.8	Unknown		n/a																				
aly1188.9	Major facilitator superfamily domain-containing protein 6	GO:0016021,GO:0016020,GO:0055085	CG12858-PA						PF07690,PF12832				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473									
aly119.1	Ommochrome-binding protein		n/a										G3DSA:2.120.10.30,G3DSA:2.120.10.30	SSF63829,SSF63829									
aly119.2	Potassium voltage-gated channel protein Shaw	GO:0071805,GO:0006813,GO:0016021,GO:0051260,GO:0008076,GO:0022843,GO:0005249,GO:0005886,GO:0005251,GO:0055085,GO:0030431	CG2822-PC				SM00225		PF00520,PF02214		PR01491,PR01491,PR01491,PR01491,PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR01498,PR01498,PR01498,PR01498,PR01498		G3DSA:1.20.120.350,G3DSA:1.10.287.70,G3DSA:3.30.710.10	SSF54695,SSF81324									
aly119.3	Unknown	GO:0006813,GO:0051260,GO:0008076,GO:0022843,GO:0005249,GO:0005251,GO:0055085	CG34366-PC																				
aly1191.1	Ecdysteroid UDP-glucosyltransfe	GO:0016758,GO:0015020,GO:0008152	CG15661-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1191.2	Unknown		CG7031-PA																				
aly1191.3	Gloverin	GO:0045087,GO:0005576,GO:0042742	n/a						PF10793														
aly1191.4	Attacin-A	GO:0005615,GO:0019731,GO:0045087,GO:0050830,GO:0005576,GO:0042742,GO:0050829,GO:0006959	CG10146-PA						PF03769,PF03768														
aly1191.5	Unknown		n/a																				
aly11932.1	Anoctamin-4	GO:0005229,GO:0017128,GO:0061589,GO:0061591,GO:0061590,GO:0016021,GO:0005622,GO:0005886	CG6938-PC						PF04547														
aly11941.1	Vitamin K-dependent protein C	GO:0004252,GO:0005615,GO:0007596,GO:0048803,GO:0043066,GO:0005509,GO:0006508,GO:0008233,GO:0030195	CG11066-PB				SM00020		PF00089	PS50240			G3DSA:2.40.10.10	SSF50494									
aly119444.1	E3 ubiquitin-protein ligase MARCH5	GO:0090344,GO:0005783,GO:0004842,GO:0016021,GO:0051865,GO:0005741,GO:0008270,GO:0016874,GO:0090140	CG9855-PA																				
aly11945.1	Unknown		n/a																				
aly11945.10	Inhibitor of growth protein 5	GO:0008285,GO:0006351,GO:0035064,GO:0043966,GO:2001235,GO:0005634,GO:0070776,GO:0043065,GO:0006260,GO:0008270,GO:0016573,GO:0045926,GO:0003682,GO:0006473,GO:0045893	CG9293-PA				SM00249		PF12998	PS50016		PS01359	G3DSA:3.30.40.10	SSF57903	97~117								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly11945.11	Wiskott-Aldrich syndrome protein family member 3	GO:0051125,GO:0006909,GO:0030031,GO:0030032,GO:0008335,GO:0060305,GO:0030037,GO:0014003,GO:0001764,GO:0034314,GO:0001745,GO:0005737,GO:0007413,GO:0000902,GO:0048846,GO:0005634,GO:0051491,GO:0003779,GO:0005856,GO:0031941,GO:0030029,GO:0030027,GO:0008360,GO:0030036,GO:0007409,GO:0007520,GO:0070062,GO:0007015,GO:0007030,GO:0010592,GO:0007010,GO:0030866,GO:0031643,GO:0005515,GO:0031209	CG4636-PD																				
aly11945.12	Diphosphomevalonate decarboxylase	GO:0008284,GO:0004163,GO:0030544,GO:0005829,GO:0005575,GO:0008299,GO:0006695,GO:0019287,GO:0005524,GO:0042803	CG8239-PA			PIRSF015950		TIGR01240	PF00288				G3DSA:3.30.230.10,G3DSA:3.30.70.890	SSF55060,SSF54211		00900+4.1.1.33		PWY-922,PWY-7391					
aly11945.13	Guanine nucleotide-binding protein subunit beta-like protein	GO:0005737,GO:0007626,GO:0005829,GO:0042335,GO:0018991,GO:0009267,GO:0044829,GO:0071011,GO:0005080,GO:0071013,GO:0048477,GO:0005776,GO:0035220,GO:0075522,GO:0000398,GO:0005515,GO:0045725,GO:0016243,GO:0005875,GO:0046716	CG7111-PC				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50082,PS50082,PS50082,PS50294,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly11945.14	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	GO:0055059,GO:0006909,GO:0046677,GO:0006470,GO:0019208,GO:0008022,GO:0009416,GO:0090162,GO:0007406,GO:0007067,GO:0051225,GO:0000278,GO:0005737,GO:0070062,GO:0043161,GO:0005634,GO:0005814,GO:0000922,GO:0046872,GO:0048477,GO:0006914,GO:0016787,GO:0051298,GO:0051297,GO:0007051,GO:0008360,GO:0046580,GO:0007155,GO:0007059,GO:0000775,GO:0007015,GO:0008637,GO:0034976,GO:0000159,GO:0060070,GO:0042542,GO:0007465,GO:0004722,GO:0004721,GO:0010468,GO:0007098,GO:0007099,GO:0000226,GO:0046982,GO:0045880	CG7109-PC				SM00156		PF00149		PR00114,PR00114,PR00114,PR00114,PR00114,PR00114,PR00114	PS00125	G3DSA:3.60.21.10	SSF56300										
aly11945.15	Graves disease carrier protein	GO:0045089,GO:0016021,GO:0005740,GO:0005743,GO:0022857,GO:0050829,GO:0055085	CG4241-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920	PR00928,PR00928,PR00928,PR00928,PR00928,PR00926,PR00926,PR00926,PR00926,PR00926,PR00926,PR00926		G3DSA:1.50.40.10	SSF103506									
aly11945.16	Sialin	GO:0006865,GO:0006820,GO:0030054,GO:0005737,GO:0044267,GO:0015992,GO:0006488,GO:0016021,GO:0016020,GO:0043687,GO:0018279,GO:0015739,GO:0005351,GO:0006811,GO:0005316,GO:0005887,GO:0005886,GO:0055085,GO:0030672,GO:0015136,GO:0005764,GO:0005765	CG4726-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473										
aly11945.17	5-methylcytosine rRNA methyltransferase NSUN4	GO:0008168,GO:0003723,GO:0005739,GO:0006364	CG4749-PA						PF01189	PS51686	PR02008,PR02008,PR02008		G3DSA:3.40.50.150	SSF53335									
aly11945.18	Unknown		n/a				SM01052		PF01302	PS50245			G3DSA:2.30.30.190	SSF74924	26~53								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly11945.19	Unknown		n/a																				
aly11945.2	Beta-1,4-N-acetylgalactosaminyltransferase bre-4	GO:0075015,GO:0005794,GO:0005975,GO:0033207,GO:0006486,GO:0009636,GO:0006044,GO:0016021,GO:0009247,GO:0033842,GO:0007528,GO:0045747,GO:0007291,GO:0008376,GO:0046872,GO:0008344	CG8536-PA						PF02709,PF13733		PR02050,PR02050,PR02050,PR02050		G3DSA:3.90.550.10	SSF53448					UPA00378				
aly11945.20	Diphosphomevalonate decarboxylase	GO:0008284,GO:0004163,GO:0030544,GO:0005829,GO:0005575,GO:0008299,GO:0006695,GO:0019287,GO:0005524,GO:0042803	CG8239-PA										G3DSA:3.30.230.10,G3DSA:3.30.70.890	SSF55060									
aly11945.3	Beta-1,4-galactosyltransferase 4	GO:0005794,GO:0032580,GO:0005975,GO:0006486,GO:0006044,GO:0016021,GO:0009247,GO:0033842,GO:0007528,GO:0007291,GO:0016757,GO:0008376,GO:0046872,GO:0008344,GO:0003945	CG8536-PA						PF02709		PR02050,PR02050		G3DSA:3.90.550.10	SSF53448					UPA00378				
aly11945.4	Sperm flagellar protein 2	GO:0005737,GO:0005794,GO:0010259,GO:0060541,GO:0060271,GO:0048702,GO:0035082,GO:0048854,GO:0097225,GO:0009566,GO:0048705,GO:0007283,GO:0005515,GO:0002177,GO:0002520	n/a						PF06294	PS50021			G3DSA:3.40.50.300		337~357								
aly11945.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly11945.6	Coiled-coil domain-containing protein 47	GO:0005737,GO:0005791,GO:0006983,GO:0007029,GO:0016021,GO:0016020,GO:0009791,GO:0055074,GO:0030433,GO:0044822,GO:0001649,GO:0005509	CG17593-PA						PF07946						395~415								
aly11945.7	Lysozyme	GO:0019835,GO:0005615,GO:0032504,GO:0003796,GO:0005576,GO:0042742	CG6426-PA						PF05497					SSF53955								
aly11945.8	Lysozyme	GO:0019835,GO:0005615,GO:0032504,GO:0003796,GO:0005576,GO:0042742	CG6426-PA						PF05497														
aly11945.9	Low density lipoprotein receptor adapter protein 1	GO:0030159,GO:0055037,GO:0009898,GO:0030424,GO:0043393,GO:0048260,GO:0090003,GO:0042982,GO:0005737,GO:0001540,GO:0009967,GO:0005546,GO:0009925,GO:0050750,GO:0001784,GO:0005883,GO:0030276,GO:0030122,GO:0042632,GO:0030121,GO:0008203,GO:0031623,GO:0005829,GO:0006898,GO:0090118,GO:0035591,GO:0035612,GO:0005102,GO:0005769,GO:0035615	CG14968-PB				SM00462		PF00640	PS01179			G3DSA:2.30.29.30	SSF50729	117~137								
aly1196.1	Venom carboxylesterase-6	GO:0005576,GO:0052689	CG6414-PA						PF00135	PS51257		PS00122	G3DSA:3.40.50.1820	SSF53474									
aly1196.10	Unknown		n/a																				
aly1196.11	Phosphopantothenoylcysteine decarboxylase	GO:0003824,GO:0004633,GO:0015937	CG30290-PA						PF02441				G3DSA:3.40.50.1950	SSF52507									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1196.12	Nitrogen permease regulator 2-like protein	GO:0015840,GO:0033673,GO:0006468,GO:0005096,GO:0048813,GO:0015824,GO:0004672,GO:0016247,GO:0035859	CG9104-PA						PF06218,PF06218														
aly1196.13	Unknown	GO:0031519	CG4877-PB						PF01753	PS50865		PS01360		SSF144232	259~286,64~84								
aly1196.14	Cyclin-dependent kinase 12	GO:0006468,GO:0006909,GO:0030332,GO:0051726,GO:0070816,GO:0005703,GO:0005700,GO:0046579,GO:0019908,GO:0004693,GO:0008353,GO:0022008,GO:0070374,GO:0000228,GO:0005524	CG7597-PB				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112	427~447								
aly1196.15	Myosin-IB	GO:0005737,GO:0042623,GO:0007498,GO:0007368,GO:0032528,GO:0003779,GO:0048803,GO:0016459,GO:0042742,GO:0008152,GO:0005903,GO:0003774,GO:0005524,GO:0005938	CG9155-PD				SM00015,SM00015,SM00242		PF00612,PF00612,PF00063,PF06017	PS50096,PS51456,PS50096	PR00193,PR00193,PR00193,PR00193,PR00193		G3DSA:3.40.50.300	SSF52540										
aly1196.2	Venom carboxylesterase-6	GO:0005576,GO:0052689	CG6414-PA						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly1196.3	B-cell receptor associated protein 31	GO:0005811,GO:0005783,GO:0033116,GO:0005789,GO:0051561,GO:0030136,GO:0070973,GO:0006888,GO:0016021,GO:0016020,GO:0005739,GO:0035584,GO:1904154,GO:0032403,GO:2001244,GO:0042288,GO:1903071,GO:0007283,GO:0005887,GO:0043280,GO:0032580,GO:0005829,GO:0007204,GO:0000139,GO:0006886,GO:0032471	CG13887-PC						PF05529						156~211								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1196.4	Probable dynactin subunit 2	GO:0005737,GO:0007017,GO:0031982,GO:0008283,GO:0005874,GO:0016020,GO:0007018,GO:0005739,GO:0003774,GO:0022008,GO:0007051,GO:0007052,GO:0003674,GO:2001019,GO:0005869,GO:0030286,GO:0051028,GO:0051642,GO:0007067	CG8269-PA						PF04912						99~126,128~148,232~252									
aly1196.5	60S ribosomal protein L27	GO:0051298,GO:0022625,GO:0051297,GO:0005622,GO:0003735,GO:0007052,GO:0000022,GO:0006412,GO:0005840	CG4759-PD				SM00739		PF01777,PF00467			PS01107	G3DSA:2.30.30.30	SSF50104										
aly1196.6	Palmitoyltransferase ZDHHC5	GO:0018345,GO:0016021,GO:0019706,GO:0030425,GO:0005575,GO:0008150,GO:0008270,GO:0005886,GO:0003674	CG32705-PB						PF01529	PS50216													
aly1196.7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box	GO:0045089,GO:0006281,GO:0004003,GO:0005634,GO:0004386,GO:0016568,GO:0003677,GO:0050829,GO:0005524	CG5899-PA				SM00487,SM00490		PF00176,PF00271	PS51192,PS51194			G3DSA:1.10.150.320,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF46934									
aly1196.8	CBP80/20-dependent translation initiation factor	GO:0005737,GO:0000184,GO:0006446,GO:0003723,GO:0005515,GO:0048471	CG13124-PA				SM00543		PF02854				G3DSA:1.25.40.180	SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1196.9	Formin-like protein CG32138	GO:0003779,GO:0005575,GO:0048812,GO:0017048,GO:0030036	CG32138-PA				SM00498		PF02181,PF06371,PF06371,PF06367	PS51232,PS51231,PS51444				SSF48371,SSF48371,SSF101447	672~692,913~933,859~879,394~460									
aly119677.1	Unknown		n/a																				
aly119677.2	Unknown		n/a										G3DSA:3.30.40.10,G3DSA:1.20.5.340	SSF57903	146~180								
aly119963.1	60S ribosomal protein L18a	GO:0005840,GO:0022625,GO:0003735,GO:0007052,GO:0000022,GO:0006412,GO:0051298	CG6510-PA						PF01775														
aly12.1	Unknown		n/a																				
aly12.2	Unknown		n/a																				
aly120.1	Larval cuticle protein LCP-14	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG10533-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly120.2	Larval cuticle protein LCP-17	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG30045-PB						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly120.3	Larval cuticle protein LCP-14	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG8634-PA						PF00379	PS51155		PS00233											
aly120.4	Putative polypeptide N-acetylgalactosaminyltransferase 9	GO:0005794,GO:0031985,GO:0006493,GO:0032504,GO:0016021,GO:0004653,GO:0030246,GO:0000139,GO:0046872,GO:0005829	CG30463-PA				SM00458		PF00652,PF00535	PS50231			G3DSA:2.80.10.50,G3DSA:3.90.550.10	SSF50370,SSF53448									
aly120.5	Putative polypeptide N-acetylgalactosaminyltransferase 9	GO:0005794,GO:0031985,GO:0006493,GO:0032504,GO:0016021,GO:0004653,GO:0030246,GO:0000139,GO:0046872,GO:0005829	CG30463-PA				SM00458		PF00535,PF00652	PS50231			G3DSA:2.80.10.50,G3DSA:3.90.550.10	SSF50370,SSF53448									
aly1200.1	Lysine-specific histone demethylase 1A	GO:1902166,GO:0034720,GO:0007596,GO:0050681,GO:0019899,GO:0003700,GO:0003677,GO:0021983,GO:0043426,GO:0016491,GO:0032091,GO:0006482,GO:0050660,GO:0006355,GO:0006325,GO:0005634,GO:0070828,GO:0007474,GO:0005654,GO:0016458,GO:0030851,GO:0033169,GO:0045944,GO:0048477,GO:2000179,GO:0055001,GO:2000648,GO:0017053,GO:0008283,GO:0008134,GO:0045648,GO:0007264,GO:0030374,GO:0000790,GO:0001701,GO:0045892,GO:0043392,GO:0046886,GO:0008593,GO:0051572,GO:0051573,GO:0043433,GO:0055114,GO:0044212,GO:0051091,GO:0034648,GO:0006357,GO:0000122,GO:0045654,GO:0032451,GO:0032452,GO:0032453,GO:0032454,GO:0006351,GO:0005667,GO:0010725,GO:0003682,GO:0002039,GO:0043518	CG17149-PA						PF01593				G3DSA:3.90.660.10	SSF51905,SSF51905,SSF54373									
aly1200.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1200.3	Protein toll	GO:0009897,GO:0007416,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0007165,GO:0008063,GO:0006955,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0002229,GO:0042802,GO:0016201,GO:0009880,GO:0007507,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005886,GO:0007155,GO:0007352,GO:0043234,GO:0006952,GO:0009950,GO:0009620,GO:0004888,GO:0045944,GO:0005515,GO:0030097,GO:0045610,GO:0005769,GO:0035007	CG7250-PA				SM00255,SM00082,SM00082,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00369		PF01582,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS50104,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR01537,PR01537,PR01537		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.40.50.10140,G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52058,SSF52058,SSF52200,SSF52058									
aly1200.4	Unknown		n/a																				
aly120215.1	Zinc finger protein 135	GO:0005737,GO:0022604,GO:0005819,GO:0007010,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0005876,GO:0006351	CG8474-PA				SM00355,SM00355,SM00355		PF12874,PF12874	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly120294.1	Unknown		n/a																				
aly1204.1	Glycerol-3-phosphate acyltransferase 4	GO:0004366,GO:0016021,GO:0005789,GO:0003841,GO:0016746,GO:0008152,GO:0016024	CG3209-PD				SM00563		PF01553														
aly1204.2	Alpha-centractin	GO:0005737,GO:0019896,GO:0005200,GO:0007010,GO:0015629,GO:0043209,GO:0005813,GO:0070062,GO:0008089,GO:0003779,GO:0005884,GO:0005869,GO:0007067,GO:0005875,GO:0005524,GO:0008090	CG6174-PA				SM00268		PF00022		PR00190,PR00190,PR00190,PR00190,PR00190,PR00190,PR00190	PS01132	G3DSA:3.90.640.10,G3DSA:3.30.420.40	SSF53067,SSF53067										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1204.3	GDP-fucose protein O-fucosyltransferase 2	GO:0005794,GO:0016266,GO:0005783,GO:0051046,GO:0010717,GO:0008417,GO:0036066,GO:0006004,GO:0046922,GO:0010468,GO:0001707	CG14789-PA						PF10250							00514+2.4.1.221			UPA00378				
aly1204.4	ATP synthase subunit e, mitochondrial	GO:0000276,GO:0015992,GO:0005811,GO:0005753,GO:0015986,GO:0008553,GO:0015078	CG3321-PA						PF05680						38~58								
aly120497.1	Unknown	GO:0008494	CG17514-PA																				
aly1205.1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1	GO:0048639,GO:0006651,GO:0004871,GO:2000344,GO:0007613,GO:0008277,GO:0048009,GO:0007165,GO:0070498,GO:0045444,GO:0035556,GO:0007215,GO:0021987,GO:0005737,GO:0070062,GO:0043209,GO:0007213,GO:0005546,GO:0016042,GO:0035723,GO:0035722,GO:0045663,GO:0060466,GO:0006661,GO:0005509,GO:0016607,GO:0006629,GO:0031965,GO:0005096,GO:0007629,GO:0000790,GO:0045892,GO:0045893,GO:0004435,GO:0040019,GO:0005829,GO:0046330,GO:0080154,GO:2000438,GO:0032735,GO:1900087,GO:2000560	CG4574-PD				SM00149,SM00148,SM00239		PF00388,PF09279,PF00387	PS50007,PS50008,PS50004	PR00390,PR00390,PR00390,PR00390,PR00390,PR00390		G3DSA:1.20.1230.10,G3DSA:3.20.20.190,G3DSA:3.20.20.190,G3DSA:1.10.238.10,G3DSA:2.60.40.150	SSF49562,SSF51695,SSF47473	723~743,784~804	00562+3.1.4.11			PWY-6367,PWY-6351,PWY-7039					
aly1205.2	Malate dehydrogenase, mitochondrial	GO:0044262,GO:0005739,GO:0006099,GO:0030060,GO:0005759,GO:0005975,GO:0006108,GO:0055114,GO:0016491	CG10749-PA						PF00056				G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1205.3	Unknown	GO:0005811,GO:0044262,GO:0016615,GO:0016616,GO:0006919,GO:0035209,GO:0035070,GO:0006099,GO:0005739,GO:0006108,GO:0003824,GO:0043067,GO:0030060,GO:0005759,GO:0005975,GO:0043068,GO:0055114	CG7998-PA						PF02866				G3DSA:3.90.110.10	SSF56327									
aly1205.4	Carotenoid isomerooxygenase	GO:0004497,GO:0016063,GO:0035238,GO:0007604,GO:0007603,GO:0007602,GO:0010436,GO:0003834,GO:0009110,GO:0016119,GO:0042572,GO:0046872,GO:0042574,GO:0004744	CG9347-PA						PF03055														
aly1205.5	Carotenoid isomerooxygenase	GO:0004497,GO:0016063,GO:0035238,GO:0007604,GO:0007603,GO:0007602,GO:0010436,GO:0003834,GO:0009110,GO:0016119,GO:0042572,GO:0046872,GO:0042574,GO:0004744	CG9347-PA						PF03055														
aly12053.1	Neogenin (Fragment)	GO:0007432,GO:0050773,GO:0016021,GO:0070983,GO:0030425,GO:0005042,GO:0048813,GO:0008045,GO:0016199,GO:0005515,GO:0005886,GO:0007155,GO:0007411,GO:0030424,GO:0043025,GO:0008347	CG8581-PA				SM00060,SM00060,SM00060,SM00060		PF06583,PF00041,PF00041,PF00041	PS50853,PS50853,PS50853,PS50853	PR00014,PR00014,PR00014,PR00014		G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF49265,SSF49265			REACT_18266						
aly12053.2	Neogenin	GO:0030425,GO:0030424,GO:0007155,GO:0055072,GO:0004872,GO:0008045,GO:0051149,GO:0007411,GO:0007432,GO:0050709,GO:0016021,GO:0043025,GO:0005887,GO:0005886,GO:0007520,GO:0030513,GO:0008347,GO:0050773,GO:0070983,GO:0016199,GO:0005042,GO:0006355,GO:0048813,GO:0005515,GO:0042692	CG8581-PA				SM00409,SM00409,SM00408,SM00408		PF07679,PF07679	PS50835,PS50835,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF48726,SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly12053.3	Unknown	GO:0007432,GO:0050773,GO:0016021,GO:0070983,GO:0030425,GO:0005042,GO:0048813,GO:0008045,GO:0016199,GO:0005886,GO:0007411,GO:0030424,GO:0043025,GO:0008347	CG8581-PA						PF06583						46~66		REACT_18266							
aly120593.1	Unknown		n/a																				
aly12063.1	Facilitated trehalose transporter Tret1-2 homolog	GO:0005355,GO:0035428,GO:0015992,GO:0016021,GO:0016020,GO:0046323,GO:0005887,GO:0005886,GO:0005351,GO:0055085	CG1213-PA						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	211~231								
aly12063.10	H(+)/Cl(-) exchange transporter 7	GO:0050975,GO:0030554,GO:0031410,GO:0016021,GO:0016020,GO:0015297,GO:0005765,GO:0006821,GO:0005247,GO:0009268,GO:0005254,GO:0055085,GO:0005524	CG8594-PA						PF00654		PR00762,PR00762,PR00762,PR00762,PR00762,PR00762		G3DSA:1.10.3080.10,G3DSA:1.10.3080.10	SSF81340,SSF81340									
aly12063.11	Transcription factor grauzone	GO:0043565,GO:0007343,GO:0005634,GO:0007349,GO:0007279,GO:0006355,GO:0006357,GO:0045944,GO:0008270,GO:0006366,GO:0000987,GO:0045143,GO:0007143,GO:0000981	CG5034-PA				SM00868		PF07776					SSF57716									
aly12063.12	Leucine-rich repeat-containing protein 4B	GO:0005515,GO:0042734,GO:0016021,GO:0051965,GO:0030054,GO:0044300	CG7702-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly12063.13	WD repeat-containing protein 3	GO:0034388,GO:0032040,GO:0030515,GO:0005730,GO:0005634,GO:0031965,GO:0000462,GO:0022008,GO:0044822	CG8064-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF04003	PS50294,PS50082,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50998	254~274								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly12063.14	Phosphoribosyl pyrophosphate synthase-associated protein 2	GO:0043234,GO:0002189,GO:0000287,GO:0060348,GO:0004749,GO:0009165	CG2246-PA					TIGR01251	PF14572,PF13793				G3DSA:3.40.50.2020,G3DSA:3.40.50.2020,G3DSA:3.40.50.2020	SSF53271,SSF53271		00030+2.7.6.1,00230+2.7.6.1			UPA00087				
aly12063.15	Tyrosine--tRNA ligase, mitochondrial	GO:0006437,GO:0004812,GO:0070184,GO:0005829,GO:0005739,GO:0000166,GO:0043039,GO:0003723,GO:0006418,GO:0005759,GO:0004831,GO:0006412,GO:0005524	CG16912-PA	MF_02006				TIGR00234	PF00579		PR01040,PR01040,PR01040,PR01040	PS00178	G3DSA:3.10.290.10,G3DSA:3.40.50.620,G3DSA:1.10.240.10	SSF55174,SSF52374		00970+6.1.1.1	REACT_71						
aly12063.16	Rho GTPase-activating protein 17	GO:0005737,GO:0051056,GO:0007480,GO:0005829,GO:0005543,GO:0005096,GO:0045887,GO:0031594,GO:1900144,GO:0043089,GO:0005515,GO:0005886,GO:0005100,GO:0007264,GO:0007274,GO:0005923	CG4755-PA				SM00721,SM00324		PF03114,PF00620	PS50238			G3DSA:1.20.1270.60,G3DSA:1.10.555.10	SSF48350,SSF103657	22~49,174~194		REACT_11044						
aly12063.17	UNC93-like protein MFSD11	GO:0016021	CG18549-PA						PF05978				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly12063.18	Transmembrane protein 70 homolog, mitochondrial	GO:0033615,GO:0032592,GO:0003674	CG7506-PA						PF06979														
aly12063.19	Meteorin-like protein	GO:0005179,GO:0050728,GO:0005615,GO:0050873,GO:2000507,GO:0014850,GO:0090336,GO:0009409	n/a																				
aly12063.2	Eukaryotic translation initiation factor 3 subunit D	GO:0005737,GO:0005852,GO:0005829,GO:0016282,GO:0006446,GO:0006412,GO:0033290,GO:0001731,GO:0006413,GO:0005634,GO:0003743	CG10161-PB	MF_03003		PIRSF016281			PF05091															

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly12063.20	Testis-expressed sequence 2 protein	GO:0016021,GO:0005575,GO:0008150,GO:0007165,GO:0003674,GO:0006665	CG43783-PG												904~924,507~550								
aly12063.21	Serine/threonine-protein kinase/endoribonuclease ire-1	GO:0002119,GO:0005783,GO:0090305,GO:0030176,GO:0006986,GO:0016020,GO:0004521,GO:0004674,GO:0004672,GO:0006402,GO:0005524,GO:0006468,GO:0061541,GO:0043484,GO:0001751,GO:0001752,GO:0090502,GO:0007030,GO:0006990,GO:0030968,GO:0030969,GO:0070055,GO:0035966,GO:1902255,GO:0034976	CG4583-PB				SM00564,SM00564,SM00564,SM00564,SM00564,SM00580,SM00220		PF00069,PF06479	PS51392,PS50011		PS00108	G3DSA:2.140.10.10,G3DSA:2.140.10.10,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF50998,SSF56112									
aly12063.22	Ankyrin repeat domain-containing protein 27	GO:0042470,GO:0007016,GO:0005200,GO:0045170,GO:0008092,GO:0005770,GO:0045169,GO:0005764,GO:0030659,GO:0007165,GO:0005515,GO:0005886,GO:0015031,GO:0005769	CG1651-PB				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796,PF12796,PF02204	PS50088,PS50088,PS51205,PS50297,PS50088,PS50088,PS50088,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403,SSF109993	437~457								
aly12063.23	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0005515,GO:0048812,GO:0005887,GO:0005886,GO:0007155,GO:0007156,GO:0042802	CG31190-PE				SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00060,SM00060,SM00060,SM00060,SM00060		PF00041,PF00041,PF00041,PF13895,PF13895,PF13927,PF13927,PF07679,PF07679	PS50835,PS50835,PS50835,PS50835,PS50853,PS50835,PS50835,PS50853,PS50835,PS50835,PS50835,PS50853,PS50835,PS50853,PS50853	PR00014,PR00014,PR00014		G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF49265,SSF49265,SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726									
aly12063.24	Unknown		n/a																				
aly12063.25	Cyclic nucleotide-gated olfactory channel	GO:0030552,GO:0007608,GO:0006813,GO:0050896,GO:0016021,GO:0005216,GO:0008076,GO:0007605,GO:0022843,GO:0005249,GO:0055085	CG3182-PA				SM00100		PF00027	PS50042			G3DSA:1.10.287.70,G3DSA:2.60.120.10	SSF51206,SSF81324									
aly12063.26	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly12063.27	Unknown		n/a																				
aly12063.28	Ubiquitin carboxyl-terminal hydrolase 7	GO:0043234,GO:0005737,GO:0016605,GO:0051090,GO:0006342,GO:0005634,GO:0005700,GO:0004843,GO:0006511,GO:0005515,GO:0007275,GO:0035328,GO:0016579,GO:0016578	CG1490-PB				SM00061		PF00917,PF00443	PS50235,PS50144		PS00973,PS00972	G3DSA:2.20.210.10,G3DSA:2.60.210.10	SSF54001,SSF49599									
aly12063.29	Cyclic nucleotide-gated cation channel subunit A	GO:0030553,GO:0042391,GO:0005249,GO:0071805,GO:0005221,GO:0006812,GO:0005223,GO:0005222,GO:0005622,GO:0019934,GO:0005887,GO:0001666,GO:0055085,GO:0017071	CG42701-PB						PF00027	PS50042,PS50042,PS50042			G3DSA:2.60.120.10,G3DSA:2.60.120.10,G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:2.60.120.10	SSF81324,SSF51206,SSF81324,SSF51206,SSF51206									
aly12063.3	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG1213-PA						PF00083	PS50850	PR00171,PR00171,PR00171	PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						
aly12063.30	Unknown		n/a																				
aly12063.4	Gem-associated protein 6	GO:0005737,GO:0000387,GO:0016604,GO:0000245,GO:0032797,GO:0005634,GO:0097504,GO:0000398,GO:0005654,GO:0010467,GO:0034660,GO:0034719,GO:0005829	n/a						PF06372														
aly12063.5	Probable E3 ubiquitin-protein ligase sinah	GO:0007423,GO:0016874,GO:0005634,GO:0010498,GO:0045676,GO:0016567,GO:0006511,GO:0008270,GO:0004842,GO:0007275	CG2681-PA						PF03145	PS50089,PS51081			G3DSA:3.30.40.10,G3DSA:3.90.890.10	SSF57850,SSF49599					UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly12063.6	60S ribosomal protein L29	GO:0005840,GO:0022625,GO:0005622,GO:0003735,GO:0003682,GO:0006412	CG10071-PA						PF01779														
aly12063.7	Signal recognition particle subunit SRP68	GO:0005786,GO:0030942,GO:0005783,GO:0005047,GO:0005048,GO:0006614,GO:0045047,GO:0008312,GO:0003729	CG5064-PA						PF16969,PF16969						240~260								
aly12063.8	Zinc finger protein 598	GO:0007067,GO:0046872,GO:0008270	CG11414-PA				SM00355,SM00355,SM00355,SM00355		PF13920	PS50089		PS00028	G3DSA:3.30.40.10	SSF57850									
aly12063.9	Protein abnormal spindle	GO:0032027,GO:0051383,GO:0030037,GO:0000226,GO:0007067,GO:0005815,GO:0005874,GO:0005875,GO:0005737,GO:0030954,GO:0005813,GO:0005634,GO:0030706,GO:0000922,GO:0030723,GO:0048477,GO:0008017,GO:0051295,GO:0051297,GO:0007051,GO:0007052,GO:0007282,GO:0048132,GO:0051642,GO:0007017,GO:0000132,GO:0048854,GO:0005515,GO:0007097	CG6875-PA				SM00015,SM00033		PF00307,PF00612,PF00612,PF00612,PF00612,PF00612,PF00612,PF00612,PF00612,PF00612,PF00612	PS50096,PS50096,PS50096,PS50021,PS50096,PS50096,PS50096,PS50096,PS50096,PS50096,PS50096,PS50096		G3DSA:4.10.270.10,G3DSA:1.10.418.10	SSF47576,SSF52540	1032~1052,1949~1969									
aly12072.1	Unknown		n/a																				
aly12072.2	Unknown	GO:0006909	CG16791-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly12072.3	Serine/threonine-protein kinase BRSK2	GO:0006887,GO:0060590,GO:0000086,GO:0036503,GO:0018105,GO:0030010,GO:0007067,GO:0051301,GO:0005783,GO:0005737,GO:0043462,GO:0006487,GO:0031532,GO:0005813,GO:0000287,GO:1904152,GO:0004674,GO:0048471,GO:0005524,GO:0006468,GO:0030182,GO:0051117,GO:0007528,GO:0007409,GO:0061178,GO:0070059,GO:0050321	CG6114-PA																				
aly12072.4	Unknown		n/a																				
aly120763.1	Unknown		n/a																				
aly12082.1	Unknown		n/a																				
aly12082.2	Unknown		n/a																				
aly12082.3	Unknown		n/a																				
aly12089.1	Unknown		n/a																				
aly12089.2	Unknown		n/a																				
aly121005.1	Unknown		n/a												35~53								
aly121157.1	Unknown		n/a																				
aly1215.1	Unknown		n/a										G3DSA:3.40.525.10	SSF46938									
aly1215.2	Unknown		n/a																				
aly1215.3	Unknown		n/a																				
aly1215.4	Unknown	GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG2663-PA						PF00650				G3DSA:3.40.525.10	SSF52087									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1215.5	Alpha-tocopherol transfer protein-like	GO:0005215,GO:0016020,GO:0006810,GO:0005622	CG30339-PA						PF00650	PS50191	PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087									
aly12152.1	Flexible cuticle protein 12	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG6956-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly12152.2	Neurexin-4	GO:0008104,GO:0045216,GO:0019991,GO:0007163,GO:0003015,GO:0016021,GO:0048786,GO:0097105,GO:0060857,GO:0035151,GO:0016081,GO:0016080,GO:0008039,GO:0008366,GO:0005887,GO:0005886,GO:0005919,GO:0005918,GO:0008065,GO:0072553,GO:0007391,GO:0004888,GO:0061343,GO:0021682	CG6827-PA				SM00282,SM00282,SM00181,SM00181		PF02210,PF02210,PF00008,PF00008	PS50025,PS50026,PS50026,PS50025			G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.10.25.10,G3DSA:2.60.120.200	SSF49899,SSF49899,SSF49899,SSF57196									
aly12161.1	Pyruvate carboxylase, mitochondrial	GO:0046872,GO:0006629,GO:0005811,GO:0004736,GO:0009374,GO:0005743,GO:0010629,GO:0005739,GO:0019074,GO:0003677,GO:0005759,GO:0044791,GO:0004075,GO:0006090,GO:0005875,GO:0005524,GO:0006094	CG1516-PI						PF02436					SSF89000									
aly121921.1	Peptidyl-prolyl cis-trans isomerase CWC27 homolog	GO:0000413,GO:0006457,GO:0071011,GO:0071013,GO:0000398,GO:0003755	CG10907-PA												22~42								
aly12195.1	Peroxisomal targeting signal 2 receptor	GO:0007031,GO:0006909,GO:0006635,GO:0001958,GO:0005829,GO:0016558,GO:0005777,GO:0005053,GO:0019899,GO:0001764,GO:0005515,GO:0005782,GO:0008611,GO:0042803	CG6486-PA				SM00320,SM00320		PF00400,PF00400	PS50082,PS50082,PS50294			G3DSA:2.130.10.10	SSF50978									
aly122.1	Unknown		n/a																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly122176.1	Equilibrative nucleoside transporter 1	GO:0006139,GO:0016020,GO:0005337,GO:0016324,GO:0016021,GO:0006810,GO:0015862,GO:0071456,GO:0016323,GO:0007595,GO:0030431,GO:0005887,GO:0071333,GO:0060079,GO:1901642,GO:0005886,GO:0015858,GO:0055085	CG11907-PA						PF01733		PR01130,PR01130						REACT_1698,REACT_15518						
aly1222.1	Gamma-aminobutyric acid type B receptor subunit 2	GO:0038039,GO:0016021,GO:0007214,GO:0045211,GO:0005887,GO:0004965,GO:0007186,GO:0030054	CG3022-PA						PF00003,PF01094	PS50259	PR01177,PR01177,PR01177,PR01177,PR01177,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176		G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300	SSF53822	740~760								
aly1222.10	Neutral ceramidase	GO:0005737,GO:0035187,GO:0017040,GO:0016079,GO:0031629,GO:0005576,GO:0007268,GO:0046514,GO:0006665,GO:0045494	CG1471-PB						PF17048,PF04734							00600+3.5.1.23		PWY-6483,PWY-7119					
aly1222.11	Triokinase/FMN cyclase	GO:0004371,GO:0005975,GO:0070062,GO:0005829,GO:0050354,GO:0005634,GO:0046835,GO:0006071,GO:0044281,GO:0061624,GO:0034012,GO:0044262,GO:0046872,GO:0006000,GO:0045087,GO:0005524,GO:0045088	n/a						PF02733,PF02734	PS51480,PS51481			G3DSA:3.40.50.10440,G3DSA:3.30.1180.20	SSF82549,SSF101473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1222.12	STE20-related kinase adapter protein alpha	GO:0060439,GO:0032147,GO:0030036,GO:0042981,GO:0007049,GO:0043408,GO:0005737,GO:0007346,GO:0007430,GO:0005634,GO:0019991,GO:0031098,GO:0006611,GO:0023014,GO:0004672,GO:0016477,GO:0005524,GO:0006468,GO:0007266,GO:0030295,GO:0007015,GO:0004702	CG5169-PA										G3DSA:1.10.510.10	SSF56112									
aly1222.13	STE20-related kinase adapter protein alpha	GO:0005737,GO:0006468,GO:0006611,GO:0005634,GO:0032147,GO:0004674,GO:0005524,GO:0004672,GO:0030295,GO:0007049	CG40293-PA						PF00069	PS50011			G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1222.14	Nesprin-1	GO:0005640,GO:0015629,GO:0007498,GO:0060361,GO:0008335,GO:0030017,GO:0007303,GO:0030018,GO:0005737,GO:0005654,GO:0090286,GO:0040023,GO:0016021,GO:0005635,GO:0007519,GO:0003779,GO:0006366,GO:0048471,GO:0016477,GO:0042803,GO:0005794,GO:0044822,GO:0031965,GO:0051015,GO:0008305,GO:0045211,GO:0034993,GO:0005884,GO:0090292,GO:0007523,GO:0051640,GO:0040011,GO:0007015,GO:0007030,GO:0005521,GO:0007010,GO:0008092,GO:0005856,GO:0003725,GO:0042692,GO:0005634	CG42768-PL				SM00150,SM00033,SM00033		PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00307,PF00307	PS50021,PS50021	PS00019,PS00020	G3DSA:1.20.58.60,G3DSA:1.10.418.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.10.418.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60	SSF46966,SSF47576,SSF46966	4920~4944,6483~6503,5241~5261,6900~6941,5694~5714,7176~7196,4967~4987,6270~6290,4428~4448,6000~6020,2403~2441,5407~5438,1486~1511,4754~4774,6371~6391,6773~6793,892~912,2462~2489,2923~2943,6515~6535,5948~5968,2672~2699,5192~5212,1637~1657,7778~7805,2730~2750,5617~5637,4385~4412,7600~7637,859~882,4597~4617,2603~2641,7328~7386,7861~7864,7288~7315,5090~5110,4015~4035,7438~7458,3091~3111,151~171,51								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1222.15	Nesprin-1	GO:0005640,GO:0015629,GO:0007498,GO:0060361,GO:0008335,GO:0030017,GO:0007303,GO:0030018,GO:0005737,GO:0005654,GO:0090286,GO:0040023,GO:0016021,GO:0005635,GO:0007519,GO:0003779,GO:0006366,GO:0048471,GO:0016477,GO:0042803,GO:0005794,GO:0006997,GO:0044822,GO:0031965,GO:0051015,GO:0008305,GO:0045211,GO:0034993,GO:0005884,GO:0090292,GO:0007523,GO:0051640,GO:0040011,GO:0007015,GO:0007030,GO:0005521,GO:0007010,GO:0008092,GO:0005856,GO:0003725,GO:0042692,GO:0005634	CG33715-PG						PF10541	PS51049			G3DSA:1.20.58.60,G3DSA:1.20.58.60	SSF46966,SSF46966,SSF46966,SSF46966	1227~1247,6875~6895,7592~7612,7774~7801,7902~7929,2082~2102,7048~7068,395~429,8213~8233,8033~8063,7462~7482,3291~3311,6491~6511,3339~3366,3248~3268,8128~8148,3370~3390								
aly1222.16	Peripherin-2	GO:0016021,GO:0007601,GO:0008150,GO:0007155,GO:0003674,GO:0009645	CG14936-PA						PF00335					SSF48652,SSF48652									
aly1222.17	Dynein-1-beta heavy chain, flagellar inner arm I1 complex	GO:0036156,GO:0008152,GO:0031514,GO:0008017,GO:0036159,GO:0060294,GO:0005875,GO:0003774,GO:0003777,GO:0016887,GO:0005874,GO:0005930,GO:0005524	CG9068-PA						PF08385						292~312								
aly1222.18	SprT-like domain-containing protein Spartan	GO:0016607,GO:0004478,GO:0006281,GO:0006556,GO:0005634,GO:0019985,GO:0006974,GO:0009411,GO:0031398,GO:0003677,GO:0070530,GO:0046872,GO:0005694,GO:0043130	CG9203-PA				SM00731,SM00734,SM00734,SM00734		PF10263														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1222.19	Dynein heavy chain 2, axonemal	GO:0036156,GO:0042623,GO:0031512,GO:0007018,GO:0005858,GO:0003774,GO:0001539,GO:0003777,GO:0016887,GO:0030286,GO:0005874,GO:0005875,GO:0005524	CG17866-PB				SM00382,SM00382		PF12777,PF12774,PF12781,PF08393,PF12780,PF12775,PF03028,PF03028				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540	452~479,2497~2562,2301~2321,401~428,53~73,941~961								
aly1222.2	Probable ATP-dependent RNA helicase DDX28	GO:0005737,GO:0042645,GO:0016063,GO:0005730,GO:0005634,GO:0004004,GO:0004386,GO:0005739,GO:0003676,GO:0010501,GO:0044822,GO:0005524	CG3561-PA				SM00487,SM00490		PF00270,PF00271	PS51192,PS51194,PS51195			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									
aly1222.20	Unknown	GO:0035099,GO:0005172,GO:0008083,GO:0016020,GO:0008039,GO:0007435,GO:0048010	CG31629-PA						PF00341	PS50278			G3DSA:2.10.90.10	SSF57501									
aly1222.21	Protein FAM151A	GO:0016021	CG7231-PE						PF10223	PS50007													
aly1222.22	Protein croquemort	GO:0006909,GO:0042116,GO:0005886,GO:0048102,GO:0050764,GO:0016063,GO:0016021,GO:0016020,GO:0090382,GO:0035071,GO:0006915,GO:0007602,GO:0006952,GO:0005887,GO:0006955,GO:0007155,GO:0006911,GO:0005044,GO:0043052,GO:0006898,GO:0016116,GO:0002433	CG12789-PA						PF01130		PR01609,PR01609,PR01609,PR01609,PR01609												
aly1222.23	Protein croquemort	GO:0050764,GO:0006915,GO:0006909,GO:0035071,GO:0006898,GO:0042116,GO:0005044,GO:0002433,GO:0016020,GO:0090382,GO:0006911,GO:0006952,GO:0048102,GO:0005887,GO:0006955,GO:0007155,GO:0005886,GO:0016021	CG4280-PA						PF01130		PR01609,PR01609,PR01609,PR01609												
aly1222.24	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1222.25	Protein croquemort	GO:0050764,GO:0006915,GO:0006909,GO:0035071,GO:0006898,GO:0042116,GO:0005044,GO:0002433,GO:0016020,GO:0090382,GO:0006911,GO:0006952,GO:0048102,GO:0005887,GO:0006955,GO:0007155,GO:0005886,GO:0016021	CG4280-PA						PF01130		PR01609,PR01609,PR01609,PR01609,PR01609												
aly1222.26	Stress-induced-phosphoprotein 1	GO:0005737,GO:0005634,GO:0006457,GO:0051082,GO:0005515	CG2720-PA				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00727,SM00727		PF13414,PF13414,PF13414,PF00515,PF00515,PF00515	PS50005,PS50005,PS50293,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452	105~136								
aly1222.27	Protein mothers against dpp	GO:0042078,GO:0008586,GO:0003705,GO:0045887,GO:0048100,GO:0003677,GO:0035556,GO:0001745,GO:0005737,GO:0043565,GO:2000134,GO:0005634,GO:0007476,GO:0030707,GO:0061353,GO:0046872,GO:0045705,GO:0005667,GO:0007480,GO:0007424,GO:0007488,GO:0001105,GO:0045595,GO:0001102,GO:0035019,GO:0007179,GO:0035290,GO:0007507,GO:0030618,GO:0003700,GO:0010629,GO:0007391,GO:0005622,GO:0006355,GO:0006357,GO:0045944,GO:0005515,GO:0060799,GO:0000980,GO:0030718	CG12399-PB				SM00524,SM00523		PF03165,PF03166	PS51075,PS51076			G3DSA:3.90.520.10,G3DSA:2.60.200.10	SSF56366,SSF49879	48~68								
aly1222.28	Unknown	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG15884-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly1222.29	Unknown	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG6131-PA						PF00379	PS51257,PS51155													
aly1222.3	Glucose dehydrogenase [FAD, qui]	GO:0005575,GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0045455,GO:0055114,GO:0016491	CG45065-PA			PIRSF000137			PF05199,PF00732			PS00623,PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1222.30	Unknown	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG6131-PA						PF00379	PS51155													
aly1222.31	Unknown	GO:0042302	CG8927-PC						PF00379	PS51155	PR00947,PR00947,PR00947				351~386								
aly1222.32	DDB1- and CUL4-associated factor 7	GO:0005737,GO:0043234,GO:0007517,GO:0045927,GO:0080008,GO:0005654,GO:0016567,GO:0016363,GO:0007275,GO:0035332	CG14614-PA				SM00320,SM00320,SM00320,SM00320,SM00320			PS50294,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978										
aly1222.33	Spermatogenesis-associated protein 5	GO:0005737,GO:0005783,GO:0030154,GO:0005739,GO:0007283,GO:0016887,GO:0007275,GO:0005524	CG5776-PA				SM00382,SM00382		PF00004,PF00004			PS00674	G3DSA:1.10.8.60,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.8.60	SSF52540,SSF52540										
aly1222.34	Gamma-secretase subunit Aph-1	GO:0055037,GO:0007219,GO:0016021,GO:0005770,GO:0070765,GO:0004175,GO:0005887,GO:0005886,GO:0016485,GO:0008593,GO:0043085	CG2855-PA						PF06105								REACT_299,REACT_11061						
aly1222.35	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1222.36	Embryonic polarity protein dorsal	GO:0035206,GO:0007498,GO:0038061,GO:0008063,GO:0006964,GO:0031594,GO:0007419,GO:0008358,GO:0001077,GO:0035006,GO:0003677,GO:0008354,GO:0070491,GO:0005737,GO:0043565,GO:0000381,GO:0000122,GO:0005634,GO:0007369,GO:0009950,GO:0005654,GO:0006366,GO:0033256,GO:0042387,GO:0034097,GO:0070379,GO:0016015,GO:0006952,GO:0045892,GO:0045893,GO:0006954,GO:0006955,GO:0009953,GO:0007507,GO:0001715,GO:0009952,GO:0007398,GO:0003700,GO:0005829,GO:0007501,GO:0007249,GO:0010629,GO:0006355,GO:0010004,GO:0045944,GO:0000977,GO:0005515,GO:0048935,GO:0003682,GO:0003705	CG6667-PF				SM00429		PF16179,PF00554	PS50254	PR00057,PR00057,PR00057,PR00057	PS01204	G3DSA:2.60.40.10,G3DSA:2.60.40.340	SSF49417,SSF81296										
aly1222.37	Apoptosis-resistant E3 ubiquitin protein ligase 1	GO:0005737,GO:0016874,GO:0005634,GO:0006915,GO:0043066,GO:0042787,GO:0004842,GO:0005829	CG4238-PD				SM00119		PF00632	PS50237			G3DSA:3.30.2160.10	SSF56204					UPA00143				
aly1222.38	Apoptosis-resistant E3 ubiquitin protein ligase 1	GO:0005737,GO:0016874,GO:0005634,GO:0006915,GO:0043066,GO:0042787,GO:0004842,GO:0005829	CG4238-PD										G3DSA:2.60.40.10	SSF81296									
aly1222.39	Peroxiredoxin-5, mitochondrial	GO:0045824,GO:0051920,GO:0005829,GO:0005777,GO:0005739,GO:0006979,GO:0043066,GO:0004601,GO:0008340,GO:0045454,GO:0005634,GO:0016209,GO:0016491	CG7217-PA						PF08534	PS51352			G3DSA:3.40.30.10	SSF52833									
aly1222.4	Transcriptional protein SWT1		CG7206-PB				SM00670		PF13638	PS50020			G3DSA:3.40.50.1010,G3DSA:2.20.70.10	SSF51045,SSF88723	51~71								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1222.40	Transportin-3	GO:0005737,GO:0043231,GO:0035048,GO:0008536,GO:0005634,GO:0006606,GO:0042802,GO:0005515,GO:0048024,GO:0022008,GO:0006406	CG2848-PA						PF08389				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371									
aly1222.41	Chromatin assembly factor 1 subunit B	GO:0031497,GO:0006281,GO:0006355,GO:0006334,GO:0003677,GO:0006333,GO:0045747,GO:0006260,GO:0006351,GO:0005515,GO:0033186,GO:0005634,GO:0007049	CG12892-PA				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50294,PS50082,PS50082,PS50082	PR00319,PR00319,PR00319	PS00678	G3DSA:2.130.10.10	SSF50978									
aly1222.42	WASH complex subunit CCDC53	GO:0043231,GO:0015031,GO:0071203,GO:0015629,GO:0005769	CG7429-PA						PF10152						44~71								
aly1222.43	Pre-mRNA-splicing factor SPF27	GO:0005730,GO:0071011,GO:0071013,GO:0000398,GO:0008380,GO:0005681,GO:0006397	CG4980-PA						PF05700						186~206								
aly1222.44	Ubiquitin thioesterase otubain-like	GO:0005575,GO:0019538,GO:0008242,GO:0071108,GO:0004843	CG4968-PA			PIRSF013503			PF10275	PS50802				SSF54001									
aly1222.45	Putative E3 ubiquitin-protein ligase UBR7	GO:0016874,GO:0004842,GO:0008270,GO:0016567	CG15141-PA				SM00396		PF02207	PS51157			G3DSA:3.30.40.10	SSF57903									
aly1222.46	Radial spoke head protein 9 homolog	GO:0005737,GO:0005856,GO:0003674,GO:0035082,GO:0005575,GO:0008150,GO:0005929,GO:0003341	CG31803-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1222.47	Fork head domain transcription factor slp2	GO:0030154,GO:0009792,GO:0009653,GO:0043565,GO:0007346,GO:0045787,GO:0000122,GO:0007380,GO:0006355,GO:0005634,GO:0045665,GO:0003690,GO:0000981,GO:0048665,GO:0035058,GO:0008134,GO:0009888,GO:0008301,GO:0007367,GO:0051090,GO:0009953,GO:0003700,GO:0007365,GO:0003705,GO:0016199,GO:0002052,GO:0006357,GO:0045944,GO:0006351,GO:0005667	CG2939-PA				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00658	G3DSA:1.10.10.10	SSF46785									
aly1222.48	Fork head domain transcription factor slp2	GO:0030154,GO:0009792,GO:0009653,GO:0043565,GO:0007346,GO:0045787,GO:0000122,GO:0007380,GO:0006355,GO:0005634,GO:0045665,GO:0003690,GO:0000981,GO:0048665,GO:0035058,GO:0008134,GO:0009888,GO:0008301,GO:0007367,GO:0051090,GO:0009953,GO:0003700,GO:0007365,GO:0003705,GO:0016199,GO:0002052,GO:0006357,GO:0045944,GO:0006351,GO:0005667	CG2939-PA				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00658	G3DSA:1.10.10.10	SSF46785									
aly1222.49	Unknown		n/a																				
aly1222.5	Acylglycerol kinase, mitochondrial	GO:0043231,GO:0016301,GO:0007205,GO:0001729,GO:0005739,GO:0046513,GO:0007280,GO:0047620,GO:0003951,GO:0046486,GO:0031966,GO:0004143,GO:0006672,GO:0005524	CG31873-PA				SM00046		PF00781	PS50146				SSF111331,SSF111331									
aly1222.50	Unknown		n/a																				
aly1222.51	Protein lethal(2)denticless	GO:0005737,GO:0051726,GO:0005634,GO:0016567,GO:0005515,GO:0022008,GO:0007049	CG11295-PA				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50082,PS50082,PS50294,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10	SSF50978,SSF50978									
aly1222.52	Protein lethal(2)denticless	GO:0005737,GO:0051726,GO:0005634,GO:0016567,GO:0022008,GO:0007049	CG11295-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1222.53	Unknown		n/a																				
aly1222.54	Unknown		n/a																				
aly1222.55	Transmembrane protein 147	GO:0016021,GO:0006909	CG5861-PA						PF09767														
aly1222.56	Unknown		n/a																				
aly1222.57	Unknown		n/a						PF00804				G3DSA:1.20.58.70	SSF47661			REACT_11184						
aly1222.58	POU domain, class 2, transcription factor 3	GO:0035220,GO:0007419,GO:0001077,GO:0003677,GO:0008544,GO:0005737,GO:0007389,GO:0005634,GO:0036022,GO:0005654,GO:0006366,GO:0030216,GO:0043565,GO:0042060,GO:0043922,GO:0007402,GO:0007400,GO:0003700,GO:0048813,GO:0006357,GO:0045944,GO:0005667,GO:0000978	CG6246-PA				SM00389,SM00352		PF00046,PF00157	PS51179,PS50071	PR00028,PR00028,PR00028,PR00028,PR00028	PS00035,PS00465,PS00027	G3DSA:1.10.260.40,G3DSA:1.10.10.60	SSF47413,SSF46689										
aly1222.59	Unknown		n/a																				
aly1222.6	Probable methyltransferase TARBP1	GO:0008173,GO:0005634,GO:0006357,GO:0003723,GO:0006396	CG18596-PA						PF00588				G3DSA:3.40.1280.10	SSF75217									
aly1222.60	Unknown		n/a																				
aly1222.61	Unknown		n/a							PS51257				SSF57567									
aly1222.62	Dynein heavy chain 2, axonemal	GO:0008152,GO:0042623,GO:0007018,GO:0005858,GO:0003774,GO:0001539,GO:0005524,GO:0016887,GO:0030286,GO:0005874,GO:0005875,GO:0003777	CG17866-PB						PF03028														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1222.63	Embryonic polarity protein dorsal	GO:0035206,GO:0007498,GO:0038061,GO:0008063,GO:0006964,GO:0031594,GO:0007419,GO:0008358,GO:0001077,GO:0035006,GO:0003677,GO:0008354,GO:0070491,GO:0005737,GO:0043565,GO:0000381,GO:0000122,GO:0005634,GO:0007369,GO:0009950,GO:0005654,GO:0006366,GO:0033256,GO:0042387,GO:0034097,GO:0070379,GO:0016015,GO:0006952,GO:0045892,GO:0045893,GO:0006954,GO:0006955,GO:0009953,GO:0007507,GO:0001715,GO:0009952,GO:0007398,GO:0003700,GO:0005829,GO:0007501,GO:0007249,GO:0010629,GO:0006355,GO:0010004,GO:0045944,GO:0000977,GO:0005515,GO:0048935,GO:0003682,GO:0003705	CG6667-PF																					
aly1222.7	DDB1- and CUL4-associated factor 8	GO:0005737,GO:0005634,GO:0005515	CG8001-PA				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50082,PS50082,PS50294			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978										
aly1222.8	Unknown		n/a												68~88								
aly1222.9	Neutral ceramidase	GO:0005737,GO:0035187,GO:0017040,GO:0016079,GO:0031629,GO:0005576,GO:0007268,GO:0046514,GO:0006665,GO:0045494	CG1471-PB						PF04734,PF17048	PS51257						00600+3.5.1.23		PWY-6483,PWY-7119					
aly12255.1	Unknown		n/a																				
aly122637.1	Beta-1,3-glucan-binding protein	GO:0045087,GO:0005975,GO:0045088,GO:0008329,GO:0009620,GO:0009986,GO:0002758,GO:0005576,GO:0004553,GO:0052736,GO:0032491,GO:0001872	CG5008-PA										G3DSA:2.60.120.200	SSF49899									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly12285.1	Protein takeout	GO:0007631,GO:0007623,GO:0005615,GO:0032504,GO:0007617,GO:0005576,GO:0042594,GO:0042595,GO:0008343,GO:0008049,GO:0007622	CG10407-PA				SM00700		PF06585														
aly12285.2	3-oxoacyl-[acyl-carrier-protein] reductase FabG	GO:0050661,GO:0051287,GO:0030497,GO:0004316,GO:0008152,GO:0016491	CG31548-PA				SM00822		PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080	PS00061	G3DSA:3.40.50.720	SSF51735									
aly12285.3	Tubulin alpha chain	GO:0045298,GO:0051258,GO:0005200,GO:0019730,GO:0007017,GO:0005813,GO:0009987,GO:0003924,GO:0005737,GO:0007052,GO:0005819,GO:0000235,GO:0007094,GO:0006184,GO:0005874,GO:0005525	CG1913-PA				SM00864,SM00865		PF00091,PF03953		PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162	PS00227	G3DSA:3.30.1330.20,G3DSA:3.40.50.1440,G3DSA:1.10.287.600	SSF52490,SSF55307	416~435									
aly1229.1	Unknown		n/a																				
aly1229.10	Senecionine N-oxygenase	GO:0050661,GO:0050660,GO:0043231,GO:0009820,GO:0005829,GO:0051289,GO:0004499,GO:0004497,GO:0005739,GO:0005576,GO:0033784,GO:0055114	CG3006-PA						PF00743,PF00743		PR00370,PR00370,PR00370,PR00370,PR00370		G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905									
aly1229.11	Sodium-independent sulfate anion transporter	GO:0005794,GO:0005783,GO:0015301,GO:0005215,GO:0016021,GO:0005886,GO:0015116,GO:0005765,GO:0008271,GO:0008272,GO:0098656,GO:0008509,GO:0015381,GO:0070062	CG5002-PA						PF00916														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1229.2	Unknown	GO:0003677	CG8359-PA				SM00595		PF02944,PF10545	PS51029,PS51031													
aly1229.3	Unknown		n/a																				
aly1229.4	Solute carrier family 23 member 2	GO:0006810,GO:0005215,GO:0016021,GO:0016020,GO:0070890,GO:0008520,GO:0055085	CG6293-PA						PF00860,PF00860			PS01116											
aly1229.5	Unknown	GO:0005575,GO:0008150,GO:0003674	CG40498-PG																				
aly1229.6	Unknown		n/a																				
aly1229.7	Unknown		n/a																				
aly1229.8	Transcription factor Adf-1	GO:0040011,GO:0006366,GO:0050773,GO:0007616,GO:0005634,GO:0005705,GO:0007613,GO:0007611,GO:0001077,GO:0048813,GO:0006357,GO:0045944,GO:0045893,GO:0005667,GO:0003677,GO:0008345,GO:0003712,GO:0007416,GO:0008355	CG15845-PE				SM00595		PF10545,PF02944	PS51029,PS51031													
aly1229.9	Protein winged eye	GO:0031507,GO:0006342,GO:0030154,GO:0007560,GO:0005654,GO:0000785,GO:0005677,GO:0000976,GO:0003682	CG31151-PD				SM00439		PF01426	PS51038					864~884,928~955,1080~1100								
aly123.1	Unknown	GO:0046872,GO:0003676	CG32767-PC				SM00355,SM00355		PF13894	PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60	SSF57667									
aly123.10	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly123.11	Transmembrane protease serine 11D	GO:0004252,GO:0070062,GO:0045087,GO:0007585,GO:0050832,GO:0050830,GO:0005576,GO:0005887,GO:0045752,GO:0050829,GO:0006508,GO:0008233	CG2056-PB				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly123.12	Unknown		CG7031-PA																				
aly123.13	Zinc finger protein 45	GO:0006367,GO:0003700,GO:0005634,GO:0005654,GO:0006355,GO:0010467,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0007275	CG6808-PA				SM00868,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57716									
aly123.14	Unknown	GO:0005575,GO:0007606,GO:0003674	CG33996-PB				SM00409,SM00409,SM00408,SM00408		PF00047,PF07686	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly123.15	Unknown		n/a																				
aly123.2	Unknown	GO:0000166	n/a										G3DSA:3.30.70.330	SSF54928	848~869								
aly123.3	Endoplasmic reticulum metallopeptidase 1	GO:0016021,GO:0005789,GO:0006508,GO:0008233,GO:0046872,GO:0008237	CG11961-PA						PF04389				G3DSA:3.40.630.10	SSF53187									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly123.4	Insulin gene enhancer protein ISL-1	GO:0008284,GO:0035066,GO:0008258,GO:0060413,GO:0008045,GO:0071385,GO:0032760,GO:0001158,GO:0021559,GO:0001077,GO:0043524,GO:0008270,GO:0003677,GO:0043388,GO:0007411,GO:0035310,GO:0003139,GO:0007362,GO:0060913,GO:0050728,GO:0003266,GO:0003203,GO:0060384,GO:0010575,GO:0005634,GO:0005654,GO:0048880,GO:0008407,GO:0005739,GO:0045665,GO:0032024,GO:0007521,GO:0032729,GO:0021520,GO:0048936,GO:0032725,GO:0010468,GO:0000980,GO:0090090,GO:0031290,GO:0033147,GO:0031016,GO:0031103,GO:0030331,GO:0060379,GO:0090074,GO:0032735,GO:0060037,GO:0006366,GO:0001105,GO:0022416,GO:0055010,GO:0001102,GO:0045766,GO:0001755,GO:0046665,GO:0042517,GO:0016922,GO:0043433,GO:0021983,GO:0007507,GO:0000122,GO:0003215,GO:0071657,GO:0003148,GO:0070983,GO:0043565,GO:0003705,GO:0007391,GO:0007390,GO:0006355,GO:0021524,GO:0045944,GO:0000977,GO:0005515,GO:0008293,GO:0048542,GO:0000978,GO:0003682,GO:0032731,GO:0032730,GO:0032755	CG10619-PA				SM00389,SM00132,SM00132		PF00412,PF00412,PF00046	PS50023,PS50023,PS50071		PS00027,PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:1.10.10.60,G3DSA:2.10.110.10	SSF57716,SSF57716,SSF46689	274~294									
aly123.5	Unknown		n/a																				
aly123.6	S phase cyclin A-associated protein in the endoplasmic reticulum	GO:0005737,GO:0005819,GO:0005783,GO:0005634,GO:0005654,GO:0000022,GO:0046872	CG18397-PA						PF16501						1685~1712,1756~1776,1489~1509,1657~1677,1540~1570,1297~1324,1326~1368								
aly123.7	40S ribosomal protein S11	GO:0005737,GO:0016020,GO:0022627,GO:0005730,GO:0044822,GO:0022008,GO:0019843,GO:0003735,GO:0007052,GO:0000022,GO:0000228,GO:0005925,GO:0006412,GO:0001649,GO:0070062	CG8857-PC	MF_01345_B				TIGR03630	PF00366,PF16205		PR00973,PR00973,PR00973	PS00056	G3DSA:2.40.50.140	SSF50249									
aly123.8	MIP18 family protein CG30152	GO:0005737,GO:0016226,GO:0005575,GO:0008150,GO:0007059,GO:0003674	CG30152-PA						PF01883					SSF117916									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly123.9	Autophagy-related protein 13 homolog	GO:0019901,GO:0045850,GO:0000407,GO:0019887,GO:0006914,GO:0070969,GO:0034273,GO:0032147,GO:0035096,GO:0003674,GO:0000045,GO:0010506,GO:0005829	CG7331-PA						PF10033														
aly1231.1	Leucine zipper putative tumor suppressor 2 homolog	GO:0000910,GO:0005737,GO:0051168,GO:0051013,GO:0005813,GO:0016055,GO:0030496,GO:0051255,GO:0007067,GO:0005874,GO:0030178	CG15365-PB						PF06818						386~406,241~328,432~452								
aly1231.2	Glutamate receptor ionotropic, kainate 2	GO:0007268,GO:0019228,GO:0050806,GO:0030425,GO:0030424,GO:0008066,GO:0043524,GO:0050907,GO:0005929,GO:0060080,GO:0046328,GO:0048169,GO:0035249,GO:0030054,GO:0001662,GO:0045202,GO:0032983,GO:0071683,GO:0006886,GO:0016020,GO:0015277,GO:0004970,GO:0042802,GO:0042803,GO:0007165,GO:0007608,GO:0032839,GO:0035235,GO:0006874,GO:0006811,GO:0031624,GO:0005234,GO:0034220,GO:0051402,GO:0030165,GO:0014069,GO:0005887,GO:0005886,GO:0060079,GO:0043204,GO:0008328,GO:0031625,GO:0043195,GO:0042734,GO:0045211,GO:0051967,GO:0048172,GO:0043113,GO:0016021,GO:0043525	CG15627-PC				SM00918,SM00079		PF10613,PF00060		PR00177,PR00177,PR00177		G3DSA:1.10.287.70,G3DSA:3.40.190.10	SSF81324,SSF53850,SSF53850,SSF53850,SSF53822									
aly1231.3	Unknown		n/a																				
aly1231.4	Catalase-2	GO:0005737,GO:0020037,GO:0004601,GO:0042744,GO:0004096,GO:0008340,GO:0046872,GO:0006979,GO:0055114	CG9314-PA			PIRSF038928	SM01060		PF00199,PF06628	PS51402	PR00067,PR00067,PR00067,PR00067,PR00067,PR00067,PR00067		G3DSA:2.40.180.10	SSF56634		00630+1.11.1.6,00380+1.11.1.6		PWY-5506					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1231.5	Diuretic hormone class 2	GO:0007218,GO:0005184,GO:0005615,GO:0010579,GO:0007589,GO:0007186,GO:0010841,GO:0001664,GO:0008613	CG13094-PC																				
aly1231.6	Unknown	GO:0005549	n/a										G3DSA:1.10.238.20										
aly1231.7	Serpin B10	GO:0005737,GO:0005615,GO:0005634,GO:0005575,GO:0008150,GO:0004867	CG43366-PB				SM00093		PF00079			PS00284	G3DSA:2.30.39.10,G3DSA:2.30.39.10,G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574,SSF56574	879~899								
aly12325.1	Unknown	GO:0006952	n/a				SM00505,SM00505,SM00505,SM00505																
aly12325.2	Membrane-associated progesterone receptor component 2	GO:0035100,GO:0020037,GO:0016021,GO:0016020,GO:0012505,GO:0005886,GO:0005496	CG9066-PA						PF00173				G3DSA:3.10.120.10	SSF55856									
aly1236.1	Probable nucleoporin Nup58	GO:0005643,GO:0006913,GO:0048812,GO:0015031,GO:0005487,GO:0051028	CG7360-PA						PF15967						330~350								
aly1236.2	B-box type zinc finger protein ncl-1	GO:0006909,GO:1900242,GO:0008270,GO:0007411,GO:0035282,GO:0008356,GO:0022008,GO:0005737,GO:0050767,GO:0045179,GO:0008582,GO:0048477,GO:0008285,GO:0030182,GO:0030371,GO:0009303,GO:0055060,GO:0045180,GO:0045182,GO:0007406,GO:0007405,GO:0007402,GO:0016072,GO:0007420,GO:0051726,GO:0043025,GO:0090071,GO:0005515,GO:0006417	CG10719-PE				SM00336,SM00336,SM00184,SM00502		PF00643,PF01436,PF01436,PF01436,PF00097	PS51125,PS51125,PS50089,PS51125,PS50119,PS51125,PS50119,PS51125		PS00518	G3DSA:3.30.40.10,G3DSA:2.120.10.30,G3DSA:4.10.45.10	SSF57845,SSF57850,SSF101898									
aly1236.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1236.4	Unknown		n/a																				
aly123719.1	Unknown		n/a																				
aly1238.1	MORN repeat-containing protein 5		CG3222-PA				SM00698,SM00698		PF02493,PF02493				G3DSA:2.20.110.10	SSF82185									
aly1238.10	Kv channel-interacting protein 4	GO:0005737,GO:0005267,GO:0005244,GO:0005509,GO:0005886	CG44422-PA				SM00054,SM00054,SM00054		PF13833,PF13499	PS50222,PS50222,PS50222	PR00450,PR00450,PR00450,PR00450,PR00450,PR00450	PS00018,PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly1238.2	DnaJ homolog subfamily C member 21	GO:0006457,GO:0005840,GO:0044822,GO:0008270,GO:0003676,GO:0046872	CG2790-PA				SM00355,SM00355,SM00451,SM00271		PF00226,PF12171	PS50157,PS50076	PR00625,PR00625,PR00625,PR00625	PS00028,PS00028,PS00636	G3DSA:1.10.287.110	SSF57667,SSF46565	39~59,220~240,180~200								
aly1238.3	Unknown		n/a																				
aly1238.4	Unknown		n/a																				
aly1238.5	Unknown	GO:0008080	CG15628-PA						PF08445	PS51186			G3DSA:3.40.630.30	SSF55729									
aly1238.6	Protein SON	GO:0000910,GO:0016607,GO:0006351,GO:0051726,GO:0050733,GO:0043484,GO:0044822,GO:0043066,GO:0005654,GO:0006355,GO:0003725,GO:0000226,GO:0003723,GO:0003676,GO:0003677,GO:0008380,GO:0006397	CG8273-PA				SM00443,SM00358		PF01585,PF14709	PS50137,PS50174			G3DSA:3.30.160.20	SSF54768	225~248,279~299								
aly1238.7	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	GO:0005737,GO:0097428,GO:0006879,GO:0051539,GO:0051536,GO:0051537,GO:0009399,GO:0005739,GO:0016226,GO:0008198,GO:0036455,GO:0032947,GO:0044571,GO:0005759,GO:0005506,GO:0005634,GO:0005829,GO:0044281	CG9836-PA					TIGR01999	PF01592				G3DSA:3.90.1010.10	SSF82649									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1238.8	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	GO:0005737,GO:0005794,GO:0006982,GO:0005739,GO:0006979,GO:0004602,GO:0007275,GO:0004601,GO:0055114,GO:0047066	CG12013-PD			PIRSF000303			PF00255	PS51355	PR01011,PR01011,PR01011	PS00763,PS00460	G3DSA:3.40.30.10	SSF52833									
aly1238.9	Lamin-B receptor	GO:0005635,GO:0016628,GO:0005637,GO:0016021,GO:0016020,GO:0004872,GO:0003677,GO:0005521	CG17952-PC						PF01222								REACT_22258						
aly1239.1	Tachykinin-like peptides receptor 99D	GO:0007218,GO:0042048,GO:0016021,GO:0008188,GO:0007217,GO:0050805,GO:0050911,GO:0005887,GO:0005886,GO:0004995,GO:0007186	CG7887-PC							PS50262			G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly12397.1	Unknown		n/a																				
aly12397.2	Unknown		n/a																				
aly1244.1	Unknown		CG30053-PA																				
aly1244.10	Unknown		n/a																				
aly1244.11	Unknown	GO:0046872	CG15725-PA							PS50157		PS00028											
aly1244.12	Unknown		n/a								PR01217,PR01217,PR01217,PR01217												

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1244.13	Nuclear receptor corepressor 2	GO:0003714,GO:0006909,GO:0044281,GO:0003677,GO:0005654,GO:0007346,GO:0007219,GO:0000122,GO:0006325,GO:0005634,GO:0016020,GO:0007476,GO:0045746,GO:0010467,GO:0006367,GO:0016363,GO:0042826,GO:0005112,GO:0017053,GO:0016604,GO:0045892,GO:0044255,GO:0007179,GO:0047485,GO:0072365,GO:0005700,GO:0006351,GO:0005515,GO:0003682	CG4013-PG				SM00717		PF15784	PS51293				SSF46689	165~185									
aly1244.14	Transcription factor Adf-1	GO:0040011,GO:0006366,GO:0050773,GO:0003700,GO:0005634,GO:0005705,GO:0007613,GO:0007611,GO:0007616,GO:0048813,GO:0001077,GO:0045892,GO:0045893,GO:0005667,GO:0003677,GO:0045944,GO:0008345,GO:0003712,GO:0007416,GO:0008355	CG45071-PA				SM00595		PF10545,PF02944	PS51029,PS51031														
aly1244.15	Unknown	GO:0003677	CG8359-PA				SM00595		PF02944,PF10545	PS51031,PS51029														
aly1244.16	Unknown	GO:0003677	CG8359-PA				SM00595		PF10545,PF02944	PS51031,PS51029														
aly1244.2	Unknown		n/a																				
aly1244.3	Unknown		n/a																				
aly1244.4	Ataxin-2 homolog	GO:0006909,GO:0042051,GO:0009994,GO:0007616,GO:0034063,GO:0046959,GO:0090328,GO:0005737,GO:0032092,GO:0030833,GO:0097167,GO:0048749,GO:0044822,GO:0010603,GO:0060965,GO:0022416,GO:0045475,GO:1901216,GO:0022008,GO:0010494,GO:0005515,GO:0051823	CG5166-PB						PF06741,PF14438															
aly1244.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1244.6	Retinol dehydrogenase 11	GO:0016614,GO:0016062,GO:0004745,GO:0016021,GO:0052650,GO:0005789,GO:0001917,GO:0008152,GO:0042572,GO:0005622,GO:0042574	CG7675-PB						PF00106		PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735	99~119								
aly1244.7	Unknown		n/a																				
aly1244.8	Vacuolar protein sorting-associated protein 45	GO:0008021,GO:0016021,GO:0006897,GO:0016192,GO:0006904,GO:0006886,GO:0016082,GO:0000149,GO:0006605,GO:0048227,GO:0015031,GO:0005515,GO:0007040,GO:0007269,GO:0000139,GO:0005769,GO:0034058,GO:0010008	CG8228-PA			PIRSF005715			PF00995				G3DSA:1.25.40.60,G3DSA:3.90.830.10,G3DSA:3.40.50.2060,G3DSA:3.40.50.1910,G3DSA:3.40.50.1910	SSF56815	354~374									
aly1244.9	Malate dehydrogenase, mitochondrial	GO:0046554,GO:0035209,GO:0006475,GO:0006734,GO:0006099,GO:0044281,GO:0006094,GO:0044262,GO:0070062,GO:0043209,GO:0005634,GO:0005811,GO:0005739,GO:0005654,GO:0043067,GO:0005759,GO:0043068,GO:0006919,GO:0044822,GO:0030060,GO:0019752,GO:0005886,GO:0035070,GO:0055114,GO:0005975,GO:0016615,GO:0016616,GO:0044237,GO:0005743,GO:0006107,GO:0006006,GO:0006108	CG7998-PA			PIRSF000102		TIGR01772	PF00056,PF02866			PS00068	G3DSA:3.90.110.10,G3DSA:3.40.50.720	SSF51735,SSF56327		00630+1.1.1.37,00680+1.1.1.37,00720+1.1.1.37,00710+1.1.1.37,00620+1.1.1.37,00270+1.1.1.37,00020+1.1.1.37	REACT_474	PWY-561,PWY-5913,PWY-1622,PWY-7383,PWY-5392,PWY-6969,PWY-6728,PWY-7115,PWY-5690						
aly12480.1	Unknown	GO:0046872	n/a							PS50157		PS00028			286~306								
aly12480.2	Oxysterol-binding protein-related protein 8	GO:0046628,GO:0030336,GO:0015485,GO:0006869,GO:0008142,GO:0016020,GO:0031965,GO:0010891,GO:0090204,GO:0045444,GO:0051897	CG42668-PM										G3DSA:2.30.29.30	SSF50729	117~137								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly12484.1	Oxysterol-binding protein-related protein 9	GO:0008142,GO:0006869,GO:0031902,GO:0008289,GO:0005794	CG1513-PA						PF01237			PS01013		SSF144000									
aly124852.1	PiggyBac transposable element-derived protein 3		n/a						PF13843						54~74								
aly1249.1	Autophagy-related protein 16-1	GO:0039689,GO:0000421,GO:0005776,GO:0000045,GO:0005575,GO:0003674,GO:0005515,GO:0015031,GO:0034045,GO:0010506,GO:0005930,GO:0042802	CG31033-PF				SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50082,PS50082,PS50294	PR00320,PR00320,PR00320	PS00678,PS00678	G3DSA:2.130.10.10	SSF50978										
aly1249.10	Unknown		n/a																				
aly1249.11	Myosin light chain alkali	GO:0000146,GO:0006936,GO:0007498,GO:0005859,GO:0016459,GO:0005509	CG5596-PB				SM00054,SM00054			PS50222,PS50222			G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473										
aly1249.12	Microtubule-associated protein 2	GO:0043234,GO:0015631,GO:0007017,GO:0072375,GO:0005790,GO:0001578,GO:0008017,GO:0005791,GO:0032355,GO:0030425,GO:0030424,GO:0005881,GO:0046331,GO:0043025,GO:0043005,GO:0032570,GO:0021954,GO:0005874,GO:0005875,GO:0008355	CG45110-PG						PF00418,PF00418,PF00418,PF00418,PF00418	PS51491,PS51491,PS51491,PS51491		PS00229												
aly1249.13	Unknown		n/a																				
aly1249.14	Iporin	GO:0031410,GO:0005829,GO:0008157,GO:0017137,GO:0070062	CG7029-PA				SM00326		PF02759	PS50826			G3DSA:2.30.30.40	SSF140741,SSF50044										
aly1249.15	Solute carrier family 46 member 3	GO:0016021,GO:0055085	CG15890-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1249.16	Unknown	GO:0022008	CG13321-PA				SM00696,SM00696		PF11901														
aly1249.17	Unknown		n/a																				
aly1249.18	Unknown		n/a																				
aly1249.19	Pyrroline-5-carboxylate reductase 3	GO:0055129,GO:0004735,GO:0055114,GO:0006561	CG6009-PA	MF_01925		PIRSF000193		TIGR00112	PF03807,PF14748			PS00521	G3DSA:3.40.50.720,G3DSA:1.10.3730.10	SSF48179,SSF51735		00330+1.5.1.2		PWY-6344,PWY-4981,PWY-3341	UPA00098				
aly1249.2	Transcription elongation factor B polypeptide 3	GO:0008023,GO:0005634,GO:0007474,GO:0070449,GO:0035327,GO:0006351,GO:0003677,GO:0006368,GO:0042787,GO:0032968,GO:0016021	CG6755-PA				SM00509		PF08711,PF06881	PS51319			G3DSA:1.20.930.10	SSF47676	665~685,160~180								
aly1249.20	Protein lap4	GO:0016333,GO:0016332,GO:0016331,GO:0045198,GO:0016336,GO:0016335,GO:0016334,GO:0006963,GO:0045197,GO:0008105,GO:0030714,GO:0031594,GO:0005923,GO:0035088,GO:0048863,GO:0000902,GO:0000122,GO:0007472,GO:0030100,GO:0001708,GO:0019991,GO:0008406,GO:0030707,GO:0005179,GO:0050803,GO:0007318,GO:0048749,GO:0008285,GO:0016328,GO:0007608,GO:0046425,GO:0008283,GO:0042048,GO:0042067,GO:0016327,GO:0016323,GO:0007280,GO:0045186,GO:0001738,GO:0060581,GO:0008593,GO:0072002,GO:0042058,GO:0001737,GO:0005918,GO:0051726,GO:0007464,GO:0007391,GO:0045169,GO:0005576,GO:0045823,GO:0005515,GO:0045571,GO:0072089,GO:0050680	CG43398-PL				SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365		PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1249.21	Protein lap4	GO:0016333,GO:0016332,GO:0016331,GO:0045198,GO:0016336,GO:0016335,GO:0016334,GO:0006963,GO:0045197,GO:0008105,GO:0030714,GO:0031594,GO:0005923,GO:0035088,GO:0048863,GO:0000902,GO:0000122,GO:0007472,GO:0030100,GO:0001708,GO:0019991,GO:0008406,GO:0030707,GO:0005179,GO:0050803,GO:0007318,GO:0048749,GO:0008285,GO:0016328,GO:0007608,GO:0046425,GO:0008283,GO:0042048,GO:0042067,GO:0016327,GO:0016323,GO:0007280,GO:0045186,GO:0001738,GO:0060581,GO:0008593,GO:0072002,GO:0042058,GO:0001737,GO:0005918,GO:0051726,GO:0007464,GO:0007391,GO:0045169,GO:0005576,GO:0045823,GO:0005515,GO:0045571,GO:0072089,GO:0050680	CG43398-PL				SM00228,SM00228,SM00228,SM00228		PF00595,PF00595,PF00595,PF00595	PS50106,PS50106,PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156,SSF50156,SSF50156	1538~1558								
aly1249.22	Putative inner dynein arm light chain, axonemal	GO:0030286,GO:0007018,GO:0003774,GO:0008152,GO:0042623	CG6971-PA						PF10211						171~195,199~233								
aly1249.23	Mediator of RNA polymerase II transcription subunit 4	GO:0007517,GO:0005515,GO:0005634,GO:0006366,GO:0003713,GO:0001104,GO:0048813,GO:0006357,GO:0006351,GO:0006367,GO:0007095,GO:0016592	CG8609-PA						PF10018						59~100								
aly1249.24	Unknown		n/a																				
aly1249.25	Chorion peroxidase	GO:0060967,GO:0020037,GO:0006727,GO:0006979,GO:0005764,GO:0005576,GO:0042744,GO:0007306,GO:0046872,GO:0004601,GO:0055114	CG6969-PA						PF03098	PS50292	PR00457,PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									
aly1249.26	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098	PS50292			G3DSA:1.10.640.10	SSF48113									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1249.27	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098	PS50292	PR00457,PR00457,PR00457,PR00457,PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									
aly1249.28	Unknown		n/a																				
aly1249.29	Unknown		n/a																				
aly1249.3	Glutamate dehydrogenase, mitochondrial	GO:0005737,GO:0005829,GO:0004352,GO:0004353,GO:0005739,GO:0005524,GO:0006116,GO:0006536,GO:0009060,GO:0042802,GO:0019551,GO:0005759,GO:0046693,GO:0005525	CG5320-PA				SM00839		PF00208,PF00208,PF02812		PR00082,PR00082,PR00082,PR00082	PS00074	G3DSA:1.10.287.140,G3DSA:3.40.192.10,G3DSA:3.40.50.720	SSF51735,SSF53223									
aly1249.30	Unknown		n/a												268~288								
aly1249.31	Unknown		n/a																				
aly1249.4	Transmembrane emp24 domain-containing protein 3	GO:0006892,GO:0033116,GO:0000003,GO:0005793,GO:0048193,GO:0005215,GO:0016021,GO:0006810,GO:0032580,GO:0005789,GO:0061357,GO:0015031,GO:0048042,GO:0005794,GO:0030126,GO:0030133,GO:0030135,GO:0022008,GO:0005783	CG1967-PA						PF01105	PS50866				SSF101576									
aly1249.5	Protein YIPF5	GO:0016192,GO:0016021,GO:0016020,GO:0005789,GO:0015031,GO:0000139	CG12404-PA						PF04893														
aly1249.6	Unknown		n/a																				
aly1249.7	Unknown		CG8516-PA																				
aly1249.8	Nucleoporin NDC1	GO:0005737,GO:0017056,GO:0031081,GO:0005643,GO:0016020,GO:0031965,GO:0007129,GO:0051292,GO:0007283,GO:0015031,GO:0022008,GO:0051028	CG5857-PA						PF09531														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1249.9	Protein unc-80 homolog	GO:0005261,GO:0006812,GO:0045475,GO:0055080,GO:0098655,GO:0034703	CG18437-PF						PF15778														
aly125.1	Diacylglycerol kinase theta	GO:0033613,GO:0016310,GO:0016607,GO:0019933,GO:0003951,GO:0035556,GO:0070493,GO:0005737,GO:0019992,GO:0005634,GO:0046872,GO:0007186,GO:0005524,GO:0005856,GO:0019900,GO:0046331,GO:0043274,GO:0008152,GO:0005886,GO:0004143,GO:0005829,GO:0007205,GO:0070528,GO:0006357,GO:0033198	CG31140-PH				SM00109,SM00109,SM00109,SM00046,SM00314,SM00314,SM00045		PF00781,PF00609,PF00130,PF00130,PF00130,PF00788,PF00788	PS50081,PS50081,PS50081,PS50200,PS50146	PR00008,PR00008,PR00008,PR00008	PS00479,PS00479,PS00479	G3DSA:3.30.60.20,G3DSA:3.30.60.20,G3DSA:3.30.60.20	SSF54236,SSF57889,SSF54928,SSF57889,SSF57889,SSF111331		00561+2.7.1.107,00564+2.7.1.107	REACT_14797,REACT_604	PWY-7039						
aly125.10	Protein SMG8	GO:0005575,GO:0003674,GO:0000184,GO:0008150	CG6729-PA						PF10220,PF10220,PF10220														
aly125.11	Cytoplasmic polyadenylation element-binding protein 1-A	GO:0007294,GO:0003676,GO:0032869,GO:0007309,GO:0005815,GO:0046012,GO:0005737,GO:0000900,GO:0000922,GO:0005634,GO:0016020,GO:0000166,GO:0048134,GO:0071456,GO:0045727,GO:0048477,GO:0071230,GO:0046011,GO:0017131,GO:0030529,GO:0007281,GO:0007315,GO:0007314,GO:0007310,GO:0000578,GO:0045451,GO:0043234,GO:0046872,GO:2000766,GO:0008298,GO:0005515,GO:0006378,GO:0006397,GO:0035925,GO:0003729	CG10868-PA						PF16366,PF16367	PS50102			G3DSA:3.30.70.330	SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly125.12	Cell division cycle protein 16 homolog	GO:0045842,GO:0051439,GO:0090302,GO:0051437,GO:0051436,GO:0030071,GO:0051301,GO:0005737,GO:0005819,GO:0070979,GO:0005813,GO:0005654,GO:0007088,GO:0000278,GO:0007067,GO:0008283,GO:0031145,GO:0022008,GO:0004842,GO:0005829,GO:0005515,GO:0007094,GO:0005680	CG6759-PA				SM00028,SM00028		PF13414	PS50005,PS50005,PS50293			G3DSA:1.25.40.10	SSF48452										
aly125.13	Xylulose kinase	GO:0042732,GO:0005737,GO:0005975,GO:0070062,GO:0005998,GO:0005997,GO:0046835,GO:0006091,GO:0004856,GO:0005524	CG3534-PA						PF00370				G3DSA:3.30.420.40	SSF53067									
aly125.14	Unknown		n/a																				
aly125.15	Unknown		n/a																				
aly125.2	F-box only protein 9	GO:0005737,GO:0031146,GO:0016567,GO:0019005,GO:0005515,GO:0032006	CG5961-PA						PF12937	PS50293,PS50005			G3DSA:1.20.1280.50	SSF81383									
aly125.3	AP-1 complex subunit sigma-2	GO:0008021,GO:0042051,GO:0006901,GO:0036465,GO:0005905,GO:0060612,GO:0045444,GO:0030135,GO:0008542,GO:0008565,GO:0016183,GO:0050885,GO:0006886,GO:0048749,GO:0005794,GO:0030659,GO:0030276,GO:0007269,GO:0030121,GO:0016192,GO:0046907,GO:0007411,GO:0030117	CG5864-PA			PIRSF015588			PF01217			PS00989	G3DSA:3.30.450.60	SSF64356									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly125.4	Lipid storage droplets surface-binding protein 2	GO:0005737,GO:0030730,GO:0006629,GO:0006869,GO:0031887,GO:0005811,GO:0007476,GO:0005875,GO:0051049,GO:0005515,GO:0019915,GO:0050995	CG9057-PA						PF03036														
aly125.5	Unknown		CG11504-PB				SM00595		PF10545	PS51029													
aly125.6	Unknown		n/a																				
aly125.7	Unknown		n/a																				
aly125.8	Peroxisomal membrane protein 11C	GO:0043234,GO:0005779,GO:0016559,GO:0044375,GO:0005777,GO:0046331,GO:0031231	CG13827-PB						PF05648														
aly125.9	Peroxisomal membrane protein 11C	GO:0043234,GO:0005779,GO:0016559,GO:0044375,GO:0005777,GO:0046331,GO:0031231	CG13827-PB						PF05648														
aly1250.1	Protein rolling stone	GO:0016021,GO:0016020,GO:0007519,GO:0008150,GO:0007520,GO:0003674	CG43778-PA																				
aly1250.2	Protein rolling stone	GO:0007520,GO:0016021,GO:0016020,GO:0007519	CG13101-PA																				
aly1250.3	Protein rolling stone	GO:0016021,GO:0016020,GO:0007519,GO:0008150,GO:0007520,GO:0003674	CG43778-PA																				
aly1250.4	Protein rolling stone	GO:0007520,GO:0016021,GO:0016020,GO:0007519	CG13101-PA																				
aly1250.5	Protein rolling stone	GO:0007520,GO:0016021,GO:0016020,GO:0007519	CG13101-PA																				
aly1250.6	Unknown		n/a																				
aly1250.7	Unknown		n/a				SM00355,SM00355			PS50157		PS00028	G3DSA:3.30.160.60										
aly1251.1	GTP-binding protein REM 1	GO:0016020,GO:0003924,GO:0005622,GO:0006184,GO:0007264,GO:0005525	CG15069-PA				SM00174,SM00173,SM00175		PF00071	PS51421	PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly12511.1	Gypsy retrotransposon integrase-like protein 1	GO:0015074,GO:0003676	n/a						PF00665	PS50994			G3DSA:3.30.420.10	SSF53098									
aly12514.1	Unknown	GO:0005737,GO:0007294,GO:0030717,GO:0007317,GO:0007293,GO:0007282,GO:0003676,GO:0007310,GO:0007309,GO:0007067,GO:0048477,GO:0048134	CG10847-PF																				
aly12517.1	Cytoplasmic FMR1-interacting protein	GO:0005737,GO:0045177,GO:0006909,GO:0000902,GO:0030031,GO:0050807,GO:0030866,GO:0017048,GO:0008360,GO:0045202,GO:0007411,GO:0001745,GO:0022416,GO:0031209	CG4931-PA			PIRSF008153			PF05994		PR01698,PR01698												
aly12517.2	Collagen-like protein 1	GO:0019012	n/a																				
aly12520.1	CCR4-NOT transcription complex subunit 1	GO:0030014,GO:0048387,GO:0005737,GO:0007517,GO:0000289,GO:0000122,GO:0005634,GO:1900153,GO:0006402,GO:0033147,GO:0030331,GO:0006417,GO:0060213,GO:0031047,GO:0022008,GO:0010606,GO:0000932,GO:0048813,GO:0006351,GO:0005515,GO:0017148,GO:0042974,GO:0007095	CG34407-PH						PF04054														
aly12520.2	CCR4-NOT transcription complex subunit 1	GO:0030014,GO:0048387,GO:0005737,GO:0007517,GO:0000289,GO:0000122,GO:0005634,GO:1900153,GO:0006402,GO:0033147,GO:0030331,GO:0006417,GO:0060213,GO:0031047,GO:0022008,GO:0010606,GO:0000932,GO:0048813,GO:0006351,GO:0005515,GO:0017148,GO:0042974,GO:0007095	CG34407-PH						PF16415,PF12842,PF16418,PF16417														
aly12520.3	Unknown		n/a																				
aly12520.4	Unknown		n/a																				
aly125336.1	Unknown		n/a																				
aly1254.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1254.2	Nuclear inhibitor of protein phosphatase 1	GO:0003677,GO:0007411,GO:0043086,GO:0016607,GO:0008995,GO:0005634,GO:0005654,GO:0006401,GO:0008380,GO:0006351,GO:0005737,GO:0008283,GO:0035308,GO:0008157,GO:0004864,GO:0004865,GO:0008599,GO:0090501,GO:0004519,GO:0006355,GO:0003723,GO:0005515,GO:0003729,GO:0005681,GO:0006397	CG8980-PA				SM00240		PF00498	PS50006			G3DSA:2.60.200.20	SSF49879									
aly1254.3	Peroxisome biogenesis factor 10	GO:0048137,GO:0005779,GO:0007031,GO:0016558,GO:0005777,GO:0008022,GO:0045046,GO:0007112,GO:0007285,GO:0008270,GO:0005515,GO:0007286,GO:0042760	CG7864-PA						PF04757	PS50089			G3DSA:3.30.40.10	SSF57850									
aly1254.4	Peptidyl-prolyl cis-trans isomerase FKBP1A	GO:0005737,GO:0006457,GO:0018208,GO:0016020,GO:0006974,GO:0005528,GO:0003755	CG11001-PA						PF00254	PS50059			G3DSA:3.10.50.40	SSF54534									
aly1254.5	MRG/MORF4L-binding protein	GO:0006325,GO:0005634,GO:0043189,GO:0005654,GO:0006355,GO:0006351,GO:0022008,GO:0040008,GO:0016568	CG13746-PA						PF07904														
aly1254.6	Unknown	GO:0005488	CG12702-PA											SSF48371,SSF48371									
aly1254.7	Venom dipeptidyl peptidase 4	GO:0004177,GO:0016020,GO:0008239,GO:0005576,GO:0006508,GO:0008236	CG11319-PB						PF00326,PF00930				G3DSA:2.140.10.30,G3DSA:2.140.10.30,G3DSA:3.40.50.1820	SSF53474,SSF82171,SSF82171									
aly1254.8	Unknown		n/a																				
aly125427.1	Unknown		n/a																				
aly1256.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1256.2	Octopamine receptor	GO:0004930,GO:0007608,GO:0010578,GO:0008226,GO:0016021,GO:0007211,GO:0005887,GO:0005886,GO:0004989,GO:0007186,GO:0008227,GO:1900738	CG7485-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00664,PR00664,PR00664,PR00664,PR00664,PR00664	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly1256.3	Microsomal glutathione S-transferase 1	GO:0005778,GO:0045177,GO:0004364,GO:0070207,GO:0005783,GO:0033327,GO:0016021,GO:0010243,GO:0042493,GO:0005739,GO:0005789,GO:0005743,GO:0005741,GO:0055114,GO:0006749,GO:0032496,GO:0071449,GO:0005634,GO:0004602,GO:0043295	CG33177-PA										G3DSA:1.20.120.550	SSF161084									
aly12560.1	PiggyBac transposable element-derived protein 1	GO:0003700,GO:0005044,GO:0016020	n/a						PF13843														
aly12583.1	Unknown		n/a																				
aly12583.2	Unknown		n/a																				
aly12585.1	Acetylcholine receptor subunit alpha-like	GO:0006811,GO:0015464,GO:0005892,GO:0045211,GO:0004889,GO:0016021,GO:0030054	CG12414-PC					TIGR00860	PF02932,PF02931		PR00252,PR00252,PR00252,PR00252,PR00252,PR00254,PR00254,PR00254,PR00254	PS00236	G3DSA:1.20.120.370,G3DSA:1.20.120.370,G3DSA:2.70.170.10	SSF90112,SSF63712			REACT_13685						
aly12585.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1259.1	Unknown	GO:0005737,GO:0008017,GO:0007476,GO:0016321,GO:0051015,GO:0003779,GO:0008157,GO:0030517,GO:0007411	CG1822-PF																				
aly1259.10	Unknown		n/a																				
aly1259.11	Unknown		n/a																				
aly1259.12	Protein transport protein Sec16A	GO:0070971,GO:0048208,GO:0070973,GO:0005794,GO:0007029,GO:0005829,GO:0016020,GO:0007030,GO:0017016,GO:0003400,GO:0005789,GO:0034198,GO:0015031,GO:0021762,GO:0000139,GO:0070863,GO:0005737	CG32654-PI						PF12931						382~402								
aly1259.13	Unknown	GO:0004252,GO:0006508	CG10405-PB						PF00089				G3DSA:2.40.10.10	SSF50494									
aly1259.14	U11/U12 small nuclear ribonucleoprotein 35 kDa protein	GO:0000381,GO:0030619,GO:0030532,GO:0071011,GO:0005634,GO:0005692,GO:0000398,GO:0000166,GO:0007052,GO:0003723,GO:0005515,GO:0048025,GO:0022008,GO:0071013,GO:0005685,GO:0003729	CG8749-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly1259.15	Protein FAM188A homolog	GO:0005575,GO:0008150,GO:0005509	CG7332-PA						PF13898				G3DSA:1.10.238.10	SSF47473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1259.16	Protein crumbs	GO:0016332,GO:0045198,GO:0042052,GO:0042051,GO:0033157,GO:0034332,GO:0045197,GO:0035002,GO:0061024,GO:0008104,GO:0007043,GO:0001745,GO:0035330,GO:0030507,GO:0002009,GO:0035088,GO:0007435,GO:0007431,GO:0016021,GO:0016334,GO:0045746,GO:0005509,GO:0005080,GO:0032880,GO:0048477,GO:0008284,GO:0035239,GO:0061336,GO:0016324,GO:0046621,GO:0016327,GO:0061541,GO:0045186,GO:0016028,GO:0005913,GO:0005886,GO:0045218,GO:0001738,GO:0005918,GO:0007443,GO:0007424,GO:0042327,GO:0007399,GO:0035003,GO:0035090,GO:0046664,GO:0007163,GO:0032435,GO:0045570,GO:0050821,GO:0045494	CG6383-PC										G3DSA:2.60.120.200	SSF49899									
aly1259.17	Protein crumbs	GO:0016332,GO:0045198,GO:0042052,GO:0042051,GO:0033157,GO:0034332,GO:0045197,GO:0035002,GO:0061024,GO:0007163,GO:0007043,GO:0001745,GO:0035330,GO:0030507,GO:0002009,GO:0035088,GO:0007435,GO:0007431,GO:0016021,GO:0016334,GO:0008104,GO:0005509,GO:0005080,GO:0032880,GO:0048477,GO:0008284,GO:0035239,GO:0061336,GO:0016324,GO:0046621,GO:0016327,GO:0061541,GO:0045186,GO:0016028,GO:0005913,GO:0005886,GO:0045218,GO:0005918,GO:0007443,GO:0042327,GO:0007399,GO:0035003,GO:0035090,GO:0046664,GO:0045746,GO:0001738,GO:0032435,GO:0045570,GO:0050821,GO:0045494	CG6383-PC				SM00179,SM00179,SM00179,SM00181,SM00181,SM00181		PF00008,PF00008,PF07645	PS50026,PS50026,PS50026	PR00010,PR00010,PR00010,PR00010	PS01187,PS00010,PS01186,PS00010,PS01186,PS00022,PS00022,PS01187	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57184									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1259.18	Delta-like protein 4	GO:0016318,GO:0018149,GO:0045926,GO:0003209,GO:0016339,GO:0060579,GO:0044344,GO:0010629,GO:0045198,GO:0007164,GO:0004872,GO:0048105,GO:0016337,GO:0001525,GO:0003344,GO:0030178,GO:0050767,GO:0000904,GO:0000122,GO:0040008,GO:0001569,GO:0007476,GO:0003208,GO:0003222,GO:0008015,GO:0050839,GO:0005509,GO:0042067,GO:1903588,GO:0005112,GO:0035912,GO:0061314,GO:0008285,GO:0090051,GO:0008283,GO:0046620,GO:0035159,GO:0007601,GO:0007219,GO:0045317,GO:0005887,GO:0005886,GO:0035329,GO:0007156,GO:0001737,GO:0001736,GO:0061074,GO:0007446,GO:0007220,GO:0090176,GO:0010596,GO:0072554,GO:0035924,GO:0001974,GO:0010628,GO:0005515,GO:0045571,GO:2000179,GO:0016021,GO:0007165	CG3352-PA				SM00181,SM00181		PF00008,PF00008	PS50026,PS50026		PS00022,PS01186	G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57196										
aly1259.19	Nitric oxide-associated protein 1	GO:0043457,GO:0044822,GO:0006915,GO:0003924,GO:0042254,GO:0005739,GO:0005743,GO:0010941,GO:0032543,GO:0005525	CG10914-PA						PF01926				G3DSA:3.40.50.300	SSF52540,SSF52540	455~475								
aly1259.2	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	GO:0006561,GO:0006560,GO:0016620,GO:0005739,GO:0003842,GO:0006537,GO:0010133,GO:0007005,GO:0008152,GO:0005759,GO:0055114,GO:0016491	CG7145-PA					TIGR01236	PF00171			PS00070	G3DSA:3.40.605.10,G3DSA:3.40.309.10	SSF53720		00330+1.2.1.88,00250+1.2.1.88		PWY-6853	UPA00261				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1259.20	Protein crumbs	GO:0016332,GO:0045198,GO:0042052,GO:0042051,GO:0033157,GO:0034332,GO:0045197,GO:0035002,GO:0061024,GO:0007163,GO:0007043,GO:0001745,GO:0035330,GO:0030507,GO:0002009,GO:0035088,GO:0007435,GO:0007431,GO:0016021,GO:0016334,GO:0008104,GO:0005509,GO:0005080,GO:0032880,GO:0048477,GO:0008284,GO:0035239,GO:0061336,GO:0016324,GO:0046621,GO:0016327,GO:0061541,GO:0045186,GO:0016028,GO:0005913,GO:0005886,GO:0045218,GO:0005918,GO:0007443,GO:0007424,GO:0042327,GO:0007399,GO:0035003,GO:0035090,GO:0046664,GO:0045746,GO:0001738,GO:0032435,GO:0045570,GO:0050821,GO:0045494	CG6383-PC				SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00282,SM00282,SM00282		PF07645,PF07645,PF00008,PF00008,PF00008,PF00008,PF00008,PF00008,PF00008,PF00008,PF00054,PF00054	PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50025,PS50026,PS50026	PR00010,PR00010,PR00010,PR00010	PS01187,PS00010,PS00022,PS00022,PS00010,PS01186,PS00022,PS00010,PS01186,PS00010,PS00010,PS00010,PS01186,PS01187,PS00022,PS00022,PS00022,PS00022,PS00010,PS01187,PS01186,PS00022,PS01187,PS00022,PS00022,PS01186,PS01187,PS00010,PS01187,PS01187,PS01186,PS00010,PS00022,PS00010,PS01187,PS01186,PS00022,PS01187	G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF49899,SSF57196,SSF57196,SSF57196,SSF57196,SSF571984,SSF57196,SSF57196,SSF49899,SSF57196,SSF49899,SSF57196									
aly1259.21	Protein FAM102A	GO:0033227	CG8671-PA						PF10358														
aly1259.22	Unknown		n/a																				
aly1259.23	Probable tRNA pseudouridine synthase 2	GO:0008033,GO:0001522,GO:0009982,GO:0006396,GO:0003723	CG7849-PB						PF01509					SSF55120,SSF55120									
aly1259.24	PAXIP1-associated glutamate-rich protein 1A	GO:0005634,GO:0035097,GO:0060717,GO:0071557,GO:0003674,GO:0051568,GO:0044666	CG11750-PA						PF15364														
aly1259.25	Box C/D snoRNA protein 1	GO:0046872,GO:0048812,GO:0042254	CG1463-PA						PF04438	PS51083				SSF144232	327~347								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1259.26	NudC domain-containing protein 1	GO:0005737,GO:0002376,GO:0005634,GO:0005654	CG10347-PB																				
aly1259.27	NudC domain-containing protein 1	GO:0005737,GO:0002376,GO:0005634,GO:0005654	CG10347-PB						PF04969	PS51203			G3DSA:2.60.40.790	SSF49764									
aly1259.28	Unknown		n/a																				
aly1259.29	Vesicle-trafficking protein SEC22b-B	GO:0006890,GO:0006888,GO:0016192,GO:0016021,GO:0006906,GO:0033116,GO:0000139,GO:0012507,GO:0015031,GO:0005484,GO:0030133,GO:0005789,GO:0031201,GO:0006909,GO:0005783	CG7359-PA						PF00957,PF13774	PS50859,PS50892			G3DSA:1.10.3840.10,G3DSA:3.30.450.50	SSF58038,SSF64356									
aly1259.3	Unknown		n/a																				
aly1259.30	Ecdysone-induced protein 74EF isoform B	GO:0043565,GO:0030154,GO:0035071,GO:0003700,GO:0005634,GO:0009987,GO:0007275,GO:0006355,GO:0001077,GO:0045944,GO:0006366,GO:0008219,GO:0048477,GO:0006914,GO:0040034	CG32180-PB				SM00413		PF00178	PS50061	PR00454,PR00454,PR00454,PR00454	PS00346,PS00345	G3DSA:1.10.10.10	SSF46785									
aly1259.31	Unknown		n/a																				
aly1259.32	U7 snRNA-associated Sm-like protein LSm11	GO:0016604,GO:0000381,GO:0071254,GO:0005683,GO:0005634,GO:0035363,GO:0030529,GO:0006398,GO:0003723,GO:0005515,GO:0071204,GO:0006397	CG12924-PA				SM00651		PF01423				G3DSA:2.30.30.100	SSF50182,SSF50182	74~102								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1259.33	ADP-ribosylation factor-like protein 16	GO:0006471,GO:0003924,GO:0005622,GO:0005575,GO:0007264,GO:0005525	CG13692-PA				SM00177	TIGR00231	PF00025	PS51417			G3DSA:3.40.50.300	SSF52540									
aly1259.34	Zinc finger protein 569	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG2202-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57716,SSF57667	133~153									
aly1259.35	Dual specificity protein phosphatase 12	GO:0005737,GO:0016791,GO:0008138,GO:0006470,GO:0004725,GO:0033133,GO:0043508,GO:0046872,GO:0005634	CG14211-PB			PIRSF000941	SM00195		PF00782	PS50056,PS50054		PS00383	G3DSA:3.90.190.10	SSF52799									
aly1259.36	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG32645-PB				SM00703		PF01757														
aly1259.37	Unknown		n/a																				
aly1259.38	Unknown	GO:0016747	CG17707-PE						PF01757														
aly1259.39	Unknown		n/a				SM00360,SM00360		PF00076	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928									
aly1259.4	Protein OPI10 homolog	GO:0005575,GO:0008150,GO:0003674	CG13926-PA						PF05603														
aly1259.40	Unknown		n/a						PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928	219~239								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1259.41	Raf homolog serine/threonine-protein kinase phl	GO:2001234,GO:0007552,GO:0008586,GO:0007165,GO:0035556,GO:0007298,GO:0008069,GO:0002168,GO:0007362,GO:0007472,GO:0005057,GO:0007369,GO:0007476,GO:0046777,GO:0004674,GO:0046579,GO:0046872,GO:0016242,GO:0005524,GO:0008284,GO:0042386,GO:0035171,GO:0035309,GO:0007283,GO:0007173,GO:0009267,GO:0040014,GO:0051726,GO:0007428,GO:0005622,GO:0046534,GO:0005515,GO:0008293,GO:0030097,GO:0070374	CG2845-PA				SM00455,SM00109		PF00130,PF02196	PS50081,PS50898		PS00479	G3DSA:3.30.60.20,G3DSA:3.10.20.90	SSF54236,SSF57889	79~99,44~64									
aly1259.42	Unknown		n/a						PF13873						237~260								
aly1259.43	U3 small nucleolar ribonucleoprotein protein IMP3	GO:0032040,GO:0034457,GO:0005730,GO:0005634,GO:0044822,GO:0019843,GO:0003735,GO:0006364,GO:0003723,GO:0030515,GO:0006412,GO:0005761	CG4866-PA				SM00363		PF00163,PF01479	PS50889			G3DSA:3.10.290.10	SSF55174	47~67								
aly1259.44	Unknown		n/a												144~178,18~38								
aly1259.45	RNA-binding protein 45	GO:0005737,GO:0007399,GO:0005634,GO:0030154,GO:0000166,GO:0005654,GO:0003723,GO:0003676,GO:0044822,GO:0003729	CG1316-PA				SM00360,SM00360,SM00360,SM00360		PF00076,PF00076,PF00076	PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928,SSF54928										
aly1259.46	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 2	GO:0007424,GO:0016477,GO:0005634,GO:0006370,GO:0007426,GO:0008168,GO:0032259,GO:0016021	CG5032-PA																				
aly1259.47	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 2	GO:0005737,GO:0007424,GO:0016477,GO:0004483,GO:0005634,GO:0006370,GO:0007426,GO:0008168,GO:0097310,GO:0032259,GO:0016021	CG5032-PA						PF01728	PS51590,PS51614			G3DSA:3.40.50.150	SSF53335				PWY-7375					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1259.48	Nuclear pore complex protein Nup205	GO:0005635,GO:0019221,GO:0034605,GO:0019083,GO:0010827,GO:0044281,GO:0051028,GO:0005737,GO:0044267,GO:0042332,GO:0008645,GO:0016020,GO:0044611,GO:0015758,GO:0010467,GO:0019058,GO:0043687,GO:0007184,GO:0034399,GO:0017056,GO:0000278,GO:0051297,GO:0031965,GO:0006913,GO:0051292,GO:0007077,GO:0022008,GO:0016925,GO:0055085,GO:0000059,GO:0005975,GO:0005643,GO:1900034,GO:0006999,GO:0016032,GO:0005654	CG11943-PB						PF11894,PF11894,PF11894						1156~1176									
aly1259.49	Unknown		n/a																				
aly1259.5	Cell division cycle 7-related protein kinase	GO:0018105,GO:0006909,GO:0044770,GO:0048102,GO:0051301,GO:0005737,GO:0000727,GO:0005634,GO:0005654,GO:0004674,GO:0004672,GO:0046872,GO:0005524,GO:0008284,GO:0006468,GO:0015630,GO:0035071,GO:0016301,GO:0010971,GO:0008360,GO:0045171,GO:0006270,GO:0010571,GO:0004702	CG32742-PA				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20	SSF56112										
aly1259.50	BarH-like 2 homeobox protein	GO:0005737,GO:0043565,GO:0030516,GO:0045165,GO:0030182,GO:0003700,GO:0005634,GO:0001709,GO:0006366,GO:0005654,GO:0006355,GO:0001077,GO:0001764,GO:0003677,GO:0045944,GO:0045727	CG11085-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689	284~304									
aly1259.51	Unknown		n/a																				
aly1259.52	Unknown		n/a																				
aly1259.53	Innexin shaking-B	GO:0007630,GO:0016264,GO:0010496,GO:0009881,GO:0055085,GO:0016021,GO:0003254,GO:0007602,GO:0009416,GO:0005886,GO:0010644,GO:0005243,GO:0006811,GO:0005921	CG12678-PA						PF00876	PS51013													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1259.54	Innexin shaking-B	GO:0007630,GO:0016264,GO:0010496,GO:0009881,GO:0055085,GO:0016021,GO:0003254,GO:0007602,GO:0009416,GO:0005886,GO:0010644,GO:0005243,GO:0006811,GO:0005921	CG32508-PA						PF00876	PS51013	PR01262,PR01262,PR01262,PR01262,PR01262,PR01262												
aly1259.55	Unknown		n/a																				
aly1259.56	Unknown		n/a																				
aly1259.57	Unknown		n/a																				
aly1259.58	Unknown		n/a																				
aly1259.6	CDGSH iron-sulfur domain-containing protein 3, mitochondrial	GO:0046872,GO:0051537,GO:0043231,GO:0005739	CG3420-PA				SM00704,SM00704		PF09360,PF09360														
aly1259.7	Cytochrome b5	GO:0005811,GO:0043231,GO:0035206,GO:0051726,GO:0016021,GO:0016020,GO:0005789,GO:0020037,GO:0046872,GO:0012505,GO:0009055,GO:0045610,GO:0055114,GO:0002168	CG2140-PB						PF00173	PS50255	PR00363,PR00363,PR00363,PR00363	PS00191	G3DSA:3.10.120.10	SSF55856									
aly1259.8	Apoptosis regulatory protein Siva	GO:0005737,GO:0046718,GO:0006924,GO:0001618,GO:0005175,GO:0097191,GO:0005739,GO:0032088,GO:0005654,GO:0005164,GO:1901030,GO:0008270	n/a						PF05458														
aly1259.9	EP300-interacting inhibitor of differentiation 3	GO:0006310,GO:0044267,GO:0006281,GO:0005634,GO:0005654,GO:0030915,GO:0005737,GO:0000781,GO:0006355,GO:0006351,GO:0016925,GO:0043687,GO:0042802	CG13142-PB						PF08743														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1260.1	Bestrophin-2	GO:0007608,GO:0006884,GO:1902476,GO:0016021,GO:0005886,GO:0034707,GO:0051899,GO:0006821,GO:0005929,GO:0005254,GO:0072320	CG6264-PC						PF01062														
aly1260.10	THO complex subunit 2	GO:0031990,GO:0016607,GO:0016973,GO:0000902,GO:0006397,GO:0005634,GO:0001824,GO:0010468,GO:0005654,GO:0046784,GO:0010793,GO:0000347,GO:0000346,GO:0017145,GO:0000445,GO:0048477,GO:0008380,GO:0006406,GO:0003729	CG31671-PB						PF11262,PF11732,PF16134,PF16134				G3DSA:2.130.10.10	SSF50998	332~359,1822~1842,1611~1638,1580~1600								
aly1260.11	Translation initiation factor eIF-2B subunit epsilon	GO:0005085,GO:0035690,GO:0014002,GO:0031369,GO:0005737,GO:0042552,GO:0043547,GO:0005851,GO:0005634,GO:0032057,GO:0048708,GO:0006417,GO:0014003,GO:0009408,GO:0043434,GO:0001541,GO:0016779,GO:0005829,GO:0009749,GO:0045948,GO:0003743,GO:0006413,GO:0034976	CG3806-PA				SM00515		PF00132,PF02020	PS51363			G3DSA:2.160.10.10,G3DSA:3.90.550.10,G3DSA:1.25.40.180	SSF48371,SSF53448,SSF53448,SSF51161										
aly1260.12	Anaphase-promoting complex subunit 10	GO:0007113,GO:0045842,GO:0007067,GO:0031145,GO:0090302,GO:0022008,GO:0030071,GO:0051301,GO:0005680	CG11419-PA			PIRSF028841			PF03256	PS51284,PS51257			G3DSA:2.60.120.260	SSF49785										
aly1260.13	G1/S-specific cyclin-D2	GO:0005730,GO:0016049,GO:0005829,GO:0008283,GO:0030307,GO:0000079,GO:0009987,GO:0031965,GO:0051301,GO:0007259,GO:0019901,GO:0016538,GO:0000785,GO:0007049,GO:0005515,GO:0001934,GO:0045737,GO:0000307,GO:0005654,GO:0005634,GO:0007005	CG9096-PD				SM00385,SM00385		PF00134,PF02984			PS00292	G3DSA:1.10.472.10,G3DSA:1.10.472.10	SSF47954,SSF47954										
aly1260.14	Unknown		n/a												83~87								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1260.15	Paired mesoderm homeobox protein 2B	GO:0061452,GO:0021533,GO:0002087,GO:0048468,GO:0048894,GO:0048486,GO:0048484,GO:0001077,GO:0001764,GO:0048483,GO:0010001,GO:0003677,GO:0021723,GO:0043565,GO:0003360,GO:0005634,GO:0045665,GO:0045666,GO:0006366,GO:0035914,GO:1901166,GO:0010468,GO:0021934,GO:0060541,GO:0008285,GO:0030182,GO:0061549,GO:0000790,GO:0003358,GO:0003357,GO:0048839,GO:0003700,GO:0071542,GO:0006355,GO:0048485,GO:0045944,GO:0000977,GO:0000978,GO:0071773	CG11182-PA				SM00389		PF00046	PS50071			G3DSA:1.10.10.60	SSF46689										
aly1260.16	Unknown	GO:0003677	n/a							PS50071			G3DSA:1.10.10.60										
aly1260.17	Muscle-specific protein 20	GO:1901739,GO:0003779,GO:0007155,GO:0008360,GO:0005509,GO:0007520,GO:0043292	CG4696-PA				SM00033		PF00402,PF00307	PS50021,PS51122	PR00888,PR00888,PR00888,PR00888,PR00888,PR00888,PR00888	PS01052	G3DSA:1.10.418.10	SSF47576									
aly1260.18	Unknown		n/a																				
aly1260.19	Muscle LIM protein Mlp84B	GO:0005737,GO:0007517,GO:0015629,GO:0090175,GO:0005634,GO:0030154,GO:0007519,GO:0008307,GO:0045214,GO:0008270,GO:0060537,GO:0030018	CG1019-PA				SM00132,SM00132,SM00132,SM00132		PF00412,PF00412,PF00412,PF00412	PS50023,PS50023,PS50023,PS50023		PS00478,PS00478,PS00478,PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716,SSF57716,SSF57716,SSF57716,SSF57716,SSF57716,SSF57716,SSF57716,SSF57716										
aly1260.2	Translation initiation factor IF-3, mitochondrial	GO:0070124,GO:0008135,GO:0005739,GO:0032790,GO:0005759,GO:0006413,GO:0043024,GO:0003743	CG13163-PA						PF05198				G3DSA:3.30.110.10,G3DSA:3.10.20.80	SSF55200									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1260.20	DNA repair protein complementing XP-C cells homolog	GO:0005737,GO:0003697,GO:0005634,GO:0006289,GO:0071942,GO:0000111,GO:0003684,GO:0010777	CG8153-PC				SM01030,SM01032,SM01031		PF10405,PF10404,PF03835,PF10403					SSF54001,SSF54001	163~204,1112~1132								
aly1260.21	LIM domain only protein 3	GO:0045475,GO:0006909,GO:0005634,GO:0007476,GO:0036011,GO:0035218,GO:0022416,GO:0008270,GO:0005515,GO:0042220,GO:0002121,GO:0045893	CG44425-PD				SM00132,SM00132		PF00412,PF00412	PS50023,PS50023		PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716,SSF57716									
aly1260.22	Ankyrin repeat, SAM and basic leucine zipper domain-containing protein 1	GO:0043046,GO:0030154,GO:0006298,GO:0005739,GO:0071546,GO:0007283,GO:0046331,GO:0031047,GO:0005515,GO:0034587,GO:0007275,GO:0007140	CG2183-PA				SM00248,SM00248,SM00248,SM00248		PF12796	PS50088,PS50088,PS50297			G3DSA:1.10.150.50,G3DSA:1.25.40.20	SSF47769,SSF48403	405~425								
aly1260.23	Heat shock protein beta-1	GO:0006497,GO:0005737,GO:0030837,GO:0005634,GO:0051016,GO:0005739,GO:0042802,GO:0010998,GO:0005886,GO:0043292,GO:0009408,GO:0010506,GO:0030018	CG14207-PB						PF00011	PS01031	PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764	28~55								
aly1260.24	Synaptobrevin	GO:0043005,GO:0008021,GO:0006906,GO:0043195,GO:0016192,GO:0016081,GO:0016021,GO:0048786,GO:0035149,GO:0031201,GO:0006887,GO:0005515,GO:0005886,GO:0007269,GO:0005484,GO:0030672,GO:0000149,GO:0030054	CG17248-PJ						PF00957	PS50892	PR00219,PR00219,PR00219	PS00417	G3DSA:1.10.3840.10	SSF58038	45~65								
aly1260.25	T-complex protein 1 subunit beta	GO:0051131,GO:0072686,GO:0006457,GO:0051298,GO:0043209,GO:0005811,GO:0044297,GO:0051082,GO:0031122,GO:1901998,GO:0007052,GO:0002199,GO:0007339,GO:0005832,GO:0022008,GO:0005874,GO:0005875,GO:0005524,GO:0070062	CG7033-PA					TIGR02341	PF00118		PR00304,PR00304,PR00304,PR00304,PR00304	PS00750,PS00751,PS00995	G3DSA:1.10.560.10,G3DSA:1.10.560.10,G3DSA:3.30.260.10,G3DSA:3.30.260.10,G3DSA:3.50.7.10	SSF52029,SSF54849,SSF54849,SSF48592,SSF48592			REACT_17015						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1260.26	Probable 28S ribosomal protein S6, mitochondrial	GO:0070181,GO:0005840,GO:0006412,GO:0003735,GO:0005763,GO:0019843,GO:0032543	CG15016-PA						PF01250				G3DSA:3.30.70.60	SSF54995									
aly1260.27	15 kDa selenoprotein	GO:0008430,GO:0051084,GO:0035092,GO:0005788,GO:0008379,GO:0045454,GO:0055114,GO:0015036	CG7484-PB						PF08806					SSF52833									
aly1260.3	Unknown	GO:0005179,GO:0005576	n/a				SM00078		PF00049		PR00276,PR00276	PS00262	G3DSA:1.10.100.10	SSF56994									
aly1260.4	Unknown		n/a																				
aly1260.5	Ras-related and estrogen-regulated growth inhibitor	GO:0008285,GO:0030308,GO:0030331,GO:0009725,GO:0005829,GO:0016020,GO:0003924,GO:0005575,GO:0019003,GO:0008152,GO:0006184,GO:0022008,GO:0007264,GO:0005634,GO:0005525	CG5160-PA				SM00173,SM00175,SM00174	TIGR00231	PF00071	PS51421	PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly1260.6	Probable glutamine--tRNA ligase	GO:0005737,GO:0006425,GO:0004819,GO:0048813,GO:0005875,GO:0005524	CG10506-PA						PF03950,PF04557,PF04558,PF00749		PR00987,PR00987,PR00987	PS00178	G3DSA:3.90.800.10,G3DSA:2.40.240.10,G3DSA:2.40.240.10,G3DSA:3.40.50.620,G3DSA:3.40.50.620	SSF50715,SSF52374		00970+6.1.1.18	REACT_71						
aly1260.7	MAP kinase-activating death domain protein	GO:0000187,GO:0008021,GO:1902041,GO:0016192,GO:0051726,GO:0016021,GO:0006915,GO:0043410,GO:0017112,GO:0032483,GO:0007269,GO:0042981,GO:0043547	CG5627-PH				SM00799,SM00800,SM00801		PF02141,PF03456	PS50947,PS50946,PS50211													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1260.8	MAP kinase-activating death domain protein	GO:0000187,GO:0008021,GO:1902041,GO:0016192,GO:0051726,GO:0016021,GO:0006915,GO:0043410,GO:0017112,GO:0032483,GO:0007269,GO:0042981,GO:0043547	CG5627-PH																				
aly1260.9	Unknown	GO:0003700,GO:0006355,GO:0022008,GO:0007549,GO:0005634	CG3363-PA						PF16059														
aly1261.1	Trimethyllysine dioxygenase, mitochondrial	GO:0031418,GO:0051354,GO:0016702,GO:0008336,GO:0050353,GO:0034641,GO:0005739,GO:0005759,GO:0045329,GO:0005506,GO:0044281,GO:0055114,GO:0016491	CG4335-PA					TIGR02410	PF02668,PF06155				G3DSA:3.60.130.10	SSF51197		00310+1.14.11.8	REACT_13	PWY-6100	UPA00118				
aly12612.1	Unknown		n/a																				
aly12612.2	Unknown		n/a																				
aly12612.3	ELAV-like protein 4	GO:0005737,GO:0030529,GO:0051252,GO:0000166,GO:0008266,GO:0003723,GO:0008049,GO:0007275,GO:0003729	CG4396-PC				SM00361,SM00361,SM00361,SM00360,SM00360,SM00360	TIGR01661	PF14259,PF00076,PF00076	PS50102,PS50102,PS50102	PR00961,PR00961,PR00961,PR00961,PR00961		G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									
aly12612.4	Unknown		CG13458-PA						PF01753	PS50865		PS01360		SSF144232	360~380,807~848								
aly1264.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1264.10	Microtubule-associated protein RP/EB family member 1	GO:0031115,GO:0035371,GO:0035372,GO:0030981,GO:0017022,GO:0000226,GO:0000022,GO:0005815,GO:0005874,GO:0005875,GO:0005876,GO:0005737,GO:0040001,GO:0030951,GO:0051225,GO:0051301,GO:0030589,GO:1903031,GO:0007626,GO:0007067,GO:0007605,GO:0008017,GO:0051010,GO:0007629,GO:0005881,GO:0007052,GO:0042060,GO:0007059,GO:0035011,GO:0007017,GO:0007423,GO:0005515	CG3265-PF						PF03271,PF00307	PS51230			G3DSA:1.10.418.10	SSF47576,SSF140612	195~215								
aly1264.11	Proton-coupled folate transporter	GO:0005215,GO:0016021,GO:0031427,GO:0055085,GO:0005542	CG30344-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly1264.12	Proton-coupled folate transporter	GO:0005215,GO:0016021,GO:0031427,GO:0055085,GO:0005542	CG30344-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly1264.13	ATP-dependent RNA helicase vasa, isoform A	GO:0008104,GO:0007294,GO:0008026,GO:0045495,GO:0007293,GO:0051754,GO:0036464,GO:0003676,GO:0005875,GO:0002168,GO:0005737,GO:0043186,GO:0045170,GO:0005811,GO:0003730,GO:0016246,GO:0048471,GO:0010501,GO:0048477,GO:0010468,GO:0005524,GO:0046012,GO:0046011,GO:0004004,GO:0007316,GO:0007283,GO:0007314,GO:0007286,GO:0007076,GO:0000775,GO:0048134,GO:0045727,GO:0000070,GO:0043025,GO:0007315,GO:0030717,GO:0003724,GO:0008298,GO:0003723,GO:0006417,GO:0006378,GO:0016442,GO:0046843	CG9748-PB				SM00490,SM00487		PF00270,PF00271	PS51194,PS51195,PS51192		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1264.14	Tyrosine-protein kinase hopscotch	GO:0016318,GO:0006968,GO:0042078,GO:0035206,GO:0007616,GO:0035167,GO:0003383,GO:0048103,GO:0031234,GO:0007538,GO:0007169,GO:0007298,GO:0001745,GO:0007530,GO:0005737,GO:0007350,GO:0038083,GO:0007365,GO:0007455,GO:0046425,GO:0007476,GO:0030707,GO:0007259,GO:0004715,GO:0004713,GO:0004672,GO:0016476,GO:0048477,GO:0005524,GO:0048749,GO:0042386,GO:0006468,GO:0007480,GO:0042067,GO:0045087,GO:0035172,GO:0035171,GO:0006952,GO:0035010,GO:0045475,GO:0006955,GO:0045317,GO:0006959,GO:0001751,GO:0007262,GO:0007260,GO:0000910,GO:0007424,GO:0008283,GO:0051607,GO:0007399,GO:0030713,GO:0005856,GO:0060031,GO:0006355,GO:0007442,GO:0006351,GO:0019827,GO:0030097,GO:0045610,GO:0012505	CG1594-PA				SM00295,SM00219,SM00219		PF07714,PF07714	PS50011,PS50011,PS50057	PR00109,PR00109,PR00109,PR00109	PS00109,PS00107	G3DSA:3.30.505.10,G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF56112,SSF55550	868~888									
aly1264.15	Sex peptide receptor	GO:0045434,GO:0008528,GO:0004930,GO:0016021,GO:0005886,GO:0048042,GO:0008188,GO:0007186	CG13229-PA						PF10324	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1264.16	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly1264.17	Sex peptide receptor	GO:0045434,GO:0008528,GO:0004930,GO:0016021,GO:0005886,GO:0048042,GO:0008188,GO:0007186	CG13229-PA						PF10324	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1264.2	Unknown		n/a																				
aly1264.3	Unknown		n/a																				
aly1264.4	Unknown	GO:0005549	n/a						PF01395				G3DSA:1.10.238.20	SSF47565									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1264.5	Eukaryotic translation elongation factor 1 epsilon-1	GO:0005737,GO:0008285,GO:0070062,GO:0005829,GO:0043065,GO:0010467,GO:0006418,GO:0043517,GO:0005634,GO:0005875	CG30185-PA						PF00043	PS50405			G3DSA:1.20.1050.10	SSF47616									
aly1264.6	Solute carrier family 35 member F5	GO:0016021,GO:0016020,GO:0006810	CG8195-PA																				
aly1264.7	28S ribosomal protein S9, mitochondrial	GO:0005840,GO:0005730,GO:0044822,GO:0003735,GO:0005743,GO:0005763,GO:0006412	CG2957-PA						PF00380				G3DSA:3.30.230.10	SSF54211									
aly1264.8	Probable RNA binding protein CG14230	GO:0005575,GO:0022008,GO:0003729,GO:0003676,GO:0000166	CG14230-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly1264.9	Unknown		n/a																				
aly1265.1	Tensin	GO:0007552,GO:0045926,GO:0042052,GO:0030308,GO:0008285,GO:0006470,GO:0016314,GO:0030036,GO:0051898,GO:0009887,GO:0042594,GO:0019915,GO:0051895,GO:0007436,GO:0045786,GO:0035206,GO:0000287,GO:0003779,GO:0030165,GO:0046856,GO:0046855,GO:0010506,GO:0009986,GO:0050773,GO:0048681,GO:0030336,GO:0008286,GO:0006915,GO:0006629,GO:0008138,GO:0008283,GO:0046620,GO:0046621,GO:0006914,GO:0009987,GO:0009888,GO:0016322,GO:0046627,GO:0035011,GO:0005856,GO:0008361,GO:0008360,GO:0005912,GO:0007155,GO:0007010,GO:0007425,GO:0007015,GO:0031104,GO:0045792,GO:0040015,GO:0040014,GO:0090175,GO:0004726,GO:0004725,GO:0031647,GO:0004722,GO:0004721,GO:0005737,GO:0002164,GO:1901888,GO:0051800	CG5671-PD										G3DSA:3.90.190.10	SSF52799									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1265.10	Neural retina-specific leucine zipper protein	GO:0043565,GO:0045872,GO:0007468,GO:0003700,GO:0046548,GO:0005634,GO:0006366,GO:0043522,GO:0008585,GO:0008584,GO:0035262,GO:0006355,GO:0010467,GO:0001077,GO:0045944,GO:0006351,GO:0003677,GO:0007298,GO:0046982,GO:0000978,GO:0000981	CG10034-PC				SM00338		PF03131	PS50217			G3DSA:1.10.880.10,G3DSA:1.20.5.170	SSF57959,SSF47454	238~265								
aly1265.11	Diacylglycerol O-acyltransferase 1	GO:0043231,GO:0019992,GO:0050252,GO:0016021,GO:0030073,GO:0035220,GO:0005789,GO:0005504,GO:0019432,GO:0045477,GO:0008374,GO:0046486,GO:0004144,GO:0048477,GO:0004772,GO:0010888	CG31991-PD			PIRSF000439,PIRSF500231			PF03062							00561+2.3.1.20,00073+2.3.1.20			UPA00230				
aly1265.12	Protein slowmo	GO:0030537,GO:1990050,GO:0015914,GO:0030706,GO:0005739,GO:0007283,GO:0003674,GO:0030432,GO:0005758,GO:0008345,GO:0007275	CG9131-PA						PF04707	PS50904													
aly1265.13	Mediator of RNA polymerase II transcription subunit 11	GO:0007517,GO:0005634,GO:0006366,GO:0003713,GO:0001104,GO:0048813,GO:0006357,GO:0007406,GO:0016592	CG6884-PA						PF10280														
aly1265.14	60S ribosomal protein L3	GO:0022626,GO:0051298,GO:0022625,GO:0051297,GO:0005622,GO:0003735,GO:0007052,GO:0000022,GO:0006412,GO:0005840	CG4863-PA						PF00297			PS00474	G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:3.30.1430.10	SSF50447									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1265.15	Nuclear fragile X mental retardation-interacting protein 1	GO:0043234,GO:0030674,GO:0046872,GO:0022626,GO:0016363,GO:0005726,GO:0005730,GO:0005634,GO:0048786,GO:0005654,GO:0008023,GO:0045944,GO:0003723,GO:0030515,GO:0000492,GO:0070761,GO:0042802,GO:0003729	CG4076-PA				SM00355,SM00355		PF10453	PS50157		PS00028			132~152								
aly1265.16	Chromatin complexes subunit BAP18	GO:0008574,GO:0008017,GO:0007018,GO:0000090,GO:0016589,GO:0016568,GO:0003777,GO:0003677,GO:0005871,GO:0003682,GO:0071339,GO:0005524	CG32955-PG																				
aly1265.17	Probable RNA methyltransferase CG11342	GO:0008168	CG11342-PA						PF06859	PS51515			G3DSA:3.40.50.150	SSF53335,SSF53335									
aly1265.18	Unknown	GO:0003674,GO:0008150,GO:0005887	CG14925-PA						PF07898														
aly1265.19	Unknown		CG15712-PA						PF06757														
aly1265.2	Tensin	GO:0005737,GO:0005856,GO:0007016,GO:0009986,GO:0007476,GO:0007475,GO:0003779,GO:0005912,GO:0005925	CG9379-PA				SM00462,SM00252		PF08416,PF00017	PS50001	PR00401,PR00401,PR00401,PR00401		G3DSA:3.30.505.10,G3DSA:2.30.29.30	SSF50729,SSF55550									
aly1265.20	Unknown		n/a																				
aly1265.21	Unknown		n/a																				
aly1265.22	Unknown		n/a																				
aly1265.23	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1265.3	Unknown	GO:0007218,GO:0005184,GO:0005615,GO:0007204,GO:0007528,GO:0006940,GO:0006950,GO:0071855,GO:0008345,GO:0008344	CG18090-PA																				
aly1265.4	Unknown		n/a												10~37,48~68								
aly1265.5	Unknown		n/a																				
aly1265.6	CD109 antigen	GO:0006909,GO:0005615,GO:0061045,GO:0009986,GO:0004867,GO:0045616,GO:0030512,GO:0050431,GO:0072675,GO:0050830,GO:0004866,GO:0005886,GO:0001933,GO:0010839,GO:0001942,GO:0031225	CG7068-PA						PF01835,PF07678,PF07703,PF00207				G3DSA:1.50.10.20,G3DSA:2.60.40.690	SSF48239,SSF49410										
aly1265.7	Peptidyl-prolyl cis-trans isomerase, rhodopsin-specific isozyme	GO:0016028,GO:0016063,GO:0003755,GO:0070059,GO:0016023,GO:0007601,GO:0016021,GO:0006458,GO:0031965,GO:0005788,GO:0007602,GO:0007603,GO:0005887,GO:0006810,GO:0006457,GO:0016018,GO:0050896	CG3966-PA						PF00160	PS50072	PR00153,PR00153,PR00153,PR00153,PR00153		G3DSA:2.40.100.10	SSF50891										
aly1265.8	Transcription and mRNA export factor ENY2	GO:0031936,GO:0000785,GO:0034399,GO:0000124,GO:0001094,GO:0005634,GO:0003713,GO:0070742,GO:0006368,GO:0016578,GO:0006406,GO:0016973,GO:0030374,GO:0045893,GO:0005643,GO:0070390,GO:0045944,GO:0005515,GO:0015031,GO:0071819,GO:0003682,GO:0043035	CG15191-PA	MF_03046					PF10163														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1265.9	Multiple epidermal growth factor-like domains protein 8	GO:0035108,GO:0030326,GO:0042074,GO:0097094,GO:0060971,GO:0060972,GO:0004872,GO:0071907,GO:0007275,GO:0070062,GO:0016021,GO:0016020,GO:0048842,GO:0005509,GO:0061371,GO:0010468,GO:0048704,GO:0055113,GO:0003143,GO:0097155,GO:0030509,GO:1900164,GO:0005515,GO:0005634	CG7466-PB				SM00042,SM00042,SM00423,SM00423,SM00423,SM00423,SM00423,SM00423,SM00423,SM00423,SM00180,SM00180,SM00180,SM00180,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00179,SM00179		PF00053,PF00053,PF00053,PF13854,PF00431,PF13418,PF13418,PF13418,PF13418,PF07645	PS50027,PS01180,PS01180,PS50026,PS50027,PS50026,PS50026,PS50027,PS50027	PR00011,PR00011,PR00011	PS01186,PS01186,PS00010,PS01186,PS01248,PS01186,PS00022,PS01248,PS00022,PS01248,PS00022,PS00022,PS00022,PS01186,PS00010,PS00022,PS01186,PS01187,PS00022	G3DSA:2.120.10.80,G3DSA:2.120.10.80,G3DSA:2.120.10.80,G3DSA:2.120.10.80,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF117281,SSF117281,SSF57196,SSF117281,SSF57196,SSF117281,SSF49854,SSF49854,SSF57196,SSF57196,SSF57196										
aly12671.1	SID1 transmembrane family member 1	GO:0016021,GO:0033227,GO:0051033	n/a						PF13965														
aly12671.10	Myosin-2 essential light chain	GO:0032036,GO:0017022,GO:0030048,GO:0016461,GO:0016459,GO:0005509,GO:0005515,GO:0016460,GO:0031477,GO:0031476,GO:0031475	CG3201-PB				SM00054,SM00054		PF13405,PF00036	PS50222,PS50222		PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly12671.11	Protein turtle	GO:0030537,GO:0008039,GO:0005887,GO:0098632,GO:0098609,GO:0007638,GO:0016199,GO:0045467,GO:0070593,GO:0046331,GO:0007629,GO:0005515,GO:0007155,GO:0007411,GO:0007414,GO:0008344,GO:0048814	CG16857-PA				SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00060,SM00060		PF13895,PF07679,PF07679,PF00041	PS50835,PS50853,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF49265									
aly12671.2	Unknown		n/a												47~67								
aly12671.3	Chitotriosidase 1	GO:0009617,GO:0005975,GO:0005615,GO:0008843,GO:0006955,GO:0000272,GO:0005764,GO:0005576,GO:0008061,GO:0004553,GO:0004568,GO:0006032	CG3044-PA				SM00636		PF00704			PS01095	G3DSA:3.10.50.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF54556,SSF51445,SSF51445		00520+3.2.1.14		PWY-6902					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly12671.4	Ninein	GO:0090222,GO:0034454,GO:0005730,GO:0005813,GO:0005814,GO:0000922,GO:0005575,GO:0019900,GO:0008150,GO:0005509,GO:0003674,GO:0005874,GO:0005525	CG14025-PG												567~612,381~401,345~372,431~451,403~423,661~688								
aly12671.5	Low-density lipoprotein receptor-related protein 11	GO:0016021,GO:0051219,GO:0005886	CG6495-PA																				
aly12671.6	Low-density lipoprotein receptor-related protein 11	GO:0016021,GO:0051219,GO:0005515,GO:0005886	CG6495-PA				SM00192,SM00765		PF00057,PF07502	PS50068,PS50986		PS01209	G3DSA:4.10.400.10	SSF57424	108~128								
aly12671.7	Protein phosphatase 1 regulatory subunit 14B	GO:0005737,GO:0042325,GO:0019212,GO:0050790,GO:0008599,GO:0004864,GO:0043086	CG17124-PA						PF05361				G3DSA:1.10.150.220	SSF81790									
aly12671.8	Serine/threonine-protein kinase chk-1	GO:0009314,GO:0051225,GO:0007049,GO:0005737,GO:0001700,GO:0005634,GO:0007348,GO:0007349,GO:0007275,GO:0004674,GO:0004672,GO:0005524,GO:0033314,GO:0006468,GO:0051299,GO:0016321,GO:0042060,GO:0007050,GO:0030162,GO:0006974,GO:0000077,GO:0000075,GO:0007444,GO:0007093	CG17161-PC																				
aly12671.9	Serine/threonine-protein kinase grp	GO:0009314,GO:0051225,GO:0007049,GO:0001700,GO:0005634,GO:0007348,GO:0007349,GO:0004674,GO:0004672,GO:0005524,GO:0033314,GO:0006468,GO:0051299,GO:0016321,GO:0042060,GO:0007050,GO:0030162,GO:0000077,GO:0000075,GO:0007444,GO:0005829,GO:0007095,GO:0007093	CG17161-PC						PF00069	PS50011		PS00108	G3DSA:1.10.510.10	SSF56112									
aly127.1	PQ-loop repeat-containing protein 1	GO:0016021	CG13784-PF				SM00679,SM00679		PF04193,PF04193														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.10	Sorting nexin-21	GO:0035091,GO:0030659,GO:0015031	CG3077-PA				SM00312		PF00787	PS50195			G3DSA:3.30.1520.10	SSF64268									
aly127.11	NADH dehydrogenase [ubiqui] iron-sulfur protein 2, mitochondrial	GO:0031625,GO:0046872,GO:0051539,GO:0048812,GO:0008137,GO:0005739,GO:0006120,GO:0005654,GO:0046331,GO:0016651,GO:0006979,GO:0051287,GO:0048038,GO:0003954,GO:0055114,GO:0005747	CG1970-PA	MF_01358				TIGR01962	PF00346			PS00535	G3DSA:1.10.645.10	SSF56762									
aly127.12	Y+L amino acid transporter 2	GO:1902475,GO:0015297,GO:0060356,GO:0003333,GO:0016020,GO:0016323,GO:0050832,GO:0015807,GO:0015179,GO:0005887,GO:0015171	CG12317-PA			PIRSF006060			PF13520														
aly127.13	Homeobox protein Mohawk	GO:0043565,GO:0007517,GO:0035990,GO:0000122,GO:0003700,GO:0005634,GO:0045662,GO:0006366,GO:0006355,GO:0030199,GO:0032967,GO:0010628,GO:0002932,GO:0003677,GO:0022008,GO:0000981	CG11617-PA				SM00389		PF05920	PS50071			G3DSA:1.10.10.60	SSF46689									
aly127.14	39S ribosomal protein L10, mitochondrial	GO:0003735,GO:0042254,GO:0006412,GO:0005762,GO:0030529	CG11488-PA						PF00466					SSF160369									
aly127.15	Angio-associated migratory cell protein	GO:0005737,GO:0014909,GO:0010595,GO:0009986,GO:0030154,GO:0005515,GO:0005886,GO:0001525	CG5114-PB				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400	PS50082,PS50082,PS50294,PS50082			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.16	Large neutral amino acids transporter small subunit 1	GO:0006520,GO:0006865,GO:0007596,GO:0050900,GO:0005737,GO:0070062,GO:0005730,GO:0005634,GO:0016020,GO:0006811,GO:0015297,GO:0030154,GO:0060356,GO:0016324,GO:1902475,GO:0006810,GO:0015804,GO:0015823,GO:0015820,GO:0015827,GO:0005887,GO:0005886,GO:0015196,GO:0015192,GO:0055085,GO:0015190,GO:0043231,GO:0007399,GO:0005829,GO:0042605,GO:0015171,GO:0015175,GO:0098655,GO:0003333	CG3297-PC			PIRSF006060			PF13520														
aly127.17	Zinc transporter ZIP14	GO:1903874,GO:0005794,GO:0071578,GO:0005887,GO:0005783,GO:0016021,GO:0016020,GO:0006882,GO:0005385,GO:0030001,GO:0071577,GO:0015684,GO:0005886,GO:0015093,GO:0006826,GO:0046873,GO:0006829,GO:0055085	CG10006-PB						PF02535						463~472								
aly127.18	ER membrane protein complex subunit 4	GO:0016021,GO:0072546	CG11137-PA			PIRSF017207			PF06417														
aly127.19	Tyrosine aminotransferase	GO:0005739,GO:0006572,GO:0051384,GO:0006559,GO:0006520,GO:0006536,GO:0080130,GO:0009058,GO:0004838,GO:0014070,GO:0030170,GO:0006103,GO:0046689,GO:0016597,GO:0006979,GO:0009072,GO:0006094	CG1461-PA			PIRSF000517		TIGR01264,TIGR01265	PF00155		PR00753,PR00753,PR00753	PS00105	G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383		00400+2.6.1.5,00360+2.6.1.5,00950+2.6.1.5,00960+2.6.1.5,00350+2.6.1.5,00401+2.6.1.5,00270+2.6.1.5,00130+2.6.1.5	REACT_13	PWY-3581,PWY-5886,PWY-5151,PWY-7518,PWY-5754,PWY-7514,PWY-5048	UPA00139				
aly127.2	Mitochondrial import inner membrane translocase subunit Tim21	GO:0016021,GO:0005744,GO:0030150	CG7382-PA						PF08294														
aly127.20	NADH dehydrogenase (ubiqui) complex I, assembly factor 6	GO:0005737,GO:0032981,GO:0009058,GO:0005739,GO:0050821,GO:0005743,GO:0016740,GO:0003674	CG15738-PA						PF00494				G3DSA:1.10.600.10	SSF48576									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.21	Platelet-activating factor acetylhydrolase IB subunit beta homolog	GO:0005575,GO:0003847,GO:0008150	CG8962-PA						PF13472				G3DSA:3.40.50.1110	SSF52266									
aly127.22	OTU domain-containing protein 6B	GO:0008234	CG7857-PA						PF02338	PS50802				SSF54001	12~65								
aly127.23	Lysine--tRNA ligase	GO:0004824,GO:0005737,GO:0006430,GO:0000166,GO:0003676,GO:0046872,GO:0005875,GO:0005524	CG12141-PC	MF_00252		PIRSF039101		TIGR00499	PF01336,PF00152	PS50862	PR00982,PR00982,PR00982,PR00982,PR00982		G3DSA:2.40.50.140,G3DSA:3.30.930.10	SSF55681,SSF50249	1~34	00970+6.1.1.6	REACT_71						
aly127.24	Protein Mo25	GO:0005575,GO:0001700,GO:0003674	CG4083-PB						PF08569				G3DSA:1.25.10.10	SSF48371	18~38		REACT_11163,REACT_498						
aly127.25	Activating molecule in BECN1-regulated autophagy protein 1	GO:0030154,GO:0098779,GO:0043524,GO:0051568,GO:0005875,GO:0005737,GO:0005634,GO:0004402,GO:0005776,GO:0005739,GO:0005741,GO:0016573,GO:0008285,GO:0021915,GO:0006914,GO:0045335,GO:0031625,GO:2000785,GO:0022008,GO:0005930,GO:0005671,GO:0043552,GO:0006338,GO:0005829,GO:0048188,GO:0005515,GO:0007095,GO:0044666,GO:0044545,GO:1903599,GO:0044665	CG17437-PA				SM00320,SM00320,SM00320			PS50294,PS50082			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978									
aly127.26	Unknown		n/a																				
aly127.27	Unknown		CG2225-PE																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.28	Profilin	GO:0030717,GO:0007300,GO:0005546,GO:0007411,GO:0007436,GO:0000902,GO:0000281,GO:0051491,GO:0003779,GO:0048471,GO:0045451,GO:0005737,GO:0032507,GO:0042060,GO:0007488,GO:0008154,GO:0007283,GO:0030041,GO:0007420,GO:0007015,GO:0000915,GO:0005856,GO:0007391,GO:0035193,GO:0005515	CG9553-PF				SM00392		PF00235		PR00392,PR00392,PR00392,PR00392,PR00392,PR00392,PR01640,PR01640,PR01640,PR01640,PR01640,PR01640	PS00414	G3DSA:3.30.450.30	SSF55770										
aly127.29	Eukaryotic initiation factor 4A	GO:0008026,GO:0007279,GO:0007067,GO:0005875,GO:0002168,GO:0072686,GO:0000381,GO:0005813,GO:0005634,GO:0010501,GO:0048477,GO:0051297,GO:0005524,GO:0000339,GO:0017116,GO:0004004,GO:0006974,GO:0007052,GO:0048132,GO:0043186,GO:0030718,GO:0007446,GO:0009950,GO:0006268,GO:0005829,GO:0003724,GO:0000022,GO:0003729,GO:0006413,GO:0016281,GO:0003743	CG9075-PF				SM00487		PF00270	PS51192,PS51195		PS00039	G3DSA:3.40.50.300	SSF52540										
aly127.3	Transmembrane protein 231	GO:0045930,GO:0007030,GO:0042384,GO:0035869,GO:0060170,GO:0016021,GO:0007224,GO:0036038	CG14020-PB						PF10149														
aly127.30	Eukaryotic initiation factor 4A	GO:0071011,GO:0006413,GO:0016281,GO:0045495,GO:0005634,GO:0004004,GO:0004386,GO:0006974,GO:0000398,GO:0005515,GO:0003743,GO:0071013,GO:0008380,GO:0005524,GO:0045451	CG7483-PA				SM00490		PF00271	PS51194			G3DSA:3.40.50.300	SSF52540										
aly127.31	Unknown		CG31886-PB						PF16040,PF16041														
aly127.32	Activating signal cointegrator 1 complex subunit 1	GO:0005737,GO:0003824,GO:0006355,GO:0006351,GO:0005667,GO:0003723	CG12129-PA			PIRSF027019	SM00322		PF00013,PF10469	PS50084			G3DSA:3.90.1140.10,G3DSA:3.30.1370.10	SSF54791										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.33	Schwannomin-interacting protein 1	GO:0005737	CG5375-PB						PF10148,PF10148						303~330,578~605								
aly127.34	Zinc finger protein sens	GO:0042051,GO:0042059,GO:0045465,GO:0045464,GO:0008270,GO:0043425,GO:0007411,GO:0043565,GO:0007219,GO:0000122,GO:0005634,GO:0008407,GO:0043066,GO:0006366,GO:0016360,GO:0046872,GO:0048666,GO:0050767,GO:0007601,GO:0008594,GO:0007423,GO:0007422,GO:0003700,GO:0003705,GO:0005700,GO:0006355,GO:0048813,GO:0001077,GO:0045944,GO:0000977,GO:0030099	CG32120-PA				SM00355,SM00355,SM00355,SM00355		PF13912,PF00096	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly127.35	Carbonyl reductase [NADPH] 1	GO:0005737,GO:1903561,GO:0016614,GO:0070062,GO:0016655,GO:0042373,GO:0004090,GO:0047021,GO:0008152,GO:0030855,GO:0050221,GO:0017144,GO:0055114	CG12171-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									
aly127.36	Transmembrane 9 superfamily member 4	GO:0006909,GO:0005215,GO:0016021,GO:0035010,GO:0050829,GO:0005768	CG7364-PA						PF02990,PF02990														
aly127.37	Neuroguidin	GO:0005737,GO:0032040,GO:0005730,GO:0044822,GO:0030425,GO:0030424,GO:0030175,GO:0000462,GO:0006417,GO:0000775	CG11030-PA						PF04000						217~237								
aly127.38	Unknown		n/a						PF15139														
aly127.39	Radial spoke head 10 homolog B2	GO:0005575,GO:0003674,GO:0008150	CG30429-PA				SM00698,SM00698,SM00698,SM00698,SM00698,SM00698,SM00698,SM00698,SM00698		PF02493,PF02493,PF02493,PF02493,PF02493,PF02493,PF02493,PF02493,PF02493,PF02493,PF02493,PF02493				G3DSA:2.20.110.10,G3DSA:2.20.110.10	SSF82185,SSF82185									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.4	Hemocyte protein-glutamine gamma-glutamyltransferase	GO:0018149,GO:0042381,GO:0003810,GO:0045087,GO:0016020,GO:0046872	CG7356-PA				SM00460		PF00927,PF00927,PF00868,PF00868,PF01841				G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.90.260.10,G3DSA:2.60.40.10	SSF81296,SSF81296,SSF54001,SSF49309,SSF49309									
aly127.40	CDK5 and ABL1 enzyme substrate 2	GO:0006909,GO:0051726,GO:0016538,GO:0007049,GO:0051302,GO:0051301	CG6191-PC						PF00134				G3DSA:1.10.472.10	SSF47954									
aly127.41	E3 ubiquitin-protein ligase mind-bomb	GO:0008104,GO:0007476,GO:0008587,GO:0008270,GO:0001745,GO:0061630,GO:0000209,GO:0005737,GO:0007219,GO:0004842,GO:0045179,GO:0045747,GO:0048749,GO:0007480,GO:0046331,GO:0008593,GO:0016874,GO:0006897,GO:0007423,GO:0005829,GO:0016567,GO:0005515,GO:0045807	CG5841-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00291		PF00569,PF12796,PF12796,PF06701,PF06701	PS50088,PS51416,PS51416,PS50088,PS50088,PS50297,PS50088,PS50135	PR01415,PR01415	PS01357	G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF159034,SSF159034,SSF48403,SSF57850					UPA00143				
aly127.42	E3 ubiquitin-protein ligase mib1	GO:0048749,GO:0005737,GO:0008104,GO:0006897,GO:0007423,GO:0007480,GO:0008587,GO:0008593,GO:0045179,GO:0007219,GO:0005815,GO:0045747,GO:0016874,GO:0046331,GO:0008270,GO:0005515,GO:0016567,GO:0045807,GO:0001745,GO:0004842,GO:0007476	CG5841-PA				SM00248,SM00248,SM00248,SM00184,SM00184,SM00184		PF13857,PF13920,PF13920,PF13920,PF13920	PS50089,PS50297,PS50088,PS50089,PS50088	PR01415,PR01415		G3DSA:3.30.40.10,G3DSA:1.25.40.20	SSF57850,SSF48403									
aly127.43	WW domain-containing oxidoreductase	GO:0005737,GO:0010165,GO:0006915,GO:0016614,GO:0016055,GO:2000377,GO:0008152,GO:0050829,GO:0010212,GO:0016491	CG7221-PA						PF00106				G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.44	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	GO:0005737,GO:0071011,GO:0006396,GO:0071013,GO:0044822,GO:0004004,GO:0004386,GO:0005654,GO:0003724,GO:0000398,GO:0003676,GO:0005681,GO:0022008,GO:0008380,GO:0005524,GO:0006397	CG10689-PA				SM00847,SM00487,SM00490		PF07717,PF00271,PF04408,PF00270	PS51192,PS51194		PS00690	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	754~774								
aly127.45	Succinate dehydrogenase assembly factor 4, mitochondrial	GO:0005575,GO:0008150,GO:0005759,GO:0003674	CG7224-PA						PF07896														
aly127.46	V-type proton ATPase subunit d	GO:0015992,GO:0015991,GO:0007035,GO:0033181,GO:0033179,GO:0000220,GO:0046961,GO:0008593,GO:0005886,GO:0015078	CG2934-PA			PIRSF018497			PF01992					SSF103486									
aly127.47	Conserved oligomeric Golgi complex subunit 6	GO:0015031,GO:0006891,GO:0017119,GO:0000139	CG1968-PA				SM01087		PF06419														
aly127.48	39S ribosomal protein L15, mitochondrial	GO:0003735,GO:0015934,GO:0006412,GO:0005762	CG5219-PA	MF_01341					PF00828				G3DSA:3.100.10.10	SSF52080									
aly127.49	Adenosylhomocysteinase	GO:0004013,GO:0006730	CG11654-PA	MF_00563		PIRSF001109	SM00997,SM00996	TIGR00936	PF05221,PF00670			PS00739,PS00738	G3DSA:3.40.50.1480,G3DSA:3.40.50.1480,G3DSA:3.40.50.720	SSF52283,SSF52283,SSF51735		00270+3.3.1.1		PWY-5041	UPA00314				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.5	Annulin	GO:0018149,GO:0042381,GO:0003810,GO:0045087,GO:0005886,GO:0046872	CG7356-PA			PIRSF000459	SM00460		PF01841,PF00927,PF00868	PS51257			G3DSA:2.60.40.10,G3DSA:3.90.260.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49309,SSF54001,SSF81296,SSF49309										
aly127.50	Importin subunit beta-1	GO:0005811,GO:0006610,GO:0008565,GO:0019899,GO:0007304,GO:0007067,GO:0005875,GO:0071782,GO:0005737,GO:0016020,GO:0070062,GO:0005635,GO:0005654,GO:0043234,GO:0031965,GO:0044822,GO:0006606,GO:0006607,GO:0008320,GO:0008360,GO:0019904,GO:0000059,GO:0007015,GO:0005643,GO:0008536,GO:0051533	CG2637-PE				SM00913		PF13513,PF03810	PS50166			G3DSA:1.25.10.10	SSF48371										
aly127.51	40S ribosomal protein S18	GO:0005737,GO:0005840,GO:0005730,GO:0005829,GO:0042254,GO:0005622,GO:0003735,GO:0007052,GO:0022627,GO:0003723,GO:0000022,GO:0000228,GO:0019843,GO:0006413,GO:0006412,GO:0015935	CG8900-PA	MF_01315		PIRSF002134			PF00416	PS50159		PS00646	G3DSA:4.10.910.10,G3DSA:1.10.8.50	SSF46946										
aly127.52	Histidine-rich membrane protein KE4 homolog 2	GO:0008021,GO:0005622,GO:0016021,GO:0042069,GO:0030234,GO:0016020,GO:0055085,GO:0007300,GO:0030001,GO:0045202,GO:0005887,GO:0007298,GO:0030424,GO:0043025,GO:0046873,GO:2000274	CG10449-PA						PF02535														
aly127.53	Major facilitator superfamily domain-containing protein 1	GO:0016021,GO:0055085	CG12194-PB						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly127.54	Organic cation transporter 1	GO:0016021,GO:0015695,GO:0008513,GO:0022857,GO:0015101,GO:0008340,GO:0055085	CG9317-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.55	Junctophilin-3	GO:0040011,GO:0060314,GO:0015278,GO:0005783,GO:0050885,GO:0030314,GO:0016021,GO:0070588,GO:0007613,GO:0005789,GO:0035640,GO:0003674,GO:0005886,GO:0008150,GO:0048168,GO:0007612	CG4405-PB				SM00698,SM00698,SM00698,SM00698,SM00698,SM00698		PF02493,PF02493,PF02493,PF02493,PF02493,PF02493,PF02493				G3DSA:2.20.110.10,G3DSA:2.20.110.10,G3DSA:2.20.110.10	SSF82185,SSF82185									
aly127.56	Probable palmitoyltransferase ZDHHC24	GO:0019706,GO:0016021,GO:0018345,GO:0008270,GO:0005783	CG10344-PB							PS50216													
aly127.57	Trifunctional enzyme subunit alpha, mitochondrial	GO:0006635,GO:0051287,GO:0005739,GO:0042594,GO:0032868,GO:0003857,GO:0005875,GO:0050662,GO:0042645,GO:0005811,GO:0005777,GO:0000062,GO:0004300,GO:0003985,GO:0006644,GO:0042060,GO:0008340,GO:0044255,GO:0055114,GO:0042493,GO:0035965,GO:0005743,GO:0016508,GO:0016509,GO:0046474,GO:0016507,GO:0044281	CG4389-PA					TIGR02441	PF00725,PF00378,PF02737				G3DSA:3.40.50.720,G3DSA:3.90.226.10,G3DSA:1.10.1040.10,G3DSA:1.10.1040.10	SSF48179,SSF52096,SSF48179,SSF51735		00281+4.2.1.17,00720+4.2.1.17,00310+4.2.1.17,00120+1.1.1.35,00380+4.2.1.17,00062+4.2.1.17+1.1.1.21,00280+4.2.1.17+1.1.1.35,00281+4.2.		PWY-5177,PWY-6583,PWY-6883,PWY-5138,PWY-5136,PWY-7094,PWY-7654,PWY-7656,PWY-5789,PWY-6945,PWY-5109,PWY-7007,PWY-6435,PWY-7046,PWY-	UPA00659				
aly127.58	Aromatic-L-amino-acid decarboxylase	GO:0048082,GO:0040040,GO:0006520,GO:0004058,GO:0040007,GO:0007619,GO:0007616,GO:0043052,GO:0007615,GO:0006585,GO:0016831,GO:0035220,GO:0006584,GO:0006587,GO:0008062,GO:0042423,GO:0007611,GO:0048085,GO:0009611,GO:0048066,GO:0030170	CG10697-PC						PF00282		PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800	PS00392	G3DSA:3.90.1150.10,G3DSA:1.20.1340.10,G3DSA:3.40.640.10	SSF53383									
aly127.59	Peroxisomal N(1)-acetyl-spermine/spermidine oxidase	GO:0005737,GO:0006598,GO:0052899,GO:0005782,GO:0046208,GO:0009447,GO:0009446,GO:0046203,GO:1901307,GO:0008150,GO:0052902,GO:0052901,GO:0003674,GO:0046592,GO:0052903,GO:0052904,GO:0005102,GO:0055114,GO:0016491	CG10561-PA						PF01593				G3DSA:3.90.660.10,G3DSA:3.40.50.720	SSF54373,SSF51905,SSF51905									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.6	Protein tilB homolog	GO:0005737,GO:0045433,GO:0007605,GO:0030317,GO:0036158,GO:0036159,GO:0010378,GO:0060287,GO:0035082,GO:0005515,GO:0005929,GO:0008584,GO:0044458	CG14620-PA				SM00446,SM00365,SM00365,SM00365		PF14580	PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									
aly127.60	BTB/POZ domain-containing protein 2	GO:0000932,GO:0005515	CG11275-PA				SM00225		PF07707,PF00651	PS50097			G3DSA:3.30.710.10	SSF54695									
aly127.61	Unknown	GO:0005488	n/a											SSF48371,SSF48371	84~118,157~188,1247~1267								
aly127.62	Vacuolar protein sorting associated protein 52 homolog	GO:0005794,GO:0048611,GO:1990745,GO:0032456,GO:0015031,GO:0048471,GO:0010668,GO:0055037,GO:0010008	CG7371-PA						PF04129						523~543,59~79								
aly127.63	Probable nuclear hormone receptor HR38 (Fragment)	GO:0048082,GO:0043565,GO:0042335,GO:0006909,GO:0006351,GO:0005634,GO:0003707,GO:0006355,GO:0000977,GO:0043401,GO:0008544,GO:0004879,GO:0008270	CG1864-PB				SM00430,SM00399		PF00104,PF00105	PS51030	PR01284,PR01284,PR01284,PR01284,PR01284,PR01284,PR01284,PR01284,PR00398,PR00398,PR00398,PR00398,PR00398,PR00047,PR00047,PR00047,PR00047	PS00031	G3DSA:3.30.50.10,G3DSA:1.10.565.10	SSF48508,SSF57716			REACT_71						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.64	5'-AMP-activated protein kinase subunit gamma-2	GO:0006633,GO:0009267,GO:0010800,GO:0006469,GO:0042595,GO:0035556,GO:0008603,GO:0071901,GO:0006629,GO:0005737,GO:0045787,GO:0005634,GO:0005654,GO:0004674,GO:0006110,GO:0008607,GO:0004679,GO:0005524,GO:0006468,GO:0031588,GO:0042632,GO:0019217,GO:0006914,GO:0016208,GO:0019901,GO:0004862,GO:0043531,GO:2001020,GO:0030295,GO:0005615,GO:0030730,GO:0005977,GO:0030554,GO:0005829,GO:0045860	CG17299-PR				SM00116,SM00116,SM00116,SM00116		PF00571,PF00571	PS51371,PS51371,PS51371,PS51371			G3DSA:3.10.580.10,G3DSA:3.10.580.10	SSF54631,SSF54631	518~538								
aly127.65	COP9 signalosome complex subunit 8	GO:0005737,GO:0051726,GO:0007476,GO:0050821,GO:0042742,GO:0007095,GO:0001745,GO:0048477,GO:0008180	CG42522-PB						PF10075				G3DSA:1.10.10.10										
aly127.66	Chitin synthase 1	GO:0007443,GO:0007424,GO:0004100,GO:0007430,GO:0008362,GO:0060439,GO:0035159,GO:0016021,GO:0009611,GO:0035158,GO:0001838,GO:0071555,GO:0005886,GO:0006035	CG2666-PA						PF03142					SSF53448	1083~1103,1013~1043,1197~1217								
aly127.67	Chitin synthase 1	GO:0007443,GO:0007424,GO:0004100,GO:0007430,GO:0008362,GO:0060439,GO:0035159,GO:0016021,GO:0009611,GO:0035158,GO:0001838,GO:0071555,GO:0005886,GO:0006035	CG2666-PA						PF03142				G3DSA:3.90.550.10	SSF53448	1048~1072,1216~1236								
aly127.68	MPN domain-containing protein CG4751	GO:0008233	CG4751-PA						PF01398				G3DSA:3.40.140.10	SSF102712									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.69	Ras-related protein Rab-14	GO:0005764,GO:0055037,GO:0005802,GO:0031982,GO:0006895,GO:0006886,GO:0090387,GO:0003924,GO:0042742,GO:0032482,GO:0045335,GO:0008152,GO:0031164,GO:0032456,GO:0005525,GO:0043025,GO:0005769,GO:0016192	CG12015-PB				SM00174,SM00173,SM00175	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly127.7	T-box transcription factor TBX20	GO:0060577,GO:0035223,GO:0060045,GO:0010629,GO:0001077,GO:0001764,GO:0003015,GO:0007411,GO:0051890,GO:0003344,GO:0036306,GO:0007417,GO:0005737,GO:0003207,GO:0007367,GO:0000122,GO:0005634,GO:0001569,GO:0014018,GO:0014019,GO:0001947,GO:0055008,GO:0003175,GO:0003193,GO:0010991,GO:0042684,GO:0048665,GO:0021524,GO:0006936,GO:0008283,GO:0008015,GO:0035050,GO:0001105,GO:0003215,GO:0042659,GO:0007409,GO:0007402,GO:0007507,GO:0001227,GO:0001226,GO:0009953,GO:0007399,GO:0003700,GO:0003148,GO:0030381,GO:0003272,GO:0006355,GO:0051960,GO:0045944,GO:0000977,GO:0003180,GO:0060413,GO:0000978,GO:0035922	CG6634-PB				SM00425		PF00907	PS50252	PR00937,PR00937,PR00937,PR00937,PR00937,PR00937	PS01283	G3DSA:2.60.40.820	SSF49417										
aly127.70	Probable cysteine desulfurase, mitochondrial	GO:0005737,GO:0006523,GO:0004123,GO:0005634,GO:0005739,GO:0016226,GO:0006534,GO:0030170,GO:0031071,GO:0051536,GO:0046872,GO:0005875	CG12264-PA			PIRSF005572			PF00266			PS00595	G3DSA:3.40.640.10,G3DSA:3.90.1150.10	SSF53383		00730+2.8.1.7		PWY-6892,PWY-6891,PWY-6823,PWY-7250						
aly127.71	Negative elongation factor E	GO:0034244,GO:0032021,GO:0017053,GO:0000122,GO:0005634,GO:0032785,GO:0000166,GO:0008023,GO:0045944,GO:0003723,GO:0006368,GO:0022008,GO:0005694,GO:0007070,GO:0003729	CG5994-PA																				
aly127.72	Unknown	GO:0006952	n/a											SSF57095									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.73	Aromatic-L-amino-acid decarboxylase	GO:0048082,GO:0040040,GO:0006520,GO:0040007,GO:0007619,GO:0007616,GO:0043052,GO:0007615,GO:0006585,GO:0006584,GO:0035220,GO:0004058,GO:0003824,GO:0006587,GO:0008062,GO:0042416,GO:0007611,GO:0048085,GO:0009611,GO:0048066,GO:0030170	CG10697-PC						PF00282		PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800	PS00392	G3DSA:3.90.1150.10,G3DSA:1.20.1340.10,G3DSA:3.40.640.10	SSF53383	393~394								
aly127.74	Calponin homology domain-containing protein 2	GO:0016021	n/a										G3DSA:2.60.40.360		1728~1728								
aly127.75	LIM/homeobox protein Lhx3	GO:0021520,GO:0043565,GO:0048839,GO:0021526,GO:0007399,GO:0051726,GO:0003700,GO:0005634,GO:0021527,GO:0006366,GO:0021521,GO:0006355,GO:0001076,GO:0043066,GO:0045944,GO:0008270,GO:0005667,GO:0008045,GO:0021983	CG10699-PG				SM00132,SM00132,SM00389		PF00412,PF00412,PF00046	PS50023,PS50071,PS50023		PS00478,PS00027	G3DSA:1.10.10.60,G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF46689,SSF57716									
aly127.76	Protein phosphatase PHLPP-like protein	GO:0006470,GO:0006915,GO:0004722,GO:0005575,GO:0003824,GO:0046872,GO:0042981	CG10493-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00332,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364		PF00481,PF13855,PF13855	PS51450,PS51450,PS51450,PS51746,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.60.40.10,G3DSA:3.80.10.10,G3DSA:3.60.40.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF81606									
aly127.77	Unknown		n/a																				
aly127.78	Cysteine-rich venom protein triflin	GO:0008150,GO:0005576,GO:0003674	CG8483-PA				SM00198		PF00188,PF08562		PR00838,PR00838,PR00837,PR00837,PR00837,PR00837	PS01009	G3DSA:3.40.33.10	SSF57546,SSF55797									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.79	Protein PIH1D3	GO:0005737,GO:0030317,GO:0051087,GO:0070286	CG5048-PA						PF08190	PS51203			G3DSA:2.60.40.790	SSF49764									
aly127.8	T-box transcription factor TBX20	GO:0060577,GO:0035223,GO:0060045,GO:0010629,GO:0001077,GO:0001764,GO:0003015,GO:0007411,GO:0051890,GO:0003344,GO:0036306,GO:0007417,GO:0005737,GO:0003207,GO:0007367,GO:0000122,GO:0005634,GO:0001569,GO:0014018,GO:0014019,GO:0001947,GO:0055008,GO:0003175,GO:0003193,GO:0010991,GO:0042684,GO:0048665,GO:0021524,GO:0006936,GO:0008283,GO:0008015,GO:0035050,GO:0001105,GO:0003215,GO:0042659,GO:0007409,GO:0007402,GO:0007507,GO:0001227,GO:0001226,GO:0009953,GO:0007399,GO:0003700,GO:0003148,GO:0030381,GO:0003272,GO:0006355,GO:0051960,GO:0045944,GO:0000977,GO:0003180,GO:0060413,GO:0000978,GO:0035922	CG6634-PB				SM00425		PF00907	PS50252	PR00937,PR00937,PR00937,PR00937,PR00937,PR00937	PS01283	G3DSA:2.60.40.820	SSF49417									
aly127.80	Unknown		n/a																				
aly127.81	Probable 26S proteasome non-ATPase regulatory subunit 3	GO:0004175,GO:0005838,GO:0043161,GO:0030234,GO:0042176,GO:0000502,GO:0006508,GO:0008541	CG42641-PB				SM00753,SM00088		PF01399,PF08375				G3DSA:1.10.10.10	SSF46785	466~490								
aly127.82	Zinc finger CCHC domain containing protein 2	GO:0005737,GO:0035091,GO:0008270,GO:0003676	CG10492-PA							PS50158			G3DSA:4.10.60.10										
aly127.83	Unknown		n/a																				
aly127.84	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.85	Neural-cadherin	GO:0048675,GO:0016318,GO:0005887,GO:0016339,GO:0030425,GO:0030424,GO:0045467,GO:0045463,GO:0004872,GO:0007411,GO:0007412,GO:0007413,GO:0050839,GO:0048846,GO:0016021,GO:0016020,GO:0048841,GO:0005509,GO:0031290,GO:0042803,GO:0008013,GO:0005911,GO:0005886,GO:0007155,GO:0044331,GO:0007156,GO:0050774,GO:0045296,GO:0048814,GO:0005515	CG7100-PL				SM00112,SM00112,SM00112,SM00112,SM00112,SM00282,SM00282,SM00181,SM00181,SM00181,SM00181,SM00179,SM00179,SM00179,SM00179		PF00028,PF00028,PF00028,PF00028,PF00028,PF01049,PF00008,PF00008,PF02210,PF02210,PF12661	PS50268,PS50026,PS50268,PS50026,PS50268,PS50268,PS50268,PS50026,PS50025,PS50268,PS50025	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00022,PS00232,PS00010,PS01186,PS01186,PS00022,PS01186,PS00232,PS00022,PS01187,PS00010,PS00232,PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:4.10.900.10,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200	SSF49313,SSF49899,SSF49313,SSF49313,SSF49313,SSF57184,SSF57184,SSF49313,SSF49313,SSF49899,SSF49313									
aly127.86	Neural-cadherin	GO:0048675,GO:0016318,GO:0005887,GO:0016339,GO:0030425,GO:0030424,GO:0045467,GO:0045463,GO:0004872,GO:0007411,GO:0007412,GO:0007413,GO:0050839,GO:0048846,GO:0016021,GO:0016020,GO:0048841,GO:0005509,GO:0031290,GO:0042803,GO:0008013,GO:0005911,GO:0005886,GO:0007155,GO:0044331,GO:0007156,GO:0050774,GO:0045296,GO:0048814,GO:0005515	CG7100-PL				SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112		PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028	PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00232,PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313									
aly127.87	Broad-complex core protein isoform 6	GO:0010629,GO:0003676,GO:0003677,GO:0008219,GO:0042332,GO:0005634,GO:0007552,GO:0048808,GO:0046872,GO:0048477,GO:0071390,GO:0035075,GO:0035072,GO:0035070,GO:0006914,GO:0048747,GO:0007458,GO:0040034,GO:0003700,GO:0001752,GO:0009608,GO:0007562,GO:0048813,GO:0045944,GO:0000977	CG12236-PA				SM00355,SM00355,SM00225		PF00651,PF12874	PS50157,PS50097,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.710.10,G3DSA:3.30.160.60	SSF54695,SSF57667									
aly127.88	Geranylgeranyl transferase type-2 subunit alpha	GO:0018342,GO:0018344,GO:0005968,GO:0017137,GO:0008360,GO:0004663,GO:0007155,GO:0022008,GO:0008318,GO:0008270	CG12007-PA						PF01239,PF01239,PF01239,PF01239	PS51147,PS51147,PS51147,PS51147,PS51147			G3DSA:3.80.10.10,G3DSA:1.25.40.120,G3DSA:1.25.40.120	SSF48439,SSF48439,SSF52058									
aly127.89	Exonuclease mut-7 homolog	GO:0008408,GO:0030529,GO:0044748,GO:0003676,GO:0044747,GO:0046872	CG9247-PA				SM00474		PF01927,PF01612				G3DSA:3.30.420.10	SSF53098									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly127.9	Unknown		n/a																				
aly127.90	26S proteasome non-ATPase regulatory subunit 6	GO:0004175,GO:0005838,GO:0070062,GO:0022624,GO:0043161,GO:0009987,GO:0000502,GO:0006508,GO:0022008,GO:0008541	CG5378-PA				SM00088		PF10602,PF01399				G3DSA:1.10.10.10	SSF46785									
aly127.91	Sal-like protein 1	GO:0030325,GO:0048566,GO:0060173,GO:0003281,GO:0008586,GO:0008584,GO:0021553,GO:0003676,GO:0003677,GO:0003340,GO:0021983,GO:0021889,GO:0001078,GO:0072073,GO:0005737,GO:0000122,GO:0005634,GO:0008406,GO:0001822,GO:0016575,GO:0045666,GO:0001843,GO:0046872,GO:0072092,GO:0031129,GO:0007507,GO:0007605,GO:0048098,GO:0045879,GO:0008013,GO:0090190,GO:0000792,GO:0061034,GO:0035136,GO:0035137,GO:0001657,GO:0001658,GO:0072309,GO:0022008,GO:0042733,GO:0042473,GO:0016581,GO:0007423,GO:0003700,GO:2000177,GO:0030539,GO:0030177,GO:0003337,GO:0010369,GO:0006355,GO:0045944,GO:0006351,GO:0045892,GO:0000978,GO:0003682,GO:0045893	CG4881-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF12874,PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	1162~1182									
aly127274.1	Unknown		n/a																				
aly1274.1	Unknown	GO:0032027,GO:0005516,GO:0005515,GO:0005938	CG18285-PA				SM00015,SM00015		PF00612,PF00612	PS50096,PS50096			G3DSA:1.20.5.190,G3DSA:1.20.5.190	SSF52540	18~38								
aly1274.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1274.3	Unknown		n/a																				
aly1274.4	E3 ubiquitin-protein ligase CBL	GO:0007166,GO:0007476,GO:0017124,GO:0042059,GO:0008270,GO:0004871,GO:0008340,GO:0007298,GO:0010941,GO:0008069,GO:0005737,GO:0016874,GO:0005634,GO:0033971,GO:0033500,GO:0043066,GO:0005509,GO:0006508,GO:0046875,GO:0001784,GO:0042127,GO:0006468,GO:0007175,GO:0007173,GO:0005938,GO:0005886,GO:0001754,GO:0004842,GO:0045453,GO:0048134,GO:0006897,GO:0009950,GO:0080134,GO:0007465,GO:0005515,GO:0014068	CG7037-PB				SM00184		PF13920,PF02761,PF02762	PS50089,PS51506,PS50030		PS00518	G3DSA:1.10.238.10,G3DSA:3.30.505.10,G3DSA:1.10.8.10,G3DSA:3.30.40.10	SSF47473,SSF46934,SSF55550,SSF57850										
aly12745.1	Integrin alpha-PS3	GO:0007494,GO:0048149,GO:0030336,GO:0007614,GO:0005886,GO:0007613,GO:0007611,GO:0007160,GO:0035001,GO:0004872,GO:0007411,GO:0005925,GO:0003344,GO:0008355,GO:0005737,GO:0007431,GO:0016021,GO:0005055,GO:0005198,GO:0009925,GO:0016477,GO:0016339,GO:0006909,GO:0033627,GO:0005178,GO:0016328,GO:0016340,GO:0007507,GO:0016324,GO:0042060,GO:0008305,GO:0043277,GO:0007155,GO:0007157,GO:0050839,GO:0001555,GO:0040011,GO:0007424,GO:0007391,GO:0007229,GO:0007508,GO:0045886,GO:0046982	CG8095-PB									PS00242	G3DSA:1.20.5.930				REACT_13552						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly12745.2	Integrin alpha-4	GO:0009897,GO:0034113,GO:0034446,GO:0060710,GO:0007160,GO:0050901,GO:0004872,GO:0016337,GO:0005925,GO:0003366,GO:0070062,GO:0016020,GO:0016477,GO:0001968,GO:0009986,GO:0008305,GO:0007159,GO:0005911,GO:0005886,GO:0007155,GO:0060485,GO:0007157,GO:0050839,GO:0072678,GO:0043113,GO:0007507,GO:0046872,GO:0007229,GO:0090074,GO:0001974,GO:0061032,GO:0034669,GO:0060324	CG5372-PA				SM00191,SM00191,SM00191,SM00191		PF01839,PF01839	PS51470,PS51470,PS51470,PS51470	PR01185,PR01185,PR01185,PR01185,PR01185,PR01185,PR01185	PS00242	G3DSA:2.60.40.1510,G3DSA:2.130.10.130,G3DSA:1.20.5.930	SSF69179,SSF69318			REACT_13552						
aly127538.1	Unknown		n/a																				
aly127757.1	Nuclear envelope integral membrane protein 1	GO:0016021	CG9723-PA						PF10225														
aly127910.1	Unknown		n/a																				
aly128.1	Regulation of nuclear pre-mRNA domain-containing protein 1B	GO:0008284,GO:0070940,GO:0005634,GO:0010564,GO:0005575,GO:0045944,GO:0008150,GO:0006351,GO:0003674,GO:0016591,GO:0000993	CG9018-PA				SM00582		PF16566,PF04818	PS51391			G3DSA:1.25.40.90	SSF48464	283~310								
aly128.10	85/88 kDa calcium-independent phospholipase A2	GO:0005737,GO:0006629,GO:0006935,GO:0032049,GO:0016020,GO:0016042,GO:0005515,GO:0004623,GO:0005815,GO:0005829,GO:0047499	CG6718-PB				SM01015,SM00248,SM00248,SM00248,SM00248,SM00248		PF06456,PF01734,PF12796,PF12796	PS50088,PS50088,PS50088,PS50088,PS50870,PS50088,PS50297			G3DSA:3.40.1090.10,G3DSA:1.25.40.20,G3DSA:1.20.1270.60	SSF103657,SSF48403,SSF52151									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly128.11	Cyclin-dependent kinase 14	GO:0000308,GO:0002009,GO:0006468,GO:0016055,GO:0030332,GO:0020037,GO:0051726,GO:0000086,GO:0005634,GO:0007552,GO:0001700,GO:0004674,GO:0005886,GO:0051301,GO:0005515,GO:0004672,GO:0004693,GO:0048589,GO:0060828,GO:0005524,GO:0002168	CG10579-PN				SM00220		PF00069	PS50011		PS00191,PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly128.12	Armadillo repeat-containing protein 8	GO:0008565,GO:0005737,GO:0005643,GO:0006606,GO:0017022,GO:0008320,GO:0009411,GO:0007095,GO:0051533	CG9423-PA				SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185		PF00514	PS50077			G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371									
aly128.13	Ankyrin repeat domain-containing protein 54	GO:0005737,GO:0005634,GO:0030496	CG10809-PA				SM00248,SM00248,SM00248		PF12796	PS50088,PS50088,PS50297,PS50088			G3DSA:1.25.40.20	SSF48403									
aly128.14	Unknown		n/a																				
aly128.15	Sphingosine kinase 2	GO:0016310,GO:0008481,GO:0003951,GO:0006669,GO:0001568,GO:0016020,GO:0046834,GO:0043066,GO:0004143,GO:0006665,GO:0005524,GO:0008284,GO:0017050,GO:0038036,GO:0008283,GO:0016301,GO:0007629,GO:0003376,GO:0018991,GO:0007420,GO:0007565,GO:0005829,GO:0007205,GO:0005765,GO:0046512,GO:0006670	CG32484-PA				SM00046		PF00781	PS50146				SSF111331,SSF111331									
aly128.16	tRNA (cytosine(38)-C(5))-methyltransferase	GO:0003677,GO:0008340,GO:0000786,GO:0008168,GO:0000723,GO:0030488,GO:0005730,GO:0005634,GO:0003886,GO:0016458,GO:0016363,GO:0005737,GO:0045089,GO:0006306,GO:0000790,GO:0044026,GO:0008175,GO:0009408,GO:0006979,GO:0010494,GO:0001975,GO:0002230,GO:0003723,GO:0043045	CG10692-PC					TIGR00675	PF00145	PS51679	PR00105,PR00105,PR00105	PS00095	G3DSA:3.90.120.10,G3DSA:3.40.50.150	SSF53335		00270+2.1.1.37							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly128.17	Protein JTB	GO:0000910,GO:0005737,GO:0005819,GO:0016021,GO:0030496,GO:0005739,GO:0005815,GO:0019901,GO:0007067,GO:0045860	CG1935-PA						PF05439														
aly128.18	Maternal protein tudor	GO:0030719,GO:0005737,GO:0043186,GO:0005634,GO:0007315,GO:0005739,GO:0019090,GO:0007281,GO:0009790,GO:0007278,GO:0008298,GO:0007277,GO:0045495	CG9450-PA				SM00333,SM00333,SM00333,SM00333,SM00333,SM00333,SM00333,SM00333,SM00333		PF00567,PF00567,PF00567,PF00567,PF00567,PF00567,PF00567,PF00567,PF00567	PS50304,PS50304,PS50304,PS50304,PS50304,PS50304,PS50304,PS50304,PS50304			G3DSA:2.30.30.140,G3DSA:2.30.30.140,G3DSA:2.30.30.140,G3DSA:2.30.30.140,G3DSA:2.30.30.140,G3DSA:2.30.30.140,G3DSA:2.30.30.140,G3DSA:2.30.30.140,G3DSA:2.30.30.140	SSF63748,SSF63748,SSF63748,SSF63748,SSF63748,SSF63748,SSF63748,SSF63748,SSF63748	1614~1634,2324~2333								
aly128.19	Condensin complex subunit 2	GO:0007443,GO:0007424,GO:0000070,GO:0048567,GO:0008258,GO:0072587,GO:0005829,GO:0007422,GO:0007052,GO:0000775,GO:0000793,GO:0006099,GO:0000785,GO:0051306,GO:0007076,GO:0000796,GO:0022008,GO:0005634,GO:0007067,GO:0051301,GO:0002009	CG10726-PA						PF05786														
aly128.2	Sodium-dependent serotonin transporter	GO:0005328,GO:0006837,GO:0007626,GO:0009636,GO:0005326,GO:0005886,GO:0007613,GO:0017022,GO:0010628,GO:0042310,GO:0001666,GO:0019811,GO:0010008,GO:0051610,GO:0032355,GO:0045787,GO:0016021,GO:0051260,GO:0045665,GO:0051259,GO:0043005,GO:0017075,GO:0042803,GO:0017032,GO:0007623,GO:0005335,GO:0035176,GO:0046621,GO:0007584,GO:0051015,GO:0012505,GO:0005887,GO:0006836,GO:0010033,GO:0032227,GO:0015222,GO:0007420,GO:0042713,GO:0048854,GO:0005829,GO:0045121,GO:0042493,GO:0071300,GO:0021794,GO:0071321,GO:0021941	CG8850-PB						PF00209	PS50267	PR00176,PR00176,PR00176,PR00176,PR00176			SSF161070									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly128.20	Protein LSM14 homolog B-B	GO:0006888,GO:0005783,GO:0030036,GO:0045169,GO:0006417,GO:0000226,GO:0005515,GO:0007310,GO:0007275,GO:0043186,GO:0030529,GO:0005875	CG10686-PH						PF09532,PF12701	PS51512,PS51513,PS51536				SSF50182									
aly128.21	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0016491,GO:0005737,GO:0030728,GO:0070062,GO:0007179,GO:0004022,GO:0016323,GO:0003824,GO:0008152,GO:0045786,GO:0055114,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly128.22	Kelch-like protein 10	GO:0005737,GO:0048873,GO:0000902,GO:0006919,GO:0009566,GO:0008584,GO:0016567,GO:0007291,GO:0007286,GO:0048808,GO:0031463	CG12423-PA			PIRSF037037	SM00875,SM00612,SM00612,SM00612,SM00612,SM00612,SM00225		PF01344,PF01344,PF01344,PF01344,PF01344,PF07707,PF00651	PS50097			G3DSA:3.30.710.10,G3DSA:2.120.10.80	SSF54695,SSF117281									
aly128.23	60S ribosomal protein L18	GO:0005840,GO:0022625,GO:0005622,GO:0003735,GO:0007052,GO:0000022,GO:0006412	CG8615-PA									PS01106	G3DSA:3.100.10.10	SSF52080									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly128.24	Folliculin	GO:0035065,GO:0030308,GO:0005886,GO:2000506,GO:0035024,GO:0010629,GO:0051898,GO:0003674,GO:0010823,GO:2000973,GO:0005737,GO:0001701,GO:0005730,GO:0045785,GO:0005634,GO:0043065,GO:1901837,GO:0032403,GO:1901840,GO:0030336,GO:0031929,GO:0032465,GO:0030097,GO:2001170,GO:0030511,GO:1900181,GO:0030718,GO:0001932,GO:0000122,GO:1901723,GO:0045944,GO:0032008,GO:0032007,GO:0007043,GO:0032006,GO:0070373,GO:0001934	CG8616-PA						PF16692,PF11704														
aly128.25	Cytochrome c1, heme protein, mitochondrial	GO:0046872,GO:0020037,GO:0005743,GO:0016021,GO:0005811,GO:0006122,GO:0005739,GO:0005750,GO:0070469,GO:0005506,GO:0009055,GO:0045153,GO:0005634,GO:0055114,GO:0006119	CG4769-PB						PF02167	PS51007	PR00603,PR00603,PR00603,PR00603,PR00603,PR00603,PR00603,PR00603		G3DSA:1.10.760.10,G3DSA:1.20.5.100	SSF81496,SSF46626									
aly128.26	Protein arginine N-methyltransferase 7	GO:0005737,GO:0016274,GO:0018216,GO:0005575,GO:0035243,GO:0019918,GO:0019919	CG9882-PB						PF06325	PS51678,PS51678			G3DSA:3.40.50.150,G3DSA:3.40.50.150,G3DSA:2.70.160.11	SSF53335,SSF53335									
aly128.27	Unknown		n/a																				
aly128.3	Ubiquitin carboxyl-terminal hydrolase 10	GO:0005737,GO:0006281,GO:0016579,GO:0006914,GO:0030330,GO:0010506,GO:0005769,GO:0045747,GO:0004843,GO:0006511,GO:0004197,GO:0044325,GO:0005634,GO:0002039,GO:0036459	CG32479-PA						PF00443	PS50235		PS00973		SSF54001,SSF54001									
aly128.4	Allatotropin	GO:0007218,GO:0005184,GO:0002027,GO:0006811,GO:0043271,GO:0005576,GO:0045969	n/a									PS00018											

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly128.5	Unknown	GO:0006030,GO:0005576,GO:0008061	n/a						PF01607	PS50940			G3DSA:2.170.140.10	SSF57625	117~168								
aly128.6	Supervillin	GO:0005737,GO:0071437,GO:0036449,GO:0002102,GO:0007010,GO:0005615,GO:0032504,GO:0007519,GO:0005634,GO:0030496,GO:0032154,GO:0051015,GO:0003674,GO:0005886,GO:0032467,GO:0005925,GO:0043034,GO:0015629	CG45186-PAE				SM00262,SM00262,SM00262,SM00262		PF00626				G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10	SSF55753,SSF55753,SSF55753,SSF55753,SSF55753,SSF55753	1283~1317								
aly128.7	Unknown		n/a																				
aly128.8	Unknown	GO:0003674,GO:0005615,GO:0032504	CG45186-PAE												257~285								
aly128.9	Protein cueball	GO:0016021,GO:0005041,GO:0042813,GO:0060070,GO:0007283,GO:0007285,GO:0005886,GO:0017147,GO:0044332,GO:0048477	CG12086-PA				SM00135,SM00135,SM00135,SM00181,SM00181,SM00181		PF00058,PF00058	PS50026,PS50026,PS51120,PS51120,PS51120		PS01186,PS00022,PS00022,PS00022,PS01186	G3DSA:2.10.25.10,G3DSA:2.120.10.30,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57196,SSF63825,SSF57196									
aly128025.1	Unknown	GO:0005740,GO:0022857,GO:0055085	CG5805-PA						PF00153	PS50920			G3DSA:1.50.40.10	SSF103506									
aly1281.1	MDS1 and EVI1 complex locus protein EVI1	GO:0016607,GO:0006351,GO:0030154,GO:0071425,GO:0051726,GO:0003700,GO:0005634,GO:0006915,GO:0045892,GO:0045893,GO:0003676,GO:0003677,GO:0046329,GO:0046872,GO:0043069,GO:0042803	CG10348-PC				SM00355,SM00355,SM00355		PF00096,PF00096	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1281.10	Twist-related protein	GO:0031032,GO:0007498,GO:0007499,GO:0010629,GO:0010004,GO:0003677,GO:0005737,GO:0007435,GO:0006355,GO:0005634,GO:0007369,GO:0042803,GO:0016202,GO:0007507,GO:0048747,GO:0001710,GO:0007443,GO:0007370,GO:0007375,GO:0007500,GO:0009950,GO:0003700,GO:0007501,GO:0003705,GO:0014029,GO:0006357,GO:0045944,GO:0006351,GO:0046983,GO:0046982	CG2956-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459										
aly1281.11	ATP-dependent DNA helicase PIF1	GO:0000723,GO:0006310,GO:0000002,GO:0006281,GO:0005634,GO:0003677,GO:0005739,GO:0043141,GO:0003678,GO:0005524	CG3238-PA	MF_03176			SM00382		PF05970				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	627~637									
aly1281.12	Unknown		n/a												20~47								
aly1281.13	Protein brunelleschi	GO:0007111,GO:0007110,GO:0006891,GO:0007112,GO:0036063,GO:0000916,GO:0005794,GO:0032313,GO:0000281,GO:0017112,GO:0030008,GO:0043147,GO:0043087,GO:0048137,GO:0005737,GO:0043547	CG2478-PA						PF08626,PF08626														
aly1281.14	U6 snRNA-associated Sm-like protein LSm7	GO:0000288,GO:0005732,GO:0071011,GO:0071013,GO:0000398,GO:0010467,GO:0005688,GO:0022008,GO:0043928,GO:0005829,GO:0005681,GO:0017070	CG13277-PB			PIRSF037188	SM00651		PF01423				G3DSA:2.30.30.100	SSF50182										
aly1281.15	Unknown	GO:0005975,GO:0016810,GO:0005576,GO:0008061,GO:0005515,GO:0006030	CG17905-PA				SM00494,SM00192		PF00057,PF01607	PS50068,PS50940		PS01209	G3DSA:4.10.400.10,G3DSA:3.20.20.370,G3DSA:2.170.140.10	SSF88713,SSF57424,SSF57625										
aly1281.16	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1281.17	Chitinase domain-containing protein 1	GO:0005975,GO:0005764,GO:0005576,GO:0008061,GO:0004568,GO:0006032	CG8460-PA				SM00636		PF00704	PS51257			G3DSA:3.20.20.80	SSF51445,SSF51445									
aly1281.18	Epidermal retinol dehydrogenase 2	GO:0043616,GO:0004745,GO:0016021,GO:0005789,GO:0008152,GO:0042572,GO:0042574,GO:0016491	CG15629-PA						PF00106		PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly1281.2	Transcription factor hamlet	GO:0048666,GO:0008285,GO:0007219,GO:0050773,GO:0007423,GO:0003700,GO:0005634,GO:0006355,GO:0048813,GO:0014017,GO:0048814,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG31753-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF00096,PF00096,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly1281.3	Unknown	GO:0048666,GO:0007423,GO:0003700,GO:0005634,GO:0006355,GO:0048813,GO:0048814,GO:0003676,GO:0046872	CG31753-PB										G3DSA:2.170.270.10										
aly1281.4	Unknown		n/a																				
aly1281.5	Unknown		n/a																				
aly1281.6	Protein gustavus	GO:0005737,GO:0070449,GO:0008104,GO:0035017,GO:0007280,GO:0007472,GO:0005634,GO:0007281,GO:0045732,GO:0007315,GO:0007314,GO:0005938,GO:0005515,GO:0035556,GO:0046843,GO:0048471,GO:0031466,GO:0045495	CG2944-PG				SM00449,SM00969		PF00622,PF07525	PS50225,PS50188				SSF49899					UPA00143					
aly1281.7	Unknown		n/a												1089~1112								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1281.8	Transcriptional adapter 3	GO:0044154,GO:0000124,GO:0043966,GO:0000123,GO:0043967,GO:0043983,GO:0035066,GO:0005705,GO:0004402,GO:0043987,GO:0048096,GO:0005703,GO:0006355,GO:0005671,GO:0005700,GO:0016573,GO:0006338,GO:0003682,GO:0043970,GO:0005634,GO:0006351	CG7098-PC						PF10198														
aly1281.9	Zinc finger protein 358	GO:0019827,GO:0021915,GO:0006355,GO:0005634,GO:0035115,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG30443-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	668~688								
aly1282.1	Unknown	GO:0003676	n/a											SSF53098,SSF53098									
aly1282.10	Transmembrane protein 165	GO:0005794,GO:0035751,GO:0043231,GO:0006487,GO:0006874,GO:0016021,GO:0016020,GO:0005765,GO:0032588,GO:0003674,GO:0008150,GO:0032472,GO:0031902,GO:0031901,GO:0010008	CG42542-PE						PF01169,PF01169			PS01214			140~172								
aly1282.11	Exosome complex component MTR3	GO:0005737,GO:0034475,GO:0000178,GO:0071028,GO:0016075,GO:0005730,GO:0031125,GO:0000176,GO:0000177,GO:0000175,GO:0034427,GO:0003723,GO:0071051,GO:0010468	CG8025-PA						PF01138				G3DSA:3.30.230.70	SSF54211,SSF55666			REACT_21257						
aly1282.12	Protein phosphatase 1 regulatory subunit 42	GO:0005737,GO:0008285,GO:0015631,GO:0015630,GO:0016336,GO:0016334,GO:0005813,GO:0045502,GO:0000164,GO:0005815,GO:0003779,GO:0005515,GO:0002177,GO:0008599	CG5851-PA				SM00369,SM00369,SM00369,SM00365,SM00365,SM00365		PF12799	PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058	17~45								
aly1282.13	JmjC domain-containing protein 7	GO:0004623	CG10133-PA				SM00558		PF13621	PS51184			G3DSA:2.60.120.650,G3DSA:2.60.120.650	SSF51197,SSF51197									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1282.14	Disintegrin and metalloprotease domain-containing protein 10	GO:0005737,GO:0005794,GO:0006468,GO:0007219,GO:0004222,GO:0016021,GO:0005798,GO:0019901,GO:0007162,GO:0008270,GO:0008593,GO:0006509,GO:0005634,GO:0009986,GO:0008237,GO:0042803	CG1964-PA						PF13688	PS50215			G3DSA:3.40.390.10	SSF55486									
aly1282.15	Unknown		n/a							PS51257													
aly1282.16	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG1213-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly1282.17	Dystrobrevin beta	GO:0005737,GO:0008092,GO:0008307,GO:0016010,GO:0008270,GO:0016014,GO:0045202,GO:0005509	CG8529-PF						PF09069,PF09068				G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473,SSF47473	442~476,393~423								
aly1282.18	Sodium-dependent noradrenaline transporter	GO:0005330,GO:0005328,GO:0005329,GO:0008504,GO:0016021,GO:0015872,GO:0042745,GO:0030431,GO:0005887,GO:0006836,GO:0015844,GO:0019811,GO:0048265	CG8380-PB						PF00209,PF00209	PS50267	PR00176,PR00176,PR00176,PR00176,PR00176,PR00176	PS00610		SSF161070									
aly1282.19	Protein FAM183A		n/a						PF14886						67~87								
aly1282.2	Peroxisomal membrane protein PEX13	GO:0007626,GO:0005779,GO:0005778,GO:0043231,GO:0016021,GO:0016020,GO:0005777,GO:0098779,GO:0001967,GO:0007031,GO:0060152,GO:0001561,GO:0016560,GO:0001764,GO:0002230,GO:0048137,GO:0021795	CG4663-PA				SM00326		PF04088,PF00018	PS50002			G3DSA:2.30.30.40,G3DSA:2.30.30.40	SSF50044,SSF50044									
aly1282.20	Coiled-coil domain-containing protein 103	GO:0005737,GO:0003143,GO:0003146,GO:0031514,GO:0007368,GO:0070286,GO:0001947,GO:0003341,GO:0005930	CG13202-PA						PF15867														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1282.21	XK-related protein 6	GO:0016021	n/a						PF09815						259~279								
aly1282.22	Protein SREK1IP1	GO:0006397,GO:0008270,GO:0003676,GO:0008380	CG3918-PA						PF13917	PS50158					67~97								
aly1282.23	Protein DEK	GO:0005634,GO:2001032,GO:0003677,GO:0043292,GO:0044822,GO:0016568,GO:0006397	CG5935-PB						PF08766				G3DSA:1.10.10.60	SSF109715	102~122								
aly1282.24	Far upstream element-binding protein 1	GO:0000381,GO:0005634,GO:0044822,GO:0005654,GO:0007283,GO:0003723,GO:0005515,GO:0003677,GO:0048024,GO:0048025,GO:0005685,GO:0003729,GO:0001205,GO:0006397	CG8912-PC				SM00322,SM00322,SM00322		PF00013,PF00013,PF00013	PS50084,PS50084,PS50084			G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10	SSF54791,SSF54791,SSF54791									
aly1282.25	Unknown	GO:0016021	n/a						PF09815														
aly1282.3	40S ribosomal protein S7	GO:0032040,GO:0022627,GO:0042274,GO:0030686,GO:0005622,GO:0003735,GO:0006364,GO:0006412,GO:0005840	CG1883-PE						PF01251			PS00948											
aly1282.4	UDP-glucose 4-epimerase	GO:0050662,GO:0019388,GO:0005975,GO:0070062,GO:0005829,GO:0044237,GO:0006012,GO:0044281,GO:0003974,GO:0003978,GO:0042803	CG12030-PA						PF16363				G3DSA:3.40.50.720	SSF51735									
aly1282.5	UDP-glucose 4-epimerase	GO:0050662,GO:0006012,GO:0003978,GO:0044237,GO:0003974	CG12030-PA						PF16363				G3DSA:3.90.25.10,G3DSA:3.90.25.10	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1282.6	Longitudinals lacking protein like	GO:0006351,GO:0001700,GO:0007435,GO:0031519,GO:0006357,GO:0003700,GO:0006342,GO:0005634,GO:0000794,GO:0005700,GO:0016458,GO:0007426,GO:0031208,GO:0045893,GO:0005515,GO:0003677,GO:0045892,GO:0035167,GO:0016568,GO:0042803	CG5738-PB				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695										
aly1282.7	Ras-responsive element-binding protein 1	GO:0016318,GO:1903691,GO:0008258,GO:0016607,GO:0035160,GO:0003676,GO:0046329,GO:0007362,GO:2000394,GO:0070062,GO:0000122,GO:1900026,GO:0005634,GO:0005654,GO:0046872,GO:0048749,GO:0005737,GO:0035152,GO:0048190,GO:0033601,GO:0042067,GO:0008594,GO:0045892,GO:0046665,GO:0010634,GO:0007424,GO:0007398,GO:0003700,GO:0005730,GO:0007393,GO:0007391,GO:0007390,GO:0006355,GO:0006351,GO:0008293,GO:0000979	CG12212-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13909	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	1316~1318								
aly1282.8	Unknown		n/a																				
aly1282.9	Probable histone-lysine N-methyltransferase Mes-4	GO:0018024,GO:0042054,GO:0018992,GO:0008134,GO:0003712,GO:0005700,GO:0031490,GO:0016458,GO:0008270,GO:0000228,GO:0005721	CG4976-PA						PF00855	PS50812			G3DSA:2.30.30.160,G3DSA:3.30.40.10	SSF57903,SSF63748									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1283.1	Muscle M-line assembly protein unc-89	GO:0005089,GO:0006468,GO:0031430,GO:0043547,GO:0030241,GO:0004672,GO:0017048,GO:0031034,GO:0045214,GO:0031672,GO:0005515,GO:0035023,GO:0019902,GO:0005524,GO:0007527	CG33519-PC				SM00408,SM00409,SM00060,SM00060,SM00233,SM00325		PF00069,PF00069,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF00041,PF00041,PF00621	PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50853,PS50835,PS50835,PS50835,PS50011,PS50835,PS50003,PS50835,PS50853,PS50835,PS50835,PS50835,PS50835,PS50835,PS50010,PS50011			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:1.10.510.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.30.200.20,G3DSA:3.30.200.20,G3DSA:3.30.200.20,G3DSA:1.20.900.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:1.10.510.10,G3DSA:2.30.29.30,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF56112,SSF48726,SSF48726,SSF48726,SSF49265,SSF49265,SSF48726,SSF50729,SSF48726,SSF48065,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF56112,SSF48726,SSF48726,SSF48726,SSF48726	2330~2350,1823~1847								
aly1283.10	Chorion peroxidase	GO:0060967,GO:0020037,GO:0006727,GO:0006979,GO:0005764,GO:0005576,GO:0042744,GO:0007306,GO:0046872,GO:0004601,GO:0055114	CG6969-PA						PF03098	PS50292	PR00457,PR00457,PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									
aly1283.11	Ubiquitin-like modifier-activating enzyme 5	GO:0006777,GO:0016616,GO:0008641,GO:0008265,GO:0048037,GO:0005524,GO:0046872,GO:0055114	CG1749-PA						PF00899			PS00065	G3DSA:3.40.50.720	SSF69572	4~24								
aly1283.12	MutS protein homolog 5	GO:0008094,GO:0000400,GO:0045910,GO:0008630,GO:0006301,GO:0006281,GO:0000710,GO:0000795,GO:0006298,GO:0030983,GO:0009411,GO:0051026,GO:0032301,GO:0000228,GO:0032138,GO:0032137,GO:0007131,GO:0043570,GO:0003684,GO:0005524,GO:0045143	CG7003-PA				SM00534		PF00488				G3DSA:3.40.50.300	SSF52540,SSF48334									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1283.13	MutS protein homolog 5	GO:0008094,GO:0006298,GO:0030983,GO:0051026,GO:0000795,GO:0000228,GO:0045143,GO:0007131,GO:0005524	n/a						PF05192				G3DSA:1.10.1420.10	SSF48334									
aly1283.14	Caveolin-3	GO:0060347,GO:0055013,GO:0005783,GO:0031116,GO:0030154,GO:0060307,GO:0086005,GO:0019899,GO:0043407,GO:0042593,GO:0017080,GO:0051001,GO:0051647,GO:0038009,GO:0044325,GO:1901017,GO:0090002,GO:0014819,GO:0005737,GO:0035995,GO:0016049,GO:0031982,GO:0019870,GO:0016021,GO:0006641,GO:1901019,GO:0051896,GO:0002027,GO:0042383,GO:0031594,GO:2000649,GO:1901380,GO:0008284,GO:0043234,GO:0010831,GO:0008016,GO:0051394,GO:0050998,GO:0030315,GO:0009986,GO:1900826,GO:0017015,GO:0060373,GO:0031122,GO:2001288,GO:0046716,GO:0005886,GO:0007520,GO:0042632,GO:0060762,GO:0090279,GO:0061052,GO:0001778,GO:0060299,GO:0007015,GO:0045792,GO:0005901,GO:0051926,GO:0005829,GO:0007204,GO:0000139,GO:0016010,GO:1900744,GO:0005246,GO:0070836,GO:0032947	n/a						PF01146														
aly1283.15	Unknown		n/a												56~76								
aly1283.16	Unknown		n/a												315~335								
aly1283.17	Unknown		n/a																				
aly1283.18	Bromodomain containing protein 7	GO:0008285,GO:0003714,GO:2000134,GO:0035066,GO:0005634,GO:0016055,GO:0003713,GO:0070577,GO:0048812,GO:0045892,GO:0045893,GO:0005515,GO:0003677,GO:0002039,GO:0007049,GO:0006351	CG7154-PA						PF12024				G3DSA:1.20.920.10	SSF47370									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1283.19	Unknown		n/a																				
aly1283.2	NEDD8-conjugating enzyme UBE2F	GO:0005737,GO:0045116,GO:0016874,GO:0045879,GO:0019788,GO:0005575,GO:0004842,GO:0005524	CG7375-PC				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				
aly1283.20	Hairy/enhancer-of-split related with YRPW motif protein	GO:0048664,GO:0007219,GO:0003700,GO:0005634,GO:0045746,GO:0006355,GO:0006351,GO:0003677,GO:0046983	CG11194-PA				SM00511,SM00353		PF00010,PF07527	PS51054,PS50888			G3DSA:4.10.280.10	SSF158457,SSF47459									
aly1283.21	Unknown		n/a																				
aly1283.22	Unknown		n/a																				
aly1283.23	Spherulin-2A		n/a										G3DSA:2.170.15.10										
aly1283.24	Unknown		n/a																				
aly1283.25	Serine/threonine-protein kinase 3	GO:2001235,GO:2001233,GO:0060215,GO:0050821,GO:0045464,GO:0043524,GO:0035265,GO:0035556,GO:0051897,GO:0035329,GO:0023014,GO:0007417,GO:0005737,GO:0032092,GO:0010212,GO:0003157,GO:0046983,GO:0005634,GO:0000287,GO:0000165,GO:0031098,GO:0043065,GO:0004674,GO:0045600,GO:0060706,GO:0001841,GO:0097284,GO:0005524,GO:0042803,GO:0042127,GO:0008285,GO:0006468,GO:0016301,GO:0008283,GO:0046621,GO:0006915,GO:0007346,GO:0060253,GO:0046330,GO:0001654,GO:0046666,GO:1902043,GO:0042771,GO:0000186,GO:0051091,GO:0060800,GO:0002011,GO:0090090,GO:0005575,GO:0005515,GO:0004702,GO:0045892,GO:0072089,GO:0004709	CG11228-PA				SM00220		PF00069,PF11629	PS50951,PS50011		PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112	480~500								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1283.26	Cilia- and flagella-associated protein 20	GO:0048666,GO:0036064,GO:0007517,GO:0070062,GO:0060271,GO:0006355,GO:0003700,GO:0005634,GO:0044822,GO:0000398,GO:0060296,GO:0071011,GO:0048813,GO:2000253,GO:0005814,GO:2000147,GO:0005929,GO:0005874,GO:0071013,GO:0018095	CG5343-PA						PF05018														
aly1283.27	Nodal modulator 1	GO:0016021,GO:0016020,GO:0030246,GO:0005789	CG1371-PA						PF13620,PF13620				G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.1120	SSF49464,SSF49452,SSF49478										
aly1283.28	Unknown		n/a																				
aly1283.29	Heat shock protein Hsp-16.1/Hsp-16.11	GO:0006497,GO:0005797,GO:0030968,GO:0051082,GO:0009790,GO:0010998,GO:0009408,GO:0010506	CG4533-PA						PF00011	PS01031	PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly1283.3	Vacuolar protein-sorting associated protein 25	GO:0016197,GO:0045199,GO:0032509,GO:0008283,GO:0060429,GO:0000814,GO:0043162,GO:0030154,GO:0000046,GO:0050680,GO:0042059,GO:0005198,GO:0048803,GO:0007293,GO:0043328,GO:0008593,GO:0070086,GO:0042981,GO:0030713,GO:0010669,GO:0042803	CG14750-PA						PF05871,PF06090				G3DSA:1.10.10.570,G3DSA:1.10.10.10	SSF46785,SSF46785		00562+2.7.1.158		PWY-6362,PWY-6361,PWY-4661,PWY-6369,PWY-6554,PWY-6372					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1283.30	Phospholipid scramblase 1	GO:0017128,GO:0016020,GO:0071222,GO:0060368,GO:0017121,GO:0006955,GO:0006659,GO:0017124,GO:0019899,GO:0031012,GO:0001077,GO:0003677,GO:0045089,GO:0035455,GO:0035456,GO:0032091,GO:0070062,GO:0005730,GO:0005634,GO:0042609,GO:0045071,GO:0043065,GO:1902231,GO:0033003,GO:0005509,GO:0005886,GO:0006366,GO:0005794,GO:0070782,GO:0005154,GO:2000373,GO:0006915,GO:0006953,GO:0005887,GO:0007268,GO:0097193,GO:0051607,GO:0071345,GO:0005829,GO:0045121,GO:0010628,GO:0045944,GO:0030099	CG1893-PA						PF03803				SSF54518										
aly1283.31	Unknown		n/a																				
aly1283.32	Transcriptional adapter 2A	GO:0000123,GO:0043966,GO:0006338,GO:0043967,GO:0006357,GO:0005634,GO:0004402,GO:0005671,GO:0035327,GO:0008270,GO:0016573,GO:0003677,GO:0042789,GO:0003682	CG43663-PB				SM00717		PF00249,PF04433	PS51293,PS50934		PS00028	G3DSA:1.10.10.60	SSF46689,SSF46689,SSF57850									
aly1283.4	Solute carrier organic anion transporter family member 4C1	GO:0030154,GO:0008514,GO:0005215,GO:0016021,GO:0016020,GO:0015711,GO:0016323,GO:0007283,GO:0006810,GO:0007275,GO:0006811	CG31634-PA					TIGR00805	PF03137	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473									
aly1283.5	Dynein assembly factor with WDR repeat domains 1	GO:0060271,GO:0007368,GO:0070286,GO:0060285,GO:0005515,GO:0005929	CG7568-PE				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF00400	PS50294,PS50082,PS50082,PS50082,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978									
aly1283.6	Lysosomal Pro X carboxypeptidase	GO:0005764,GO:0006508,GO:0004180,GO:0004185,GO:0008236	CG2493-PA						PF05577				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1283.7	Cysteine-rich protein 2-binding protein	GO:0036335,GO:0043998,GO:0006325,GO:2000620,GO:0030274,GO:0006338,GO:0043967,GO:0043968,GO:0005634,GO:0004402,GO:0005737,GO:0000086,GO:0005671,GO:0008270,GO:0016573,GO:0010485,GO:0043966	CG10414-PA									PS01359	G3DSA:3.30.40.10	SSF57903									
aly1283.8	Cysteine-rich protein 2-binding protein	GO:0036335,GO:0043998,GO:0006325,GO:2000620,GO:0030274,GO:0006338,GO:0043967,GO:0043968,GO:0005634,GO:0004402,GO:0005737,GO:0000086,GO:0005671,GO:0008270,GO:0016573,GO:0010485,GO:0043966	CG10414-PA						PF00583	PS51186			G3DSA:3.40.630.30	SSF55729									
aly1283.9	DnaJ protein homolog 1	GO:0005737,GO:0009408,GO:0006457,GO:0005875,GO:0051082	CG5001-PB				SM00271		PF01556,PF00226	PS50076	PR00625,PR00625,PR00625,PR00625	PS00636	G3DSA:1.10.287.110,G3DSA:2.60.260.20,G3DSA:2.60.260.20	SSF49493,SSF49493,SSF46565									
aly128698.1	Unknown		n/a																				
aly1289.1	Unknown		n/a																				
aly1289.2	TWiK family of potassium channels protein 18	GO:0040011,GO:0005267,GO:0006936,GO:0071805,GO:0006813,GO:0016021,GO:0016020,GO:0015271	CG42340-PB						PF07885,PF07885		PR01333,PR01333		G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324,SSF81324									
aly12913.1	UDP-glucuronosyltransferase 2B15	GO:0043231,GO:0052696,GO:0016021,GO:0042493,GO:0009813,GO:0005789,GO:0032870,GO:0008152,GO:0019439,GO:0015020	CG4302-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly12913.2	UDP-glucuronosyltransferase 2B15	GO:0043231,GO:0052696,GO:0016021,GO:0042493,GO:0009813,GO:0005789,GO:0032870,GO:0008152,GO:0019439,GO:0016758,GO:0015020,GO:0003851	CG17322-PC						PF00201				G3DSA:3.40.50.2000	SSF53756									
aly1294.1	Cubilin	GO:0031419,GO:0016324,GO:0006898,GO:0005765,GO:0005509,GO:0015031,GO:0004872,GO:0008203,GO:0010008	CG32702-PB				SM00179,SM00179,SM00179,SM00179,SM00042,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181		PF07645,PF07645,PF07645,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00431,PF00008,PF00008	PS01180,PS01180,PS01180,PS50026,PS01180,PS50026,PS01180,PS50026,PS01180,PS01180,PS01180,PS01180,PS01180,PS01180,PS01180,PS01180,PS01180,PS01180,PS01180,PS01180,PS01180,PS01180,PS01180,PS01180,PS01180	PS01187,PS00010,PS00022,PS00022,PS01186,PS00022,PS00010,PS01187	G3DSA:2.60.120.290,G3DSA:2.10.25.10,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.10.25.10,G3DSA:2.60.120.290,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.10.25.10	SSF57184,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF57196,SSF49854,SSF57196,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF49854,SSF57196								
aly1294.10	Cell division cycle protein 20 homolog	GO:0006909,GO:0090129,GO:0090302,GO:0007147,GO:0007067,GO:0000922,GO:0007144,GO:0051301,GO:0005737,GO:0005819,GO:0040020,GO:0005813,GO:0005815,GO:0005654,GO:0000278,GO:0009987,GO:0031145,GO:0030162,GO:0030163,GO:0022008,GO:0000776,GO:0051488,GO:0030718,GO:0016567,GO:0005515,GO:0007096,GO:0005680,GO:0031915,GO:0008054	CG4274-PA				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50082,PS50294,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1294.11	Apoptotic protease-activating factor 1	GO:0097190,GO:0034352,GO:0046672,GO:0007291,GO:0021556,GO:0042981,GO:0007559,GO:0010332,GO:0043065,GO:0005524,GO:0035071,GO:0006919,GO:0006915,GO:0012501,GO:0046668,GO:0043531,GO:0035070,GO:0008635,GO:0008656,GO:0007423,GO:0070050,GO:0048813,GO:0043293	CG6829-PB				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00619,PF00931	PS50209			G3DSA:1.10.533.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:3.40.50.300,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF52540,SSF47986,SSF50998,SSF50998,SSF50998,SSF50998,SSF50978									
aly1294.12	Unknown		n/a																				
aly1294.13	Protein toll	GO:0009897,GO:0007416,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0007165,GO:0008063,GO:0006955,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0002229,GO:0042802,GO:0016201,GO:0009880,GO:0007507,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005886,GO:0007155,GO:0007352,GO:0043234,GO:0006952,GO:0009950,GO:0009620,GO:0004888,GO:0045944,GO:0005515,GO:0030097,GO:0045610,GO:0005769,GO:0035007	CG7250-PA				SM00369,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00255,SM00082,SM00082		PF13855,PF13855,PF13855,PF13855,PF13855,PF13306,PF01582	PS50104,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.40.50.10140,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52200,SSF52058,SSF52058,SSF52058									
aly1294.14	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1294.15	Protein toll	GO:0009897,GO:0007416,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0007165,GO:0008063,GO:0006955,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0002229,GO:0042802,GO:0016201,GO:0009880,GO:0007507,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005886,GO:0007155,GO:0007352,GO:0043234,GO:0006952,GO:0009950,GO:0009620,GO:0004888,GO:0045944,GO:0005515,GO:0030097,GO:0045610,GO:0005769,GO:0035007	CG7250-PA				SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00369,SM00013,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00255		PF13855,PF13855,PF13855,PF13855,PF13855,PF13306	PS51450,PS51450,PS50104,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.40.50.10140	SSF52058,SSF52058,SSF52200,SSF52058	602~622								
aly1294.16	Unknown		n/a																				
aly1294.17	Protein toll	GO:0009897,GO:0007416,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0007165,GO:0008063,GO:0006955,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0002229,GO:0042802,GO:0016201,GO:0009880,GO:0007507,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005886,G	CG7250-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00013		PF13855,PF13855,PF13855,PF13855,PF13855,PF00560,PF00560	PS51450,PS50104			G3DSA:3.40.50.10140,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52058,SSF52200,SSF52058									
aly1294.18	CUB and sushi domain-containing protein 2	GO:0016021,GO:0005509,GO:0005886	CG32702-PB				SM00042		PF00431	PS01180			G3DSA:2.60.120.290	SSF49854									
aly1294.19	Unknown	GO:0005615,GO:0032504	CG10407-PA						PF06585														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1294.2	Protein toll	GO:0009897,GO:0007416,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0007165,GO:0008063,GO:0006955,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0010508,GO:0002229,GO:0042802,GO:0016201,GO:0009880,GO:0008329,GO:0007507,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005886,GO:0007155,GO:0007352,GO:0043234,GO:0006952,GO:0051607,GO:0002752,GO:0009950,GO:0009620,GO:0046790,GO:0004888,GO:0045944,GO:0030097,GO:0045610,GO:0005769,GO:0035007	CG8595-PA				SM00365,SM00365,SM00365,SM00365,SM00365,SM00255,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF13855,PF13855,PF01582,PF13306	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS50104,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.40.50.10140,G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52200,SSF52058									
aly1294.20	Unknown		n/a												95~102								
aly1294.3	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	GO:0032922,GO:0035220,GO:0035020,GO:0008047,GO:0032868,GO:0008375,GO:0005547,GO:0043085,GO:0005737,GO:0006486,GO:0006325,GO:0005634,GO:0005739,GO:0005815,GO:0005654,GO:0030854,GO:0070688,GO:0031397,GO:0080182,GO:0016757,GO:0016262,GO:0007584,GO:0006915,GO:0046626,GO:0045475,GO:0005886,GO:0051571,GO:0048015,GO:0006110,GO:0090526,GO:0006493,GO:0000123,GO:0043982,GO:0005829,GO:0043981,GO:0097363,GO:0043984,GO:0061087,GO:0071300,GO:0045944,GO:0005515,GO:0045862,GO:0007165	CG10392-PC				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF13424,PF13844,PF13414,PF13414,PF13414,PF13414	PS50005,PS50005,PS50293,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452					UPA00378				
aly1294.4	Protein inturned	GO:0005737,GO:0008589,GO:0042384,GO:0007399,GO:0030216,GO:0001737,GO:0009986,GO:0060173,GO:0021513,GO:0031069,GO:0051782,GO:0007163,GO:0045880,GO:0005886,GO:0035316,GO:0001736,GO:0010839	CG16993-PA																				
aly1294.5	Unknown		n/a												146~166								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1294.6	Unknown		CG4287-PA																				
aly1294.7	Exportin-4	GO:0005737,GO:0015031,GO:0005634	n/a							PS50166			G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371										
aly1294.8	Acetyl-CoA acetyltransferase B, mitochondrial	GO:0006633,GO:0003985,GO:0005811,GO:0005777,GO:0005739,GO:0046872,GO:0007052,GO:0016747,GO:0008152,GO:0006090,GO:0005875	CG10932-PA					TIGR01930	PF02803,PF05768,PF00108			PS00737,PS00099,PS00098	G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.30.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10	SSF52833,SSF53901,SSF53901			REACT_22258						
aly1294.9	Sodium- and chloride-dependent creatine transporter 1	GO:0005309,GO:0005328,GO:0016021,GO:0007464,GO:0005887,GO:0006836,GO:0005326	CG8291-PA						PF00209	PS50267	PR00176,PR00176,PR00176			SSF161070,SSF161070									
aly12944.1	Major facilitator superfamily domain-containing protein 6	GO:0016021,GO:0055085	CG15706-PA						PF12832,PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly12944.2	Endocuticle structural glycoprotein SgAbd-1	GO:0040003,GO:0005214,GO:0008010,GO:0031012,GO:0022008,GO:0042302	CG8515-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly1295.1	Unknown		n/a																				
aly1295.10	Unknown	GO:0003824,GO:0046331,GO:0009116	CG12065-PA										G3DSA:3.40.50.1580,G3DSA:3.40.50.1580,G3DSA:3.40.50.1580	SSF53167,SSF53167									
aly1295.2	Arylsulfatase B	GO:0007584,GO:0005794,GO:0051597,GO:0008484,GO:0010632,GO:0070062,GO:0006914,GO:0005791,GO:0005739,GO:0005764,GO:0010976,GO:0008152,GO:0061580,GO:0043627,GO:0003943,GO:0009268,GO:0046872,GO:0009986,GO:0004065,GO:0007417	CG8646-PB						PF00884			PS00149	G3DSA:3.30.1120.10,G3DSA:3.30.1120.10,G3DSA:3.40.720.10	SSF53649,SSF53649									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1295.3	Unknown	GO:0005549,GO:0016020,GO:0007608,GO:0004984	n/a						PF02949														
aly1295.4	Unknown	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0004888,GO:0004984	CG3206-PA						PF02949														
aly1295.5	Arylsulfatase B	GO:0007584,GO:0005794,GO:0051597,GO:0070062,GO:0010632,GO:0006914,GO:0005791,GO:0005739,GO:0004065,GO:0005764,GO:0010976,GO:0008152,GO:0061580,GO:0043627,GO:0003943,GO:0009268,GO:0046872,GO:0009986,GO:0008484,GO:0007417	CG8646-PB						PF00884			PS00149	G3DSA:3.30.1120.10,G3DSA:3.30.1120.10,G3DSA:3.40.720.10	SSF53649,SSF53649										
aly1295.6	Arylsulfatase B	GO:0007584,GO:0005794,GO:0051597,GO:0070062,GO:0010632,GO:0006914,GO:0005791,GO:0005739,GO:0004065,GO:0005764,GO:0010976,GO:0008152,GO:0061580,GO:0043627,GO:0003943,GO:0009268,GO:0046872,GO:0009986,GO:0008484,GO:0007417	CG8646-PB						PF00884			PS00149,PS00523	G3DSA:3.40.720.10,G3DSA:3.30.1120.10	SSF53649									
aly1295.7	Inositol polyphosphate 1-phosphatase	GO:0007268,GO:0046872,GO:0004441,GO:0046855,GO:0046854	CG3028-PA						PF00459				G3DSA:3.40.190.80,G3DSA:3.30.540.10,G3DSA:3.30.540.10	SSF56655									
aly1295.8	RNA-binding motif protein, X-linked 2	GO:0071011,GO:0071013,GO:0000398,GO:0000166,GO:0003676,GO:0044822,GO:0003729	CG10466-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly1295.9	Transcription initiation factor TFIID subunit 13	GO:0005730,GO:0006355,GO:0006366,GO:0001075,GO:0006367,GO:0003677,GO:0005669,GO:0046982	CG10756-PA						PF02269				G3DSA:1.10.20.10	SSF47113									
aly129626.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly129674.1	Unknown		n/a												18~38								
aly1297.1	Protein quiver	GO:0009897,GO:0032222,GO:0045938,GO:0005886,GO:0008076,GO:0048511,GO:0045187,GO:0034235,GO:0031225	CG33472-PB						PF17064														
aly1297.10	Fibrohexamerin	GO:0005576,GO:0005198	n/a						PF07294														
aly1297.11	CLIP-associating protein	GO:0030426,GO:0005488,GO:0007411,GO:0007067,GO:0030723,GO:0051225,GO:0005876,GO:0005737,GO:0040001,GO:0045172,GO:0005813,GO:0005634,GO:0000922,GO:0005815,GO:0005875,GO:0048477,GO:0043148,GO:0005525,GO:0016325,GO:0008017,GO:0032154,GO:0007051,GO:0007052,GO:0007282,GO:0046602,GO:0046580,GO:0000775,GO:0000776,GO:0035099,GO:0019827,GO:0000070,GO:0005827,GO:0051315,GO:0045169,GO:0000022,GO:0005819	CG32435-PB										G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371										
aly1297.12	CLIP-associating protein	GO:0030426,GO:0007411,GO:0007067,GO:0030723,GO:0051225,GO:0005876,GO:0005737,GO:0040001,GO:0045172,GO:0005813,GO:0005634,GO:0000922,GO:0005815,GO:0005875,GO:0048477,GO:0043148,GO:0005525,GO:0016325,GO:0008017,GO:0032154,GO:0007051,GO:0007052,GO:0007282,GO:0046602,GO:0046580,GO:0000775,GO:0000776,GO:0035099,GO:0019827,GO:0000070,GO:0005827,GO:0051315,GO:0045169,GO:0000022,GO:0005819	CG32435-PB						PF12348	PS50077			G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371										
aly1297.13	Unknown		n/a												259~279								
aly1297.14	Unknown		n/a												226~246,445~472								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1297.15	Unknown		n/a																				
aly1297.16	Cyclin-dependent kinase 6	GO:0009615,GO:0043697,GO:0000307,GO:0050680,GO:0010628,GO:0051301,GO:0004693,GO:0048146,GO:0007049,GO:0000278,GO:0005737,GO:0001726,GO:0007219,GO:0016049,GO:0003323,GO:0005813,GO:0005634,GO:0007259,GO:0005654,GO:0004674,GO:0002244,GO:0007005,GO:0004672,GO:0045668,GO:0005524,GO:0006468,GO:0030332,GO:0033077,GO:0008283,GO:0016301,GO:0042063,GO:0045786,GO:0001558,GO:0060218,GO:0007350,GO:0007424,GO:0051726,GO:0001954,GO:0010468,GO:0045638,GO:0045646,GO:0030097,GO:2000773	CG5072-PC				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112										
aly1297.2	Cyclic AMP-dependent transcription factor ATF-2	GO:0045444,GO:0034605,GO:0031618,GO:0001077,GO:0060612,GO:0009651,GO:0002385,GO:0010866,GO:0005737,GO:0043565,GO:0031573,GO:0031453,GO:0070829,GO:0071470,GO:0004402,GO:0005654,GO:0016573,GO:0046872,GO:0000980,GO:0003151,GO:0046982,GO:0032915,GO:0006974,GO:0042803,GO:0051403,GO:0006970,GO:0030431,GO:0051091,GO:1902110,GO:0035861,GO:0005704,GO:0005701,GO:0006355,GO:0005741,GO:0045944,GO:0035497,GO:0003682,GO:0005634	CG44246-PA				SM00355			PS50157		PS00028	G3DSA:3.30.160.60	SSF57667	459~486									
aly1297.3	Unknown		n/a																				
aly1297.4	Unknown		n/a																				
aly1297.5	Protein prune homolog 2	GO:0005737,GO:0006915	CG11593-PB						PF12496														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1297.6	LYR motif-containing protein 4B	GO:0005575,GO:0008150,GO:0003674	CG3717-PA						PF13232														
aly1297.7	Unknown		n/a																				
aly1297.8	Beta-1,3-galactosyltransferase 1	GO:0007030,GO:0006486,GO:0016021,GO:0016020,GO:0000139,GO:0008378,GO:0008499	CG30036-PA						PF01762						470~473				UPA00378				
aly1297.9	Unknown		n/a												54~109								
aly129708.1	Unknown		n/a																				
aly12978.1	Unknown		n/a																				
aly13013.1	Unknown		n/a																				
aly1302.1	Transcriptional repressor CTCFL	GO:0042393,GO:0010628,GO:0051569,GO:0003677,GO:0007049,GO:0005737,GO:0043565,GO:0006349,GO:0043046,GO:0005634,GO:0043007,GO:0006366,GO:0016571,GO:0046872,GO:0045892,GO:0045893,GO:0044212,GO:0003700,GO:0007379,GO:0001077,GO:0045944,GO:0000978,GO:0043035	CG8591-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13909,PF13909,PF13909,PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1302.2	RB-associated KRAB zinc finger protein	GO:0097150,GO:0030536,GO:0046672,GO:0005634,GO:0006355,GO:0008270,GO:0014019,GO:0002052,GO:0006099,GO:2000035,GO:0046580,GO:0003676,GO:0016360,GO:0045892,GO:0022008,GO:0046872,GO:0006351	CG12296-PB				SM00355,SM00355,SM00355,SM00355		PF00096,PF00096	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly1302.3	Gamma-soluble NSF attachment protein	GO:0005737,GO:0048190,GO:0070062,GO:0051726,GO:0043209,GO:0006886,GO:0016082,GO:0005739,GO:0005774,GO:0061025,GO:0005765,GO:0019905,GO:0007269,GO:0031201,GO:0005483,GO:0016192	CG3988-PA						PF14938				G3DSA:1.25.40.10	SSF48452	166~186								
aly1302.4	Unknown		n/a																				
aly1302.5	Unknown		n/a																				
aly1302.6	Mitochondrial thiamine pyrophosphate carrier	GO:0015619,GO:0030974,GO:0016021,GO:0022857,GO:0005743,GO:0005740,GO:0055085	CG6608-PB						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920	PR00926,PR00926,PR00926,PR00926,PR00926		G3DSA:1.50.40.10	SSF103506									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1302.7	Probable 3',5'-cyclic phosphodiesterase pde-5	GO:0008081,GO:0016324,GO:0004114,GO:0032240,GO:0007165,GO:0005886,GO:0046068,GO:0046872,GO:0047555	CG8279-PC				SM00065,SM00471		PF00233,PF01590		PR00387,PR00387,PR00387,PR00387,PR00387	PS00126	G3DSA:3.30.450.40,G3DSA:1.10.1300.10	SSF109604,SSF55781									
aly1302.8	Macrophage migration inhibitory factor	GO:0005737,GO:0004167,GO:0005615,GO:0050178,GO:0045087,GO:0006954	n/a						PF01187				G3DSA:3.30.429.10	SSF55331									
aly130225.1	Unknown		n/a																				
aly13023.1	Paternally-expressed gene 3 protein	GO:0005737,GO:0003700,GO:0005634,GO:0006915,GO:0006351,GO:0003676,GO:0046872	n/a										G3DSA:2.40.10.10	SSF50494									
aly13023.2	Choline kinase alpha	GO:0004103,GO:0005737,GO:0006657,GO:0006656,GO:0004104,GO:0019695,GO:0016310,GO:0008144,GO:0006646,GO:0004305,GO:0033265,GO:0005524	CG2201-PB						PF01633				G3DSA:3.90.1200.10,G3DSA:3.90.1200.10	SSF56112,SSF56112									
aly13055.1	Acyl-CoA:lysophosphatidylglycerol acyltransferase 1	GO:0005737,GO:0008654,GO:0016021,GO:0016020,GO:0005789,GO:0016746	n/a						PF16076														
aly130730.1	Unknown		n/a																				
aly13102.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly13102.2	Odorant receptor Or2	GO:0005549,GO:0007608,GO:0042048,GO:0016021,GO:0016020,GO:0051291,GO:0050911,GO:0004888,GO:0005886,GO:0004984,GO:0032590	CG1854-PA						PF02949														
aly13102.3	Odorant receptor Or1	GO:0005549,GO:0007608,GO:0042048,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG6679-PA						PF02949														
aly13112.1	Unknown		n/a																				
aly13116.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0046427,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG10960-PB						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly13116.2	Gelsolin	GO:0006909,GO:0045010,GO:0005829,GO:0051016,GO:0051014,GO:0003779,GO:0005576,GO:0005884,GO:0030041,GO:0005509	CG1106-PB				SM00262,SM00262,SM00262,SM00262		PF00626,PF00626,PF00626		PR00597,PR00597,PR00597,PR00597,PR00597		G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10	SSF82754,SSF55753,SSF55753,SSF55753									
aly131162.1	Unknown		n/a																				
aly1312.1	Head-specific guanylate cyclase	GO:0005737,GO:0020037,GO:0016056,GO:0004383,GO:0007601,GO:0008074,GO:0046956,GO:0035556,GO:0005525,GO:0006182	CG1912-PA						PF07700,PF07701,PF00211	PS50125			G3DSA:3.90.1520.10,G3DSA:3.30.70.1230	SSF55073,SSF111126	427~447	00230+4.6.1.2							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1312.2	Unknown	GO:0005737,GO:0020037,GO:0016056,GO:0004383,GO:0008074,GO:0046956,GO:0035556,GO:0006182	CG1912-PA																				
aly1312.3	Guanylate cyclase soluble subunit beta-1	GO:0005737,GO:0046872,GO:0020037,GO:0004383,GO:0008074,GO:0055072,GO:0035556,GO:0006182,GO:0006811,GO:0005525	CG1470-PA				SM00044		PF00211,PF07701,PF07700	PS50125		PS00452	G3DSA:3.30.70.1230,G3DSA:3.90.1520.10	SSF55073,SSF111126	357~384	00230+4.6.1.2							
aly1312.4	Ankyrin repeat and SOCS box protein 17	GO:0007605,GO:0016567,GO:0035556,GO:0005622,GO:0016059	CG31006-PA				SM00969		PF07525	PS50225				SSF158235					UPA00143				
aly1312.5	Glutaredoxin domain-containing cysteine-rich protein CG31559	GO:0005575,GO:0045454,GO:0015035,GO:0005623,GO:0009055	CG31559-PA						PF00462	PS51354			G3DSA:3.40.30.10	SSF52833									
aly1313.1	Neuropeptides capa receptor	GO:0007218,GO:0036401,GO:0007589,GO:0001607,GO:0016021,GO:0051928,GO:0004930,GO:0016323,GO:0071465,GO:0005887,GO:0008188,GO:0007186	CG9918-PD						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR01565,PR01565,PR01565	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1313.10	Homeobox protein goosecoid	GO:0043565,GO:0000122,GO:0003700,GO:0005634,GO:0006355,GO:0045892,GO:0046982,GO:0001078,GO:0007275,GO:0042803	CG2851-PD				SM00389		PF00046	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689	355~375								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1313.11	Unknown		n/a						PF16009														
aly1313.12	Unknown		n/a																				
aly1313.13	Unknown	GO:0016020,GO:0006810	n/a							PS50928													
aly1313.14	Unknown		n/a						PF16009		PR00334,PR00334,PR00334												
aly1313.15	Unknown		n/a						PF16009														
aly1313.16	Eukaryotic translation initiation factor 3 subunit K	GO:0005852,GO:0016282,GO:0006446,GO:0033290,GO:0001731,GO:0043022,GO:0006413,GO:0003743	CG10306-PA	MF_03010					PF10075				G3DSA:1.25.40.250,G3DSA:1.10.10.10	SSF48371,SSF46785									
aly1313.17	TATA-box-binding protein	GO:0000126,GO:0001092,GO:0006352,GO:0001129,GO:0005634,GO:0005666,GO:0008134,GO:0006367,GO:0001075,GO:0006357,GO:0005515,GO:0003677,GO:0005669,GO:0000978,GO:0042796,GO:0042797,GO:0006359	CG9874-PA	MF_00408					PF00352,PF00352		PR00686,PR00686,PR00686,PR00686,PR00686,PR00686	PS00351,PS00351	G3DSA:3.30.310.10,G3DSA:3.30.310.10	SSF55945,SSF55945	30~52								
aly1313.18	WASH complex subunit 7	GO:0016197,GO:0007032,GO:0005654,GO:0015031,GO:0071203,GO:0005768,GO:0005769	CG13957-PB						PF14745,PF14745,PF14744,PF14746														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1313.19	Pre-mRNA-processing factor 40 homolog A	GO:0005737,GO:0016607,GO:0008360,GO:0016363,GO:0007010,GO:0071011,GO:0044822,GO:0016020,GO:0017058,GO:0000398,GO:0005654,GO:0070064,GO:0032465,GO:0005685,GO:0016477,GO:0008380,GO:0006397	CG3542-PA				SM00441,SM00441,SM00441,SM00441,SM00456,SM00456		PF00397,PF00397,PF01846,PF01846	PS50020,PS51676,PS51676,PS51676,PS50020,PS51676,PS51676		PS01159	G3DSA:2.20.70.10,G3DSA:2.20.70.10,G3DSA:1.10.10.440,G3DSA:1.10.10.440,G3DSA:1.10.10.440	SSF81698,SSF51045,SSF81698,SSF81698,SSF51045,SSF81698	424~444,486~517,573~593,633~653								
aly1313.2	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0006631,GO:0046872,GO:0006629,GO:0017105,GO:0016717,GO:0042811,GO:0004768,GO:0016021,GO:0055114	CG15531-PA						PF00487		PR00075,PR00075,PR00075,PR00075,PR00075												
aly1313.20	Barrier-to-autointegration factor	GO:0005737,GO:0005634,GO:0005635,GO:0030717,GO:0005654,GO:0003677,GO:0005694	CG7380-PA				SM01023		PF02961				G3DSA:1.10.150.40	SSF47798									
aly1313.21	Syntaxin-5	GO:0016021,GO:0006909,GO:0005783,GO:0005794,GO:0035167,GO:0006906,GO:0060305,GO:0055070,GO:0005484,GO:0031201,GO:0006888,GO:0000902,GO:0000149,GO:0006887,GO:0000281,GO:0009306,GO:0042803,GO:0045930,GO:0006878,GO:0008283,GO:0016081,GO:0048278,GO:0007283,GO:0012505,GO:0007269,G	CG4214-PB				SM00397		PF05739,PF11416	PS50192			G3DSA:1.20.58.70	SSF47661	246~266								
aly1313.22	Magnesium transporter NIPA2	GO:0016021,GO:0016020,GO:0007476,GO:0015693,GO:0045886,GO:0005886,GO:0030514,GO:0005769,GO:0015095	CG12292-PB						PF05653,PF05653					SSF103481									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1313.23	Ribonucleoside-diphosphate reductase large subunit	GO:0005971,GO:0006919,GO:0042246,GO:0004748,GO:0009263,GO:0006260,GO:0005524,GO:0055114	CG5371-PA					TIGR02506	PF00317,PF02867,PF03477	PS51161	PR01183,PR01183,PR01183,PR01183,PR01183,PR01183	PS00089	G3DSA:3.20.70.20,G3DSA:3.20.70.20,G3DSA:3.20.70.20	SSF51998,SSF51998,SSF48168		00230+1.17.4.1,00480+1.17.4.1,00240+1.17.4.1		PWY-7210,PWY-7198,PWY-7220,PWY-7184,PWY-7222,PWY-7226,PWY-7227,PWY-6545	UPA00326				
aly1313.24	TBP-related factor	GO:0001092,GO:0001093,GO:0009790,GO:0005634,GO:0003677,GO:0008134,GO:0006366,GO:0005700,GO:0006367,GO:0001075,GO:0006357,GO:0045944,GO:0005667,GO:0001046,GO:0005669,GO:0051123,GO:0000978,GO:0006384,GO:0006383,GO:0006359	CG7562-PA						PF00352,PF00352		PR00686,PR00686,PR00686,PR00686	PS00351	G3DSA:3.30.310.10,G3DSA:3.30.310.10	SSF55945,SSF55945									
aly1313.25	T-complex protein 1 subunit delta	GO:0005737,GO:0006457,GO:0042623,GO:0005811,GO:0051082,GO:0031122,GO:0007052,GO:0005832,GO:0022008,GO:0005875,GO:0005524	CG5525-PA					TIGR02342	PF00118		PR00304,PR00304,PR00304,PR00304,PR00304	PS00750,PS00995,PS00751	G3DSA:3.30.260.10,G3DSA:3.30.260.10,G3DSA:1.10.560.10,G3DSA:1.10.560.10,G3DSA:3.50.7.10	SSF52029,SSF54849,SSF54849,SSF48592,SSF48592			REACT_17015						
aly1313.26	Mediator of RNA polymerase II transcription subunit 8	GO:0051726,GO:0001104,GO:0006357,GO:0006351,GO:0006367,GO:0006366,GO:0016592	CG13867-PA						PF10232						16~36								
aly1313.27	Rab3 GTPase-activating protein regulatory subunit	GO:0008021,GO:0016192,GO:0030234,GO:0060025,GO:0005096,GO:0005097,GO:0007269,GO:0007298,GO:0046982,GO:0043087	CG7061-PA				SM00310		PF14656,PF02174,PF14655	PS51064			G3DSA:2.30.29.30	SSF50729									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1313.28	Unknown	GO:0005515	n/a				SM00409		PF07686				G3DSA:2.60.40.10	SSF48726									
aly1313.29	Exocyst complex component 3	GO:0045921,GO:0042052,GO:0007009,GO:0007298,GO:0002168,GO:0005737,GO:0016020,GO:0016028,GO:0000145,GO:0000149,GO:0006887,GO:0043001,GO:0016081,GO:0016080,GO:0008594,GO:0005915,GO:0007269,GO:0072659,GO:0045313,GO:0072697,GO:0016192,GO:0032456,GO:0015031,GO:0045494	CG5341-PA						PF06046						68~88,527~547								
aly1313.3	Glutamate receptor ionotropic, kainate 3	GO:0043197,GO:0035235,GO:0016021,GO:0016020,GO:0007216,GO:0005234,GO:0045211,GO:0004970,GO:0001640,GO:0030054,GO:0007196	n/a						PF00060				G3DSA:1.10.287.70	SSF53850	103~123								
aly1313.30	UDP-N-acetylglucosamine--dolichyl phosphate N-acetylglucosaminephosphotransferase	GO:0051259,GO:0016757,GO:0006487,GO:0008963,GO:0016020,GO:0006047,GO:0003975,GO:0005789,GO:0019408,GO:0016021,GO:0019348	CG5287-PA						PF00953							00550+2.7.8.13		PWY-6470,PWY-6471,PWY-5265	UPA00219				
aly1313.31	Vacuolar protein sorting associated protein 54	GO:0005794,GO:0006896,GO:0000938,GO:0005739,GO:0007291,GO:0019905,GO:0042147,GO:0007286,GO:0015031	CG3766-PA						PF10475,PF07928														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1313.32	Unknown	GO:0009755,GO:0005179,GO:0046982,GO:0005615,GO:0001664	CG17878-PB						PF03045				G3DSA:2.10.90.10										
aly1313.33	Tetratricopeptide repeat protein 8	GO:0048560,GO:0061326,GO:0060170,GO:0001103,GO:0003674,GO:0035264,GO:0005929,GO:0045444,GO:0032880,GO:0036064,GO:0005813,GO:0016020,GO:0051492,GO:0005814,GO:0032391,GO:0042384,GO:0035058,GO:0034260,GO:0021772,GO:0060219,GO:0007411,GO:0015031,GO:0007608,GO:0034464	CG13691-PA				SM00028,SM00028,SM00028,SM00028,SM00028		PF13414,PF13371,PF00515	PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452										
aly1313.34	Transcription initiation factor TFIID subunit 7	GO:0044212,GO:0051123,GO:0006355,GO:0003700,GO:0005634,GO:0003713,GO:0035035,GO:0001075,GO:0006357,GO:0006367,GO:0005669,GO:0008134	CG2670-PA						PF04658,PF08477				G3DSA:3.40.50.300	SSF52540	322~349								
aly1313.35	E3 ubiquitin-protein ligase HECTD1	GO:0005737,GO:0005838,GO:0060708,GO:0060707,GO:0016874,GO:0005634,GO:1903077,GO:0051865,GO:0042787,GO:0061630,GO:0001843,GO:0046872,GO:0004842,GO:0070534,GO:0001779	CG5604-PA				SM00248,SM00248,SM00248		PF07738,PF06701,PF12796	PS50297,PS50088,PS50088			G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.40.20,G3DSA:2.60.120.260	SSF48403,SSF49785,SSF48371					UPA00143				
aly1313.36	E3 ubiquitin-protein ligase UPL3	GO:0005737,GO:0005838,GO:0016874,GO:0005634,GO:0010091,GO:0042023,GO:0042787,GO:0005886,GO:0046872,GO:0004842	CG5604-PA				SM00119		PF00632	PS50237			G3DSA:3.30.2160.10	SSF56204,SSF56204,SSF56204					UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1313.37	Unknown		CG16800-PB						PF16009														
aly1313.38	Unknown		CG16800-PB						PF16009														
aly1313.39	Unknown		n/a						PF16009														
aly1313.4	Unknown		n/a																				
aly1313.40	Unknown		n/a						PF16009														
aly1313.41	Unknown		n/a						PF16009														
aly1313.42	Unknown		n/a						PF15868														
aly1313.43	WASH complex subunit 7	GO:0016197,GO:0007032,GO:0005654,GO:0015031,GO:0071203,GO:0005768,GO:0005769	n/a						PF14745														
aly1313.5	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0006629,GO:0017105,GO:0016717,GO:0005789,GO:0046872,GO:0016021,GO:0055114	CG9747-PA								PR00075,PR00075,PR00075,PR00075,PR00075,PR00075												
aly1313.6	Unknown		n/a																				
aly1313.7	E3 ubiquitin-protein ligase TRIM9	GO:0005737,GO:0005856,GO:0030425,GO:0008021,GO:0043161,GO:0038007,GO:0016199,GO:0005622,GO:0045955,GO:0004842,GO:0008270,GO:0007409,GO:0035544,GO:0007411,GO:0022008,GO:0016079,GO:0016874,GO:0030054,GO:0042803	CG31721-PB				SM00502,SM00449,SM00336,SM00336,SM00060,SM00184		PF00643,PF13920,PF00622	PS50188,PS50119,PS50089,PS50853			G3DSA:2.60.40.10,G3DSA:4.10.45.10,G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF49899,SSF49265,SSF57850,SSF57850,SSF57845	256~283								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1313.8	Putative ATP-dependent RNA helicase me31b	GO:0005737,GO:0010494,GO:0043186,GO:0033962,GO:0035195,GO:0000932,GO:0004004,GO:0007279,GO:0003723,GO:0005515,GO:0046959,GO:0006417,GO:0007095,GO:0090328,GO:0010501,GO:0005875,GO:0005524,GO:0050688	CG4916-PA				SM00490,SM00487		PF00270,PF00271	PS51194,PS51195,PS51192		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									
aly1313.9	WW domain-binding protein 4	GO:0016607,GO:0030532,GO:0071011,GO:0045292,GO:0017058,GO:0000398,GO:0008270,GO:0003676,GO:0005886,GO:0005686,GO:0005681	CG4291-PA				SM00456,SM00451		PF06220,PF00397	PS50020,PS50171		PS01159	G3DSA:2.20.70.10	SSF57667,SSF51045	85~105,156~186								
aly13137.1	Uncharacterized 30.3 kDa protein		n/a											SSF54001									
aly13137.2	Uncharacterized 30.3 kDa protein		n/a											SSF54001									
aly1315.1	Putative serine/threonine-protein kinase F31E3.2	GO:0004674,GO:0006468,GO:0005524,GO:0004672	CG7001-PA				SM00220		PF00069	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly1315.10	Multidrug resistance protein 1A	GO:0015893,GO:0042626,GO:0070062,GO:0042623,GO:0000086,GO:0016021,GO:0031427,GO:0015238,GO:0008152,GO:0008559,GO:0046581,GO:0016887,GO:0005886,GO:0072089,GO:0009986,GO:0055085,GO:0005524	CG8523-PA				SM00382,SM00382		PF00005,PF00005,PF00664,PF00664	PS50929,PS50893,PS50893,PS50929		PS00211,PS00211	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.20.1560.10,G3DSA:1.20.1560.10	SSF52540,SSF90123,SSF52540,SSF90123									
aly1315.11	Methylated-DNA--protein-cysteine methyltransferase	GO:0006307,GO:0003824,GO:0005737,GO:0003908,GO:0006281	CG1303-PA					TIGR00589	PF01035			PS00374	G3DSA:1.10.10.10	SSF46767,SSF53155									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1315.12	Prostaglandin reductase 1	GO:0005737,GO:0036132,GO:0006631,GO:0005739,GO:0008270,GO:0047522,GO:0032440,GO:0019166,GO:0005875,GO:0055114,GO:0016491	CG16935-PB				SM00829		PF16884,PF00107				G3DSA:3.40.50.720,G3DSA:3.90.180.10	SSF51735,SSF50129,SSF50129									
aly1315.13	Zinc finger protein 358	GO:0019827,GO:0021915,GO:0006697,GO:0006355,GO:0007616,GO:0045938,GO:0005634,GO:0035115,GO:0008270,GO:0003676,GO:0003677,GO:0008340,GO:0046872,GO:0006351	CG34100-PD				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028			1399~1419									
aly1315.14	Transmembrane protein 120 homolog	GO:0050829,GO:0003674,GO:0016021,GO:0045089	CG32795-PA						PF07851						56~76								
aly1315.15	Lissencephaly-1 homolog	GO:0016319,GO:0008104,GO:0051383,GO:0034501,GO:0030425,GO:0030424,GO:0007303,GO:2001019,GO:0007294,GO:0031616,GO:0030286,GO:0007298,GO:0005815,GO:0005874,GO:0051225,GO:0051301,GO:0042052,GO:0005737,GO:0005938,GO:0030381,GO:0005813,GO:0045502,GO:0030706,GO:0008088,GO:0000922,GO:0005875,GO:0006810,GO:0006886,GO:0048135,GO:0048477,GO:0030473,GO:0051299,GO:0007067,GO:0072499,GO:0030234,GO:0050790,GO:0007283,GO:0010970,GO:0046716,GO:0005869,GO:0045478,GO:0051647,GO:0007405,GO:0051642,GO:0000776,GO:0030510,GO:0019827,GO:0000132,GO:0043025,GO:0005828,GO:0007018,GO:0030716,GO:0048813,GO:0008298,GO:0048814,GO:0005515,GO:0007093,GO:0042623,GO:0007312	CG8440-PA	MF_03141		PIRSF037647	SM00667,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF08513,PF00400,PF00400,PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50294,PS50082,PS50896,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678,PS00678,PS00678,PS00678,PS00678	G3DSA:2.130.10.10	SSF109925,SSF50978	58~78									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1315.16	Sarcolemmal membrane-associated protein	GO:0005737,GO:0016272,GO:0005615,GO:0006936,GO:0016021,GO:0005815,GO:0042383,GO:0005515,GO:0006457	CG17494-PA				SM00240		PF00498	PS50006			G3DSA:2.60.200.20	SSF49879	303~327								
aly1315.17	Protein xmas-2	GO:0016973,GO:0003676,GO:0005643,GO:0000166,GO:0009790,GO:0007283,GO:0045944,GO:0003723,GO:0005515,GO:0048477,GO:0007275,GO:0006406,GO:0003729	CG32562-PA						PF03399,PF00076	PS50102			G3DSA:3.30.70.330	SSF54928	1614~1634,952~1073,1664~1705								
aly1315.18	Zinc finger HIT domain-containing protein 3 (Fragment)	GO:0046872	CG8204-PA						PF04438	PS51083				SSF144232									
aly1315.19	Beta-glucuronidase	GO:0005975,GO:0005783,GO:0032504,GO:0005615,GO:0016020,GO:0043231,GO:0005764,GO:0019904,GO:0004566,GO:0005102,GO:0070062	CG15117-PB						PF02836,PF02837,PF00703		PR00132,PR00132,PR00132,PR00132,PR00132	PS00608,PS00719	G3DSA:2.60.120.260,G3DSA:2.60.40.320,G3DSA:3.20.20.80	SSF51445,SSF49303,SSF49785		00600+3.2.1.23,00052+3.2.1.23,00531+3.2.1.23,00604+3.2.1.23,00511+3.2.1.23		PWY-6807					
aly1315.2	Unknown	GO:0009593,GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0004970	CG15324-PA																				
aly1315.20	Unknown		n/a																				
aly1315.21	Unknown		n/a																				
aly1315.22	Autophagy-related protein 101	GO:0006914,GO:0000407	CG7053-PA						PF07855														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1315.3	Bifunctional coenzyme A synthase	GO:0070328,GO:0070062,GO:0015937,GO:0007476,GO:0005654,GO:0007303,GO:0007297,GO:0005759,GO:0004595,GO:0005524,GO:0004140	CG10575-PA	MF_00376				TIGR00152	PF01467,PF01121	PS51219			G3DSA:3.40.50.300,G3DSA:3.40.50.620	SSF52374,SSF52540	260~280	00770+2.7.1.24			UPA00241				
aly1315.4	G-protein coupled receptor Mth2	GO:0004930,GO:0016021,GO:0016020,GO:0006950,GO:0004888,GO:0007166,GO:0005886,GO:0008340,GO:0007186	CG17061-PB						PF00002	PS50261			G3DSA:1.20.1070.10	SSF81321									
aly1315.5	Unknown		n/a						PF06652				G3DSA:2.170.180.11	SSF63877									
aly1315.6	Multidrug resistance protein 1A	GO:0015893,GO:0042626,GO:0070062,GO:0042623,GO:0000086,GO:0016021,GO:0031427,GO:0015238,GO:0008152,GO:0008559,GO:0046581,GO:0016887,GO:0005886,GO:0072089,GO:0009986,GO:0055085,GO:0005524	CG8523-PA				SM00382,SM00382		PF00664,PF00664,PF00005,PF00005	PS50893,PS50929,PS50893,PS50929		PS00211,PS00211	G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF90123,SSF52540,SSF52540,SSF90123									
aly1315.7	Unknown		n/a																				
aly1315.8	Unknown		n/a																				
aly1315.9	Multidrug resistance protein 1A	GO:0015893,GO:0042626,GO:0070062,GO:0042623,GO:0000086,GO:0016021,GO:0031427,GO:0015238,GO:0008152,GO:0008559,GO:0046581,GO:0016887,GO:0005886,GO:0072089,GO:0009986,GO:0055085,GO:0005524	CG8523-PA				SM00382,SM00382		PF00005,PF00005,PF00664,PF00664	PS50893,PS50929,PS50929,PS50893		PS00211,PS00211	G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF90123,SSF90123,SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly13159.1	Sprouty-related, EVH1 domain-containing protein 2	GO:0005737,GO:0019901,GO:0009966,GO:0031410,GO:0090311,GO:0016020,GO:0010801,GO:0000188,GO:0005654,GO:0030658,GO:0005886,GO:0030291,GO:0043517,GO:0007275,GO:0005173	CG10155-PC																				
aly13159.2	Sprouty-related, EVH1 domain-containing protein 1	GO:0005737,GO:0019901,GO:0010923,GO:0009966,GO:0090311,GO:0016020,GO:0010801,GO:0000188,GO:0005654,GO:0005901,GO:0019902,GO:0030291,GO:0043517,GO:0007275,GO:0005173	CG10155-PC				SM00461		PF00568	PS50229			G3DSA:2.30.29.30	SSF50729										
aly13159.3	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	GO:0016020,GO:0070062,GO:0006635,GO:0005811,GO:0005777,GO:0005739,GO:0008416,GO:0003824,GO:0008152,GO:0005102,GO:0016853	CG9577-PA						PF00378				G3DSA:3.90.226.10	SSF52096									
aly1316.1	Serine protease persephone	GO:0004252,GO:0050832,GO:0045087,GO:0006967,GO:0006952,GO:0005576,GO:0008592,GO:0006508,GO:0008233	CG11842-PA						PF00089				G3DSA:2.40.10.10	SSF50494									
aly13163.1	Unknown	GO:0005575,GO:0008150,GO:0016021,GO:0003674	CG1103-PA							PS51257													
aly1317.1	Outer dense fiber protein 2	GO:0005737,GO:0030154,GO:0005815,GO:0007283,GO:0005929,GO:0005874,GO:0007275	CG3213-PA												79~99,195~215,220~254,110~172								
aly1317.10	Unknown		n/a																				
aly1317.11	Unknown		n/a												90~110								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1317.12	Unknown		n/a																				
aly1317.2	Tyrosine 3-monooxygenase	GO:0048082,GO:0042053,GO:0042136,GO:0007619,GO:0035220,GO:0048067,GO:0008049,GO:0040040,GO:0048085,GO:0009611,GO:0055114,GO:0005506,GO:2000274,GO:0006584,GO:0042417,GO:0042416,GO:0048066,GO:0008344,GO:0009072,GO:0004511,GO:0043052,GO:0005575	CG10118-PB					TIGR01269	PF00351	PS51410	PR00372,PR00372,PR00372,PR00372,PR00372,PR00372	PS00367	G3DSA:1.10.800.10	SSF55021,SSF56534		00350+1.14.16.2,00950+1.14.16.2		PWY-5394,PWY-5049	UPA00747				
aly1317.3	Unknown		n/a																				
aly1317.4	Aryl hydrocarbon receptor nuclear translocator-like protein 1	GO:0032922,GO:2000323,GO:0090263,GO:0007165,GO:0004871,GO:0003677,GO:0070888,GO:2001016,GO:0051775,GO:0005737,GO:0050767,GO:0016605,GO:0043161,GO:0005634,GO:0000976,GO:0043069,GO:0007623,GO:0043565,GO:0008134,GO:0050796,GO:0007283,GO:0042753,GO:0045892,GO:0001047,GO:0090403,GO:0033391,GO:0045599,GO:0042634,GO:0051726,GO:0003700,GO:0006355,GO:0045944,GO:0006351,GO:0005667,GO:2000074,GO:0032007,GO:0046983,GO:0046982,GO:2000772	CG42739-PG				SM00353,SM00091		PF00010,PF14598	PS50888,PS50112	PR00785,PR00785,PR00785,PR00785,PR00785		G3DSA:3.30.450.20,G3DSA:3.30.450.20,G3DSA:4.10.280.10	SSF47459,SSF55785,SSF55785									
aly1317.5	Unknown		n/a																				
aly1317.6	Unknown		n/a						PF14227														
aly1317.7	Unknown		n/a						PF03564,PF05585						57~84								
aly1317.8	Unknown		n/a																				
aly1317.9	Unknown		n/a																				
aly13170.1	Unknown		CG31248-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly13170.2	Sodium-coupled monocarboxylate transporter 2	GO:0006810,GO:0008507,GO:0070062,GO:0015129,GO:0016324,GO:0005215,GO:0016021,GO:0016020,GO:0035873,GO:0006814,GO:0015293,GO:0055085	CG9657-PA						PF00474	PS50283													
aly131821.1	Unknown	GO:0005515	CG34391-PD										G3DSA:2.60.40.10	SSF48726									
aly13198.1	Putative apoptosis-inducing factor 1, mitochondrial	GO:0050660,GO:0006915,GO:0005739,GO:0050832,GO:0003677,GO:0010623,GO:0005578,GO:0045454,GO:0042775,GO:0016491	CG7263-PB						PF14721,PF07992		PR00368,PR00368,PR00368		G3DSA:3.50.50.60,G3DSA:3.30.390.30,G3DSA:3.50.50.60	SSF55424,SSF51905,SSF51905,SSF51905									
aly13198.2	Hamartin	GO:0033596,GO:0016020,GO:0030308,GO:0060439,GO:0030426,GO:0001822,GO:0007160,GO:0046323,GO:0050808,GO:0007165,GO:0032868,GO:0042325,GO:0038202,GO:0051894,GO:0005737,GO:0006417,GO:0042552,GO:0051087,GO:0048505,GO:0021766,GO:0021987,GO:0030030,GO:0010467,GO:0006367,GO:0071456,GO:0048640,GO:0043234,GO:0001843,GO:0006407,GO:0042127,GO:0008285,GO:0008286,GO:0006629,GO:0055007,GO:0046620,GO:0046621,GO:0007584,GO:0045859,GO:0051291,GO:2000377,GO:0046627,GO:0007050,GO:0019900,GO:0001558,GO:0030027,GO:0005938,GO:0005886,GO:0008340,GO:0006813,GO:0043666,GO:0036335,GO:0035883,GO:0045792,GO:0043231,GO:0047485,GO:0051726,GO:0005829,GO:0005856,GO:0090630,GO:0001952,GO:0032320,GO:0030695,GO:0017148,GO:0032007,GO:0050821,GO:0051492	CG6147-PA						PF04388						675~678								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly13198.3	Rho GTPase-activating protein 26	GO:0005737,GO:0005856,GO:0005543,GO:0005096,GO:0030036,GO:0005622,GO:0005575,GO:0007009,GO:0007165,GO:0005100,GO:0007266,GO:0005925	CG8948-PG				SM00326		PF00620,PF14604	PS50238,PS50002			G3DSA:2.30.30.40,G3DSA:1.10.555.10	SSF48350,SSF50044			REACT_11044						
aly13198.4	Rho GTPase-activating protein 26	GO:0005737,GO:0005856,GO:0005543,GO:0005096,GO:0030036,GO:0005622,GO:0005575,GO:0007009,GO:0007165,GO:0005100,GO:0007266,GO:0005925	CG8948-PG						PF00620,PF16746	PS50238,PS50003			G3DSA:2.30.29.30,G3DSA:1.20.1270.60,G3DSA:1.10.555.10	SSF103657,SSF50729,SSF48350	31~65,241~261		REACT_11044						
aly13198.5	Zinc finger protein 330 homolog	GO:0035167,GO:0005730,GO:0005634,GO:0030496,GO:0008150,GO:0008270,GO:0046872,GO:0000775	CG10009-PA						PF06524														
aly13198.6	Lysoplasmalogenase-like protein TMEM86A	GO:0016021	CG7582-PA						PF07947														
aly1320.1	Forkhead box protein F1-B	GO:0048566,GO:0030154,GO:0030509,GO:0003677,GO:0043565,GO:0007435,GO:0000122,GO:0005634,GO:0000976,GO:0003690,GO:0008283,GO:0008134,GO:0048745,GO:0007389,GO:0008301,GO:0045893,GO:0001710,GO:0051090,GO:0003700,GO:0003705,GO:0006355,GO:0006357,GO:0045944,GO:0006351,GO:0005667	CG18647-PA				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00657,PS00658	G3DSA:1.10.10.10	SSF46785									
aly13210.1	Protein lifeguard 1	GO:0005794,GO:0005783,GO:0016021,GO:1902236,GO:0032469,GO:0017146,GO:0004972	CG3798-PD						PF01027														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly13210.2	Protein lifeguard 1	GO:0005794,GO:0005783,GO:0016021,GO:1902236,GO:0032469,GO:0017146,GO:0004972	CG3798-PD						PF01027														
aly13210.3	Unknown		CG3706-PA																				
aly1323.1	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly1323.2	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00572,PS00653	G3DSA:3.20.20.80	SSF51445									
aly1323.3	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly1323.4	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1323.5	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly1323.6	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131		G3DSA:3.20.20.80	SSF51445									
aly1323.7	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131		G3DSA:3.20.20.80	SSF51445									
aly132306.1	Unknown		n/a																				
aly13240.1	Larval cuticle protein LCP-17	GO:0040003,GO:0005214,GO:0008011,GO:0008010,GO:0031012,GO:0042302	CG7673-PA						PF00379	PS51155													
aly13284.1	Unknown		n/a																				
aly132859.1	Unknown		n/a																				
aly1329.1	Inactive dipeptidyl peptidase 10	GO:0016021,GO:0016020,GO:0008239,GO:1901379,GO:0005886,GO:0006508,GO:0072659,GO:0015459,GO:0008236	CG17684-PC						PF00930,PF00326				G3DSA:2.140.10.30,G3DSA:3.40.50.1820	SSF82171,SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1329.10	Long-chain fatty acid transport protein 4	GO:0015909,GO:0015908,GO:0005324,GO:0016021,GO:0031957,GO:0005789,GO:0003824,GO:0004467,GO:0008152,GO:0005886,GO:0070328,GO:0000166	CG7400-PD						PF00501			PS00455	G3DSA:3.40.50.980,G3DSA:3.30.300.30,G3DSA:3.40.50.980	SSF56801									
aly1329.11	Golgin subfamily A member 1	GO:0005737,GO:0005794,GO:0005819,GO:0043231,GO:0048193,GO:0000042,GO:0005813,GO:0005802,GO:0017137,GO:0000138,GO:0030306,GO:0007098,GO:0000785,GO:0048471,GO:0032580,GO:0042803	CG4840-PA				SM00755		PF01465	PS50913			G3DSA:1.10.220.60		492~512,286~327,349~397,131~186,454~474,233~253,538~558								
aly1329.12	Protein muscleblind	GO:0042052,GO:0045924,GO:0046716,GO:0009790,GO:0003676,GO:0003677,GO:0030018,GO:0005737,GO:0007517,GO:0000381,GO:0031673,GO:0007476,GO:0048471,GO:0046872,GO:0010468,GO:0006915,GO:0007601,GO:0001654,GO:0001751,GO:0007525,GO:0007422,GO:0050896,GO:0005634	CG33197-PR				SM00356,SM00356			PS50103,PS50103													
aly1329.13	Muscleblind-like protein 2	GO:0042052,GO:0045924,GO:0046716,GO:0009790,GO:0003676,GO:0003677,GO:0005737,GO:0007517,GO:0000381,GO:0005634,GO:0043484,GO:0007476,GO:0048471,GO:0046872,GO:0008380,GO:0044822,GO:0006915,GO:0001751,GO:0007525,GO:0007422,GO:0010468,GO:0006397	CG33197-PR				SM00356,SM00356			PS50103,PS50103			G3DSA:4.10.1000.10										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1329.2	Meiotic recombination protein SPO11	GO:0016787,GO:0000737,GO:0001541,GO:0034502,GO:0042140,GO:0042138,GO:0042139,GO:0007130,GO:0005694,GO:0007129,GO:0000706,GO:0000781,GO:0006265,GO:0005654,GO:0003677,GO:0007131,GO:0007286,GO:0048477,GO:0003918,GO:0005524,GO:0007141	CG7753-PA						PF04406		PR01551,PR01551,PR01551,PR01551,PR01550,PR01550,PR01550,PR01550,PR01550		G3DSA:1.10.10.10,G3DSA:3.40.1360.10	SSF56726									
aly1329.3	Transcription factor glial cells missing	GO:0035169,GO:0021782,GO:0035165,GO:0035164,GO:0001158,GO:0035289,GO:0010628,GO:0010001,GO:0003677,GO:0045687,GO:0050764,GO:0007516,GO:0005634,GO:0042688,GO:0060857,GO:0031290,GO:0010468,GO:0042387,GO:0030182,GO:0008283,GO:0042063,GO:0060252,GO:0006952,GO:0045893,GO:0042690,GO:0007403,GO:0003700,GO:0006355,GO:0048813,GO:0045944,GO:0006351,GO:0030097,GO:0045610	CG12245-PA						PF03615	PS50807				SSF90073									
aly1329.4	RB1-inducible coiled-coil protein 1	GO:0005737,GO:0007507,GO:0007254,GO:2001237,GO:0045793,GO:0001934,GO:0019901,GO:0031965,GO:0006914,GO:0070969,GO:0016236,GO:0034273,GO:0000045,GO:0034045,GO:0006355,GO:0001889,GO:0006351,GO:0010506,GO:0005829,GO:0007049	CG1347-PB										G3DSA:3.10.20.90		1000~1041,960~980,793~867,389~409,900~920,746~766								
aly1329.5	Glucose-6-phosphate 1-dehydrogenase	GO:0050661,GO:0006739,GO:0004345,GO:0006098,GO:0051156,GO:0006006,GO:0055114	CG12529-PA	MF_00966		PIRSF000110		TIGR00871	PF02781,PF00479		PR00079,PR00079,PR00079,PR00079,PR00079	PS00069	G3DSA:3.30.360.10,G3DSA:3.40.50.720	SSF51735,SSF55347		00030+1.1.1.49,00480+1.1.1.49		PWY-7268	UPA00115				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1329.6	Protein ultraspiracle homolog	GO:0016319,GO:0030425,GO:0001077,GO:0008270,GO:0043401,GO:0003677,GO:0008230,GO:0007298,GO:0008232,GO:0004879,GO:0043565,GO:0007517,GO:0005634,GO:0007552,GO:0005500,GO:0042803,GO:0048666,GO:0035075,GO:0035073,GO:0071390,GO:0008289,GO:0016322,GO:0007281,GO:0045596,GO:0045892,GO:0045893,GO:0042562,GO:0040034,GO:0003700,GO:0005700,GO:0003707,GO:0006355,GO:0048813,GO:0000976,GO:0006351,GO:0005515,GO:0046982,GO:0004884	CG4380-PA				SM00430,SM00399		PF00104,PF00105	PS51030	PR00047,PR00047,PR0047,PR00047,PR00545,PR00545,PR00545,PR00398,PR00398,PR00398,PR0398	PS00031	G3DSA:3.30.50.10,G3DSA:1.10.565.10	SSF48508,SSF57716			REACT_71						
aly1329.7	Uncharacterized protein C05D11.1	GO:0005759,GO:0006508,GO:0046872,GO:0004222,GO:0003824	CG3107-PB						PF05193,PF00675				G3DSA:3.30.830.10	SSF63411,SSF63411,SSF63411	460~487,960~961								
aly1329.8	Long-chain fatty acid transport protein 4	GO:0005324,GO:0031957,GO:0005789,GO:0005902,GO:0044539,GO:0070328,GO:0042760,GO:0006629,GO:0016021,GO:0016020,GO:0000166,GO:0004467,GO:0043588,GO:0015909,GO:0015908,GO:0007584,GO:0006810,GO:0003824,GO:0008152,GO:0005886,GO:0001676,GO:0055085,GO:0001579,GO:0031526,GO:0015245	CG7400-PD						PF00501,PF13193			PS00455	G3DSA:3.40.50.980,G3DSA:3.30.300.30,G3DSA:3.40.50.980	SSF56801									
aly1329.9	Long-chain fatty acid transport protein 4	GO:0015909,GO:0015908,GO:0005324,GO:0016021,GO:0031957,GO:0005789,GO:0003824,GO:0004467,GO:0008152,GO:0005886,GO:0070328,GO:0000166	CG7400-PD						PF00501,PF13193			PS00455	G3DSA:3.40.50.980,G3DSA:3.30.300.30,G3DSA:3.40.50.980	SSF56801									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly133.1	Deoxyhypusine hydroxylase	GO:0016049,GO:0007423,GO:0008283,GO:0019135,GO:0007451,GO:0005789,GO:0010508,GO:0042406,GO:0046872,GO:0008612	CG2245-PA	MF_03101			SM00567,SM00567,SM00567,SM00567,SM00567,SM00567		PF03130,PF13646,PF13646	PS50077,PS50077			G3DSA:1.25.10.10	SSF48371				PWY-5905	UPA00354				
aly133.10	NudC domain-containing protein 3		CG31251-PA						PF04969,PF14050	PS51203			G3DSA:2.60.40.790	SSF49764									
aly133.11	Unknown	GO:0060857,GO:0016021,GO:0007476,GO:0005918	CG6398-PA						PF13903														
aly133.12	Unknown		n/a																				
aly133.13	Usher syndrome type 1G protein	GO:0005737,GO:0042472,GO:0015629,GO:0007605,GO:0005829,GO:0050953,GO:0060122,GO:0003674,GO:0005886,GO:0050957,GO:0008150,GO:0005769,GO:0045494,GO:0030507	CG13320-PA				SM00248,SM00248,SM00248,SM00454		PF12796,PF00536	PS50297,PS50088,PS50105,PS50088			G3DSA:1.25.40.20,G3DSA:1.10.150.50	SSF47769,SSF48403									
aly133.14	Homeobox protein unc-4	GO:0043565,GO:0007399,GO:0003700,GO:0005634,GO:0030154,GO:0006355,GO:0006351	CG6269-PB																				
aly133.15	Tudor domain-containing protein 15	GO:0043186,GO:0030717,GO:0007310,GO:0048471,GO:0046872,GO:0007319	CG15707-PA						PF00567,PF00567	PS50103			G3DSA:2.30.30.140,G3DSA:2.30.30.140	SSF63748,SSF63748									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly133.16	Protein ITFG3	GO:0007155,GO:0007015,GO:0004383,GO:0008360,GO:0016021	CG3618-PA											SSF69318,SSF69318									
aly133.17	Suppressor of cytokine signaling 2	GO:0005737,GO:0032355,GO:0006469,GO:0007568,GO:0019221,GO:0043434,GO:0060396,GO:0017022,GO:0046627,GO:0004860,GO:0016567,GO:0001558,GO:0005159,GO:0046426,GO:0035556,GO:0038202	CG8146-PB				SM00252,SM00969		PF00017,PF07525	PS50225,PS50001			G3DSA:3.30.505.10	SSF55550,SSF158235					UPA00143				
aly133.18	Unknown		n/a																				
aly133.19	Unknown		n/a																				
aly133.2	Hemoglobin-3	GO:0005737,GO:0005344,GO:0019825,GO:0020037,GO:0005506,GO:0015671	CG9734-PC						PF00042	PS01033			G3DSA:1.10.490.10	SSF46458									
aly133.20	Unknown		n/a																				
aly133.21	Unknown		n/a																				
aly133.22	Unknown		n/a																				
aly133.23	Unknown		n/a																				
aly133.24	Fanconi anemia group I protein homolog	GO:0005737,GO:0070182,GO:0006281,GO:0005634,GO:0016020,GO:0005654,GO:0031398,GO:0005886,GO:0007095,GO:0043240,GO:0007049	CG13745-PA						PF14676,PF14675														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly133.25	Glucose dehydrogenase [FAD, qui]	GO:0005575,GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG45065-PA			PIRSF000137			PF00732,PF05199			PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly133.26	Intraflagellar transport protein 56	GO:0030992,GO:0042384,GO:0008594,GO:0036064,GO:0005813,GO:0007224,GO:0042073,GO:0046530,GO:0072372,GO:0005929,GO:0015031	CG4525-PA						PF07719				G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452,SSF48452									
aly133.27	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG15008-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly133.28	WD repeat-containing protein 81	GO:0016772,GO:0016230,GO:0010923	CG6734-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM01026		PF02138,PF00400,PF00400	PS50294,PS50082,PS50082,PS50197			G3DSA:1.10.1540.10,G3DSA:2.130.10.10	SSF81837,SSF50978	1117~1137								
aly133.29	Uridine 5'-monophosphate synthase	GO:0004590,GO:0006207,GO:0004588,GO:0005875,GO:0044205	CG3593-PA	MF_01208			SM00934	TIGR00336,TIGR01740	PF00215,PF00156			PS00156	G3DSA:3.40.50.2020,G3DSA:3.20.20.70	SSF51366,SSF53271		00240+4.1.1.23,00983+2.4.2.10,00240+2.4.2.10		PWY-5686	UPA00070				
aly133.3	Cytoglobin	GO:0005737,GO:0005344,GO:0019825,GO:0020037,GO:0047888,GO:0006979,GO:2000490,GO:0032966,GO:0010764,GO:0043005,GO:0004096,GO:0019395,GO:0005506,GO:0001666,GO:0043025,GO:0004601,GO:0015671	CG9734-PC						PF00042	PS01033			G3DSA:1.10.490.10	SSF46458									
aly133.30	Zinc finger protein 84	GO:0031935,GO:0003700,GO:0005634,GO:0007476,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872,GO:0008270	CG31364-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly133.31	Zinc finger protein 677	GO:0006909,GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG7368-PC				SM00355,SM00355,SM00355,SM00355		PF13912,PF13912	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly133.32	Gastrula zinc finger protein XlCGF28.1 (Fragment)	GO:0006909,GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG7368-PC				SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly133.33	Actin, cytoplasmic A3a	GO:0016319,GO:0005737,GO:0005200,GO:0007010,GO:0032507,GO:0005811,GO:0031011,GO:0000281,GO:0005856,GO:0007291,GO:0005884,GO:0006909,GO:0002121,GO:0005875,GO:0005524	CG4027-PB				SM00268		PF00022,PF00022			PS00432	G3DSA:3.30.420.40,G3DSA:3.30.420.40	SSF53067,SSF53067									
aly133.34	SUN domain-containing protein 1	GO:0034399,GO:0090286,GO:0090292,GO:0043231,GO:0005639,GO:0005637,GO:0005635,GO:0031965,GO:0007129,GO:0006998,GO:0002080,GO:0034993,GO:0048471,GO:0007097	CG44154-PA						PF07738	PS51469													
aly133.35	Coiled-coil domain-containing protein 40	GO:0005737,GO:0071910,GO:0003356,GO:0001539,GO:0070286,GO:0060287,GO:0003674,GO:0035469,GO:0005929,GO:0003341,GO:0030324,GO:0001947,GO:0071907,GO:0003351	CG41265-PA												761~788,576~603,835~890,412~432,660~687,286~320,125~152,692~733,342~362,174~220,53									
aly133.36	Zinc finger protein 491	GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG15436-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667,SSF57667,SSF57667									

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly133.37	Protein lethal(2) giant larvae	GO:0016333,GO:0008021,GO:0008105,GO:0008104,GO:0016336,GO:0016335,GO:0016334,GO:0030154,GO:0045197,GO:0045196,GO:0017022,GO:0016332,GO:0006469,GO:0007391,GO:0045159,GO:0045200,GO:0005920,GO:0035072,GO:0005856,GO:0002009,GO:0001738,GO:0005614,GO:0016082,GO:0019991,GO:0090163,GO:0045746,GO:0007049,GO:0055059,GO:0042127,GO:0008285,GO:0007559,GO:0035212,GO:0035070,GO:0016325,GO:0016327,GO:0045175,GO:0004860,GO:0007314,GO:0005938,GO:0007269,GO:0005886,GO:0051668,GO:0007406,GO:0016323,GO:0035293,GO:0007179,GO:0005918,GO:0045184,GO:0008283,GO:0007399,GO:0007423,GO:0051726,GO:0030863,GO:0030036,GO:0005829,GO:0045167,GO:0005737,GO:0008360,GO:0005515,GO:0006887,GO:0048730,GO:0005578	CG2671-PC				SM00320,SM00320,SM00320		PF08366	PS50294,PS50082,PS50082	PR00962,PR00962	PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978										
aly133.38	Thrombospondin type-1 domain-containing protein 7A	GO:0070062,GO:0005044,GO:0016021,GO:0030154,GO:0030247,GO:0005886,GO:0006955,GO:0001525	CG42339-PB				SM00209,SM00209,SM00209,SM00209,SM00209,SM00209,SM00209		PF00090,PF00090	PS50092,PS50092,PS50092,PS50092,PS50092,PS50092			G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10	SSF82895,SSF82895									
aly133.39	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	GO:0008637,GO:0051537,GO:0051539,GO:0008137,GO:0051536,GO:0016020,GO:0005739,GO:0003954,GO:0045333,GO:0005747,GO:0046872,GO:0042773,GO:0055114,GO:0009055	CG2286-PA				SM00929	TIGR01973	PF10588,PF00384,PF00384,PF13510	PS51669		PS00643,PS00642,PS00641	G3DSA:3.40.50.740,G3DSA:3.40.50.740,G3DSA:3.40.50.740	SSF54292,SSF53706,SSF54862									
aly133.4	Protein Gawky	GO:0001700,GO:0000184,GO:0003676,GO:0035195,GO:0000932,GO:0000166,GO:0045475,GO:0005515,GO:0003723,GO:0006417,GO:0006402,GO:0032880	CG31992-PE						PF12938,PF00627	PS50030			G3DSA:1.10.8.10,G3DSA:3.30.70.330	SSF54928,SSF46934	874~894,910~930								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly133.40	Uncharacterized protein C1orf194 homolog		CG5435-PA						PF12494														
aly133.41	Unknown		n/a																				
aly133.42	Protein shuttle craft	GO:0000977,GO:0007399,GO:0000122,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0006366,GO:0001078,GO:0003697,GO:0003723	CG3647-PB				SM00393,SM00438,SM00438,SM00438,SM00438,SM00438,SM00438		PF01424	PS51061			G3DSA:3.30.1370.50	SSF82708										
aly133.43	Glucose dehydrogenase [FAD, qui]	GO:0005575,GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0045455,GO:0055114,GO:0016491	CG45065-PA			PIRSF000137			PF05199,PF00732				G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905,SSF54373		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly133.5	Transmembrane protein 104 homolog	GO:0005575,GO:0008150,GO:0016021,GO:0003674	CG5262-PA						PF01490,PF01490														
aly133.6	E2/E3 hybrid ubiquitin-protein ligase UBE2O	GO:0005737,GO:0031625,GO:0030513,GO:0004842,GO:0005634,GO:0061630,GO:0070534,GO:0005654,GO:0006513,GO:0042147,GO:0061631,GO:0016874,GO:0044822,GO:0005524	CG10254-PB				SM00212		PF00179	PS50127			G3DSA:3.10.110.10	SSF54495									
aly133.7	E2/E3 hybrid ubiquitin-protein ligase UBE2O	GO:0005737,GO:0031625,GO:0030513,GO:0004842,GO:0005634,GO:0061630,GO:0070534,GO:0005654,GO:0006513,GO:0042147,GO:0061631,GO:0016874,GO:0044822,GO:0005524	CG10254-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly133.8	TBC1 domain family member 16	GO:0032313,GO:0005096,GO:0005097	CG5337-PA				SM00164		PF00566	PS50086			G3DSA:1.10.8.270	SSF47923,SSF47923									
aly133.9	Zinc-type alcohol dehydrogenase like protein SERP1785	GO:0006633,GO:0005835,GO:0016788,GO:0004312,GO:0008270,GO:0055114,GO:0016491	CG17374-PC				SM00829	TIGR02817	PF08240,PF13602			PS01162	G3DSA:3.40.50.720,G3DSA:3.90.180.10	SSF51735,SSF50129									
aly13318.1	Cysteine and glycine-rich protein 2	GO:0005634,GO:0030154,GO:0008270,GO:0007275	n/a				SM00132,SM00132			PS50023,PS50023			G3DSA:2.10.110.10,G3DSA:2.10.110.10										
aly13318.2	Unknown		CG8121-PA						PF15860														
aly13318.3	Sphingolipid delta(4)-desaturase DES1	GO:0006633,GO:0030148,GO:0006629,GO:0042284,GO:0016006,GO:0005739,GO:0005789,GO:0007283,GO:0007053,GO:0006665,GO:0070938,GO:0005886,GO:0004768,GO:0016021,GO:0055114,GO:0044281	CG9078-PA						PF00487														
aly13344.1	Fumarylacetoacetase	GO:0004334,GO:0006572,GO:0046872,GO:0009072,GO:0006559	CG14993-PA						PF09298,PF01557				G3DSA:3.90.850.10,G3DSA:2.30.30.230	SSF63433,SSF56529		00643+3.7.1.2,00350+3.7.1.2			UPA00139				
aly1335.1	Unknown		n/a																				
aly1335.2	Unknown		n/a																				
aly133840.1	Unknown		n/a																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly133951.1	Ubiquitin-like modifier-activating enzyme 5	GO:0046872,GO:0008641,GO:0005524	n/a																				
aly1340.1	Unknown	GO:0046872	n/a				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157		PS00028,PS00028,PS00028,PS00028											
aly1340.2	Zinc finger protein 366	GO:0033147,GO:0030331,GO:0000122,GO:0005634,GO:0003714,GO:0006351,GO:0003676,GO:0003677,GO:0043627,GO:0046872	CG1602-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028		SSF57667									
aly1340.3	Nuclear pore complex protein Nup98-Nup96	GO:0006909,GO:0019221,GO:0034605,GO:0019083,GO:0010827,GO:0042405,GO:0051028,GO:0005487,GO:0034399,GO:0044267,GO:0007264,GO:0042277,GO:0008645,GO:0044615,GO:0005635,GO:0044613,GO:0015758,GO:0010467,GO:0019058,GO:0006260,GO:0007184,GO:0017056,GO:0000278,GO:0005215,GO:0043687,GO:0006810,GO:0031965,GO:0006913,GO:0051292,GO:0007077,GO:0016925,GO:0055085,GO:0000059,GO:0030718,GO:0005975,GO:0031080,GO:0005643,GO:1900034,GO:0005829,GO:0006999,GO:0005515,GO:0005654,GO:0016032,GO:0044281	CG10198-PA						PF12110,PF04096	PS51434			G3DSA:3.30.1610.10	SSF82215										
aly1341.1	Facilitated trehalose transporter Tret1	GO:0006909,GO:0015771,GO:0005215,GO:0016021,GO:0015149,GO:0005886,GO:0015574,GO:0055085	CG14606-PA						PF00083	PS50850		PS00217	G3DSA:1.20.1250.20	SSF103473									
aly1341.10	Dual specificity protein phosphatase 23	GO:0005829,GO:0008138,GO:0006470,GO:0004725,GO:0005634,GO:0070062	CG7134-PA				SM00404		PF00782	PS50056		PS00383	G3DSA:3.90.190.10	SSF52799									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1341.11	Probable 26S proteasome non-ATPase regulatory subunit 9	GO:0006974,GO:0006508,GO:0005838,GO:0005515	CG9588-PA										G3DSA:2.30.42.10	SSF50156									
aly1341.12	Dystonin	GO:0016319,GO:0035147,GO:0009898,GO:0015629,GO:0035371,GO:0030426,GO:0035149,GO:0030424,GO:0030175,GO:0008090,GO:0000226,GO:0042383,GO:0030716,GO:0005874,GO:0030018,GO:0005856,GO:0001725,GO:0007517,GO:0005925,GO:0007026,GO:0016023,GO:0030056,GO:0031673,GO:0016020,GO:0051491,GO:0007475,GO:0003779,GO:0005509,GO:0097038,GO:0005635,GO:0048471,GO:0042803,GO:0016203,GO:0005737,GO:0014704,GO:0015630,GO:0005938,GO:0016204,GO:0008017,GO:0051010,GO:0005634,GO:0044295,GO:0007050,GO:0005882,GO:0000235,GO:0030036,GO:0007409,GO:0007155,GO:0030516,GO:0005789,GO:0097481,GO:0007424,GO:0007017,GO:0046907,GO:0007423,GO:0008092,GO:0045104,GO:0001578,GO:0045773,GO:0016199,GO:0045169,GO:0048813,GO:0005515,GO:0016021,GO:0005912	CG18076-PH				SM00243,SM00033,SM00033,SM00250,SM00054,SM00054,SM00150		PF00307,PF00307,PF00681,PF00681,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF02187	PS50222,PS50222,PS50021,PS50222,PS51460,PS50021		PS00018,PS00020	G3DSA:1.20.58.60,G3DSA:1.10.418.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:3.30.920.20,G3DSA:1.20.58.60,G3DSA:1.10.418.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.10.238.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10,G3DSA:3.90.1290.10	SSF75399,SSF46966,SSF75399,SSF75399,SSF75399,SSF75399,SSF75399,SSF46966,SSF75399,SSF46966,SSF75399,SSF46966,SSF46966,SSF46966,SSF75399,SSF46966,SSF46966,SSF46966,SSF75399,SSF75399,SSF46966,SSF75399,SSF46966,SSF75399,SSF46966,SSF46966,SSF47576,SSF46966,SSF46966,SSF75399,SSF75399,SSF46966,SSF46966,SSF46966,SSF47473,SSF75399,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF75399,SSF46966,SSF75399,SSF46966,SSF46966,SSF75399,SSF75399,SSF46966,SSF46966,SSF46966,SSF75399,SSF75399,SSF75399,SSF46966,SSF46966,SSF143575,SSF46966	953~973,6929~6949,7169~7189,6740~6767,5125~5166,1183~1203,8036~8056,7877~7897,346~383,596~616,5437~5457,7313~7333,7127~7147,6311~6345,922~949,747~767,7368~7388,8010~8030,5965~5999,1297~1317,411~431,5867~5887,5716~5736,5262~5282,894~914,5061~5098,6413~6440,7097~7117,7069~7092								
aly1341.13	Protein wntless	GO:0033157,GO:0005887,GO:0008587,GO:0031594,GO:0030177,GO:0031302,GO:0030285,GO:0001745,GO:0031227,GO:0030054,GO:0007367,GO:0005771,GO:0007476,GO:0005794,GO:0007480,GO:0045211,GO:0035017,GO:0005886,GO:0070062,GO:0042734,GO:0050714,GO:0002790,GO:0016055,GO:0031228,GO:0017147,G	CG6210-PA						PF06664														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1341.14	Unknown	GO:0016319,GO:0035147,GO:0030426,GO:0035149,GO:0030175,GO:0000226,GO:0030716,GO:0005874,GO:0005856,GO:0007517,GO:0007026,GO:0051491,GO:0007475,GO:0003779,GO:0005509,GO:0016203,GO:0016204,GO:0008017,GO:0044295,GO:0007050,GO:0000235,GO:0030036,GO:0007409,GO:0030516,GO:0007424,GO:0007017,GO:0007423,GO:0008092,GO:0001578,GO:0045773,GO:0016199,GO:0045169,GO:0048813,GO:0005515,GO:0005912	CG18076-PH																					
aly1341.2	Protein CASC3	GO:0005737,GO:0016607,GO:0035145,GO:0000184,GO:0008103,GO:0051028,GO:0048471,GO:0005635,GO:0003723,GO:0007318,GO:0006417,GO:0031369,GO:0045451,GO:0008380,GO:0045450,GO:0006397	CG12878-PD						PF09405														
aly1341.3	Unknown		n/a																				
aly1341.4	Tubulointerstitial nephritis antigen-like	GO:0005737,GO:0042600,GO:0005615,GO:0005044,GO:0030247,GO:0043236,GO:0070062,GO:0031012,GO:0007155,GO:0030177,GO:0004197,GO:0006955,GO:0017147,GO:0006508,GO:0008234,GO:0035593	CG3074-PB				SM00645		PF00112	PS50958		PS00640,PS00639	G3DSA:3.90.70.10	SSF54001										
aly1341.5	Caspase-1	GO:0016239,GO:0009267,GO:0097194,GO:0030036,GO:0007300,GO:0048102,GO:0007303,GO:0010623,GO:0007275,GO:0097200,GO:0005739,GO:0010508,GO:0006508,GO:0048477,GO:0005737,GO:0035071,GO:1990525,GO:0006915,GO:0016322,GO:0012501,GO:0045476,GO:0007015,GO:0009790,GO:0005829,GO:0004197,GO:1900074,GO:0005515	CG5370-PA				SM00115		PF00656	PS50207,PS50208	PR00376,PR00376,PR00376,PR00376,PR00376,PR00376	PS01122	G3DSA:3.40.50.1460	SSF52129										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1341.6	Ethanolaminephosphotransferase 1	GO:0006646,GO:0006644,GO:0006909,GO:0008654,GO:0016021,GO:0016020,GO:0005789,GO:1903955,GO:0044281,GO:0004307,GO:0046474,GO:0046872,GO:0004142	CG7149-PA			PIRSF015665			PF01066			PS00379											
aly1341.7	Coiled-coil-helix-coiled-coil-helix domain-containing protein 7	GO:0005758	CG4186-PA										G3DSA:1.10.810.10	SSF47072									
aly1341.8	Partitioning defective protein 6	GO:0016332,GO:0055059,GO:0006909,GO:0040001,GO:0030154,GO:0045197,GO:0045196,GO:0035003,GO:0007163,GO:0045200,GO:0007309,GO:0007298,GO:0005923,GO:0007416,GO:0005737,GO:0045176,GO:0009949,GO:0016021,GO:0007369,GO:0045179,GO:0051491,GO:0051301,GO:0060446,GO:0005080,GO:0006469,GO:0016324,GO:0008406,GO:0045186,GO:0008360,GO:0005938,GO:0005886,GO:0007155,GO:0007506,GO:0010592,GO:0001738,GO:0005515,GO:0007338	CG5884-PA				SM00228,SM00666		PF00564,PF00595	PS51745,PS50106			G3DSA:3.10.20.240,G3DSA:2.30.42.10	SSF54277,SSF50156									
aly1341.9	Dual specificity protein phosphatase 23	GO:0016791,GO:0005829,GO:0008138,GO:0016311,GO:0004725,GO:0005634,GO:0070062	n/a						PF00782	PS50056		PS00383	G3DSA:3.90.190.10	SSF52799									
aly13410.1	Odorant receptor 2a	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0004888,GO:0005886,GO:0004984,GO:0032590	CG3206-PA						PF02949														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly13410.10	Cell division cycle 5-like protein	GO:0005737,GO:0016607,GO:0051298,GO:0005730,GO:0006281,GO:0071011,GO:0071013,GO:0016020,GO:0044822,GO:0000398,GO:0006355,GO:0005662,GO:0071987,GO:0006351,GO:0000974,GO:0003677,GO:0072422,GO:0003682,GO:0005634,GO:0005681	CG6905-PA				SM00717,SM00717		PF13921,PF11831,PF11831	PS51294,PS51294			G3DSA:1.10.10.60,G3DSA:1.10.10.60	SSF46689	543~573,631~672,168~189,592~612,486~510								
aly13410.11	Unknown	GO:0004386,GO:0004004,GO:0005524,GO:0003677	CG7922-PA												56~76								
aly13410.12	Unknown		n/a				SM00249			PS50016		PS01359	G3DSA:3.30.40.10	SSF57903	157~184,129~149								
aly13410.2	A disintegrin and metalloprotein ase with thrombospondin motifs 14	GO:0004222,GO:0030574,GO:0042059,GO:0030199,GO:0030198,GO:0008270,GO:0006508,GO:0005578,GO:0005576	CG4096-PB						PF01421,PF01562	PS50215			G3DSA:3.40.390.10	SSF55486									
aly13410.3	A disintegrin and metalloprotein ase with thrombospondin motifs 2	GO:0004222,GO:0043588,GO:0030574,GO:0042059,GO:0030199,GO:0030198,GO:0008270,GO:0016485,GO:0006508,GO:0030324,GO:0007283,GO:0005578,GO:0008237,GO:0005576	CG4096-PB				SM00209,SM00209,SM00209		PF00090,PF00090	PS50092,PS50092			G3DSA:2.20.100.10,G3DSA:2.20.100.10	SSF82895,SSF82895									
aly13410.4	Unknown		CG6123-PA																				
aly13410.5	Unknown	GO:0005575,GO:0008150,GO:0003674	CG3955-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly13410.6	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	GO:0006457,GO:0090201,GO:0090200,GO:0071243,GO:0048102,GO:1902445,GO:0090324,GO:0008024,GO:0010849,GO:0042981,GO:0005875,GO:0005737,GO:0000413,GO:0042277,GO:0010939,GO:0005739,GO:0016538,GO:0043066,GO:0003755,GO:0005759,GO:2001243,GO:0070266,GO:2000276,GO:0035071,GO:0032780,GO:0070301,GO:0071277,GO:0019908,GO:0002931,GO:0008637,GO:0046902,GO:0005829,GO:0005743,GO:0016018	CG9916-PA			PIRSF001467			PF00160	PS50072	PR00153,PR00153,PR00153,PR00153,PR00153	PS00170	G3DSA:2.40.100.10	SSF50891										
aly13410.7	Methylthioribose-1-phosphate isomerase	GO:0005737,GO:0019509,GO:0005851,GO:0005634,GO:0035220,GO:0046523,GO:0045182,GO:0006412,GO:0019284	CG11334-PC	MF_01678				TIGR00524,TIGR00512	PF01008				G3DSA:1.20.120.420,G3DSA:3.40.50.10470	SSF100950	61~81	00270+5.3.1.23		PWY-7174,PWY-4361	UPA00904				
aly13410.8	Disintegrin and metalloproteinase domain-containing protein 10	GO:0061320,GO:0004175,GO:0006909,GO:0042117,GO:0097197,GO:0007162,GO:0008270,GO:0007411,GO:0007298,GO:0005925,GO:0008237,GO:0007417,GO:0005737,GO:0007219,GO:0051088,GO:0051089,GO:0016021,GO:0007519,GO:0030307,GO:0006509,GO:0006508,GO:0048477,GO:0034612,GO:0042803,GO:0008284,GO:0005794,GO:0006468,GO:0004222,GO:0035386,GO:0009986,GO:0035051,GO:0005798,GO:0003007,GO:0001701,GO:0014069,GO:0030516,GO:0097038,GO:0008347,GO:0007400,GO:0019901,GO:0007220,GO:0070062,GO:0000139,GO:0060537,GO:0048542,GO:0005634,GO:0010820	CG7147-PA				SM00050		PF01562,PF13574,PF00200	PS50215,PS50214			G3DSA:4.10.70.10,G3DSA:3.40.390.10	SSF55486,SSF57552										
aly13410.9	Membrane-associated protein Hem	GO:0005737,GO:0007010,GO:0000902,GO:0030031,GO:0007409,GO:0030866,GO:0030036,GO:0008407,GO:0007528,GO:0008360,GO:0001764,GO:0031209,GO:0005515,GO:0005886,GO:0007520,GO:0006909,GO:0033627,GO:0016021,GO:0001555,GO:0007417	CG5837-PA						PF09735														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1342.1	Unknown		CG14905-PA																				
aly1342.2	Unknown		n/a																				
aly1342.3	Alpha-2C adrenergic receptor	GO:0016021,GO:0004935,GO:0004938,GO:0019229,GO:0008227,GO:0006940,GO:0005887,GO:0005886,GO:0007186,GO:0032795,GO:0030168	CG18208-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1342.4	Unknown		n/a																				
aly1342.5	Unknown		n/a																				
aly1342.6	Unknown		n/a																				
aly13420.1	Unknown		n/a										G3DSA:3.60.10.10	SSF56219	268~288								
aly13468.1	Clotting factor B	GO:0004252,GO:0042381,GO:0048812,GO:0006508,GO:0005576,GO:0008236	CG9372-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly134754.1	Unknown		n/a																				
aly13485.1	Unknown		n/a												47~74								
aly1349.1	Glutamate receptor ionotropic, kainate 4	GO:0032983,GO:0042734,GO:0045211,GO:0035235,GO:0016021,GO:0016020,GO:0015277,GO:0015276,GO:0005234,GO:0034220,GO:0030054,GO:0050907,GO:0005886,GO:0030425,GO:0035249,GO:0004970,GO:0045202	CG42352-PF						PF10613,PF00060				G3DSA:1.10.287.70,G3DSA:3.40.190.10	SSF53850,SSF53850									
aly1349.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1349.3	Kinesin-like protein KIF18A	GO:0031134,GO:0007596,GO:0005901,GO:0005871,GO:0005815,GO:0007060,GO:0005876,GO:0005737,GO:0003779,GO:0001726,GO:0072686,GO:0005634,GO:0005875,GO:0051225,GO:0046785,GO:0007080,GO:0000776,GO:0003774,GO:0005524,GO:0016346,GO:0015630,GO:0051299,GO:0000278,GO:0019886,GO:0008017,GO:0051010,GO:0007052,GO:0008152,GO:0007059,GO:0007264,GO:0051231,GO:0000910,GO:0008574,GO:0000070,GO:0005829,GO:0005828,GO:0007018,GO:0007019,GO:0070463,GO:0043130,GO:0003777,GO:0015031	CG10923-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380		G3DSA:3.40.850.10	SSF52540	388~415								
aly1349.4	Odorant receptor Or2	GO:0005549,GO:0007608,GO:0042048,GO:0016021,GO:0016020,GO:0030425,GO:0050911,GO:0004888,GO:0005886,GO:0004984,GO:0043025	CG9880-PA						PF02949														
aly1349.5	Signal recognition particle subunit SRP72	GO:0005786,GO:0005047,GO:0033227,GO:0005783,GO:0005730,GO:0005829,GO:0042493,GO:0006614,GO:0008312,GO:0005886,GO:0044822	CG5434-PA			PIRSF038922	SM00028,SM00028,SM00028,SM00028		PF08492,PF17004				G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452										
aly1349.6	Probable rRNA-processing protein EBP2 homolog	GO:0003723,GO:0003674,GO:0006364,GO:0005730	CG1542-PA						PF05890						40~60								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1349.7	Histone-lysine N-methyltransferase 2E	GO:0042054,GO:0042119,GO:0019899,GO:0008270,GO:0051568,GO:0048384,GO:0016607,GO:0006306,GO:0045171,GO:0005634,GO:0003713,GO:0005654,GO:0030854,GO:0070688,GO:0048477,GO:0030218,GO:0007050,GO:0035327,GO:0045893,GO:0001047,GO:0002446,GO:0043231,GO:0042800,GO:0005700,GO:0071300,GO:0006351,GO:0005515,GO:0034401	CG9007-PA				SM00249,SM00317		PF00628	PS50280,PS50016		PS01359	G3DSA:2.170.270.10,G3DSA:3.30.40.10	SSF57903,SSF82199	1474~1518,1023~1024								
aly1350.1	Unknown		n/a																				
aly1350.10	RNA polymerase II elongation factor Ell	GO:0008023,GO:0048190,GO:0005730,GO:0005634,GO:0070063,GO:0005703,GO:0005700,GO:0035327,GO:0006368,GO:0042795,GO:0003682,GO:0032968,GO:0043620	CG32217-PA						PF07303,PF10390					SSF144292,SSF46785									
aly1350.11	SURP and G-patch domain-containing protein 1	GO:0044822,GO:0000398,GO:0005654,GO:0010467,GO:0003723,GO:0005681,GO:0008380,GO:0006396	CG31550-PD				SM00443		PF01585	PS50174					75~107								
aly1350.12	Unknown		n/a																				
aly1350.13	Unknown		n/a																				
aly1350.14	Unknown		n/a																				
aly1350.15	Unknown		n/a																				
aly1350.16	GRAM domain-containing protein 1B	GO:0016021,GO:0016020	CG34394-PE				SM00568		PF02893														
aly1350.17	Unknown		n/a																				
aly1350.18	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1350.19	Elongation factor Tu GTP binding domain-containing protein 1	GO:0043022,GO:0005850,GO:0003924,GO:0042256,GO:0003746,GO:0006414,GO:0005525	CG33158-PB						PF00679				G3DSA:3.30.70.240	SSF54980									
aly1350.2	Small conductance calcium-activated potassium channel protein	GO:0009881,GO:0071805,GO:0006813,GO:0016057,GO:0016021,GO:0016286,GO:0005516,GO:0005886,GO:0043025,GO:0015269,GO:0007165	CG10706-PS																				
aly1350.20	Protein giant-lens	GO:0016318,GO:0009996,GO:0042059,GO:0007474,GO:0007411,GO:2000737,GO:0007472,GO:0007455,GO:0007476,GO:0030707,GO:0050768,GO:0043065,GO:1900116,GO:0035215,GO:0007482,GO:0005154,GO:0060233,GO:0042067,GO:0007601,GO:0048019,GO:0045596,GO:0046331,GO:0001654,GO:0050896,GO:0005576	CG4531-PA						PF11581														
aly1350.21	Unknown	GO:0005214,GO:0040003,GO:0005576	CG32159-PB																				
aly1350.22	Elongation factor Tu GTP binding domain-containing protein 1	GO:0043022,GO:0005850,GO:0003924,GO:0042256,GO:0003746,GO:0006414,GO:0005525	CG33158-PB					TIGR00231	PF00009,PF03144	PS51722	PR00315,PR00315,PR00315,PR00315,PR00315		G3DSA:3.90.1430.10,G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:3.30.70.870,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.30.230.10,G3DSA:3.30.230.10	SSF52540,SSF52540,SSF54980,SSF54211,SSF54211,SSF50447,SSF50447	436~485								
aly1350.3	Unknown		n/a																				
aly1350.4	SH2 domain-containing adapter protein F	GO:0005575,GO:0006915,GO:0003674,GO:0090175	CG43921-PA				SM00252		PF00017	PS50001	PR00401,PR00401,PR00401,PR00401		G3DSA:3.30.505.10	SSF55550									
aly1350.5	Endocuticle structural glycoprotein SgAbd-8	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG9079-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1350.6	Endocuticle structural glycoprotein SgAbd-2	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG34270-PA						PF00379	PS51155		PS00233			894~914								
aly1350.7	Unknown	GO:0005575,GO:0003674,GO:0090175	CG43921-PA																				
aly1350.8	Unknown	GO:0003677	CG4404-PA						PF02944,PF10545	PS51031													
aly1350.9	Tyrosine--tRNA ligase, cytoplasmic	GO:0005737,GO:0006437,GO:0000049,GO:0004831,GO:0005524	CG4561-PA					TIGR00234	PF00579,PF01588	PS50886	PR01040,PR01040,PR01040,PR01040		G3DSA:1.10.240.10,G3DSA:2.40.50.140,G3DSA:3.40.50.620	SSF50249,SSF52374		00970+6.1.1.1	REACT_71						
aly135017.1	Probable proline--tRNA ligase, mitochondrial	GO:0005737,GO:0006426,GO:0004827,GO:0004820,GO:0006433,GO:0005739,GO:0005759,GO:0005524	CG12186-PA										G3DSA:3.40.50.800	SSF52954									
aly13522.1	Unknown		n/a																				
aly13533.1	Unknown	GO:0003677	n/a						PF05225,PF03184					SSF46689	39~59								
aly13542.1	Unknown		n/a																				
aly13548.1	Unknown		n/a						PF02949						31~51								
aly1357.1	Unknown		n/a																				
aly1357.10	Unknown	GO:0005576,GO:0042742	n/a										G3DSA:1.20.5.750										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1357.11	Asparagine synthetase [glutamine-hydrolyzing]	GO:0045931,GO:0043200,GO:0006529,GO:0032354,GO:0009636,GO:0009416,GO:0070981,GO:0006520,GO:0006541,GO:0031667,GO:0009612,GO:0032870,GO:0043066,GO:0048037,GO:0004066,GO:0042149,GO:0001889,GO:0031427,GO:0005524,GO:0042803	CG33486-PA					TIGR01536	PF13537,PF00733,PF00733	PS51278			G3DSA:3.60.20.10,G3DSA:3.40.50.620	SSF56235,SSF52402		00250+6.3.5.4			UPA00134				
aly1357.12	Unknown		n/a																				
aly1357.13	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	GO:0018342,GO:0018343,GO:0018344,GO:0005965,GO:0004662,GO:0004660,GO:0004661,GO:0005953,GO:0008318	CG2976-PB						PF01239,PF01239,PF01239,PF01239	PS51147,PS51147,PS51147,PS51147,PS51147,PS51147,PS50293			G3DSA:1.25.40.120	SSF48439	284~304								
aly1357.14	Pupal cuticle protein C1B	GO:0005214,GO:0042302	CG8541-PA						PF11018														
aly1357.15	Unknown		CG14280-PA							PS01180			G3DSA:2.60.120.290	SSF49854									
aly1357.16	3-ketodihydrosphingosine reductase	GO:0047560,GO:0030148,GO:0005783,GO:0005615,GO:0016021,GO:0016020,GO:0005789,GO:0044281,GO:0008152,GO:0006665,GO:0006666,GO:0016491	CG10425-PA						PF00106		PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly1357.17	Death-associated inhibitor of apoptosis 2	GO:0006964,GO:0090307,GO:0008270,GO:0050829,GO:0070936,GO:0005876,GO:0005737,GO:0043154,GO:0009966,GO:0061630,GO:0005634,GO:0043066,GO:0042787,GO:0043281,GO:0048471,GO:0070534,GO:0043027,GO:0033160,GO:0089720,GO:0045087,GO:1990001,GO:0061057,GO:0016874,GO:0031625,GO:0007423,GO:0016567	CG8293-PA				SM00238,SM00238,SM00238		PF00653,PF00653,PF00653	PS50143,PS50143,PS50143		PS01282	G3DSA:1.10.1170.10,G3DSA:1.10.1170.10,G3DSA:1.10.1170.10	SSF57924,SSF57924,SSF57924									
aly1357.18	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1357.2	Unknown		CG13408-PA																				
aly1357.3	Unknown		n/a																				
aly1357.4	Unknown		n/a																				
aly1357.5	Unknown		CG13408-PA																				
aly1357.6	Unknown	GO:0005576,GO:0042742	n/a						PF06451				G3DSA:1.20.5.750										
aly1357.7	Unknown		n/a																				
aly1357.8	Moricin-2	GO:0045087,GO:0005576,GO:0042742	n/a						PF06451				G3DSA:1.20.5.750										
aly1357.9	Moricin-2	GO:0045087,GO:0005576,GO:0042742	n/a						PF06451				G3DSA:1.20.5.750										
aly1358.1	Histidine triad nucleotide-binding protein 2, mitochondrial	GO:0016787,GO:0005730,GO:0006915,GO:0008252,GO:0005739,GO:0000166,GO:0003824,GO:0006694	CG2862-PC						PF01230	PS51084	PR00332,PR00332,PR00332		G3DSA:3.30.428.10	SSF54197									
aly1358.2	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG5065-PA						PF03015,PF07993				G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735,SSF51735			REACT_22258						
aly1358.3	Tyrosine-protein phosphatase non-receptor type 7	GO:0005737,GO:0005856,GO:0000278,GO:0006470,GO:0004725,GO:0007465,GO:0009898,GO:0000188,GO:0007265,GO:0005829	CG9856-PA				SM00404,SM00194		PF00102	PS50055,PS50056	PR00700,PR00700,PR00700,PR00700,PR00700	PS00383	G3DSA:3.90.190.10,G3DSA:3.90.190.10	SSF52799,SSF52799	591~611								
aly1358.4	Cullin-2	GO:0031625,GO:0005730,GO:0008582,GO:0000152,GO:0005654,GO:0006511,GO:0042787,GO:0030163,GO:0007295,GO:0031461,GO:0022008,GO:0031462	CG1512-PA				SM00884		PF10557			PS01256	G3DSA:1.10.10.10	SSF46785					UPA00143				
aly1358.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly135930.1	Unknown	GO:0008270	CG2991-PB										G3DSA:2.10.25.10										
aly1362.1	Hemicentin-1	GO:0005604,GO:0070062,GO:0050896,GO:0007601,GO:0005509,GO:0005515,GO:0030054,GO:0005938	CG34114-PB				SM00408,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409,SM00409		PF13927,PF13927,PF13895,PF08205,PF00047	PS50835,PS50835,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF49265,SSF48726,SSF48726,SSF48726,SSF48726									
aly1362.2	Unknown	GO:0008270,GO:0003676	n/a							PS50158													
aly1362.3	Unknown		n/a																				
aly1362.4	Unknown		n/a																				
aly1362.5	Unknown		n/a																				
aly1363.1	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG15661-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									
aly1363.10	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0002121,GO:0008152	CG17323-PA						PF00201					SSF53756									
aly1363.2	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG6649-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly1363.3	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG4302-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									
aly1363.4	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG4302-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									
aly1363.5	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG15661-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly1363.6	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0002121,GO:0008152	CG17323-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756	424~444								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1363.7	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG15661-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									
aly1363.8	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG15661-PA						PF00201,PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly1363.9	Unknown		n/a																				
aly13633.1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase classes I and II	GO:0004435,GO:0006651,GO:0007629,GO:0016042,GO:0005509,GO:0004871,GO:0006661,GO:0035556,GO:0005622	CG4574-PD											SSF50729									
aly1365.1	Unknown		n/a																				
aly1365.10	Unknown		n/a												111~138								
aly1365.11	Peptidoglycan-recognition protein SA	GO:0032500,GO:0005887,GO:0005515,GO:0008329,GO:0008745,GO:0045087,GO:0006955,GO:0006965,GO:0008063,GO:0006952,GO:0016045,GO:0050830,GO:0005576,GO:0008270,GO:0008592,GO:0009253,GO:0032494,GO:0008233,GO:0016019,GO:0042834,GO:0002221	CG11709-PA				SM00701						G3DSA:3.40.80.10	SSF55846									
aly1365.12	Unknown		n/a																				
aly1365.13	Peroxidasin	GO:0006909,GO:0020037,GO:0005578,GO:0030198,GO:0042744,GO:0046872,GO:0006979,GO:0055114,GO:0004601	CG12002-PA				SM00408,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409,SM00409,SM00369,SM00369,SM00369,SM00369,SM00369		PF03098,PF07679,PF07679,PF07679,PF07679,PF13855	PS50292,PS51450,PS50835,PS51450,PS51450,PS51450,PS50835,PS50835,PS51450,PS50835	PR00457,PR00457,PR00457,PR00457,PR00457,PR00457,PR00457,PR00457		G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:1.10.640.10,G3DSA:1.10.640.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.80.10.10	SSF48726,SSF48726,SSF48726,SSF52058,SSF48726,SSF48113									
aly1365.14	Acyl-coenzyme A thioesterase 13	GO:0016787,GO:0005829,GO:0005819,GO:0005634,GO:0005739	CG16985-PA					TIGR00369	PF03061				G3DSA:3.10.129.10	SSF54637									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1365.15	Unknown		CG15615-PB						PF16086,PF16086,PF16086,PF16086,PF16086														
aly1365.16	Bombyxin A-1 homolog	GO:0005179,GO:0005576,GO:0005615	n/a				SM00078		PF00049		PR00276,PR00276		G3DSA:1.10.100.10	SSF56994									
aly1365.17	Unknown		n/a																				
aly1365.18	Unknown		n/a																				
aly1365.19	Unknown		n/a																				
aly1365.2	Unknown		n/a																				
aly1365.20	Integrator complex subunit 6	GO:0016180,GO:0015629,GO:0034472,GO:0032039,GO:0005654,GO:0004888,GO:0003674,GO:0007165	CG3125-PA						PF15300						32~59								
aly1365.21	Unknown		n/a												517~556								
aly1365.22	Unknown		n/a																				
aly1365.23	Unknown		n/a																				
aly1365.24	Failed axon connections	GO:0005737,GO:0022008,GO:0007409,GO:0005886	CG4609-PA						PF13417,PF14497				G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF47616,SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1365.25	Protein disulfide-isomerase A5	GO:0006457,GO:0005788,GO:0003756,GO:0045454,GO:0015035,GO:0006662,GO:0034976	CG9302-PA						PF00085,PF00085,PF00085,PF00085	PS51352,PS51352,PS51352	PR00421,PR00421,PR00421	PS00194,PS00194	G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10	SSF52833,SSF52833,SSF52833,SSF52833,SSF52833									
aly1365.26	Unknown		n/a												67~87								
aly1365.27	Triosephosphate isomerase	GO:0031430,GO:0004807,GO:0050877,GO:0009612,GO:0003824,GO:0006098,GO:0008340,GO:0006096,GO:0030018,GO:0006094	CG2171-PC	MF_00147_B				TIGR00419	PF00121	PS51440		PS00171	G3DSA:3.20.20.70	SSF51351		00710+5.3.1.1,00562+5.3.1.1,00051+5.3.1.1,00010+5.3.1.1		PWY-1042,PWY-6142,PWY-5484,PWY-7003	UPA00138,UPA00109				
aly1365.28	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0006909,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0008340,GO:0035336,GO:0008611	CG30427-PC						PF07993,PF03015				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly1365.29	Unknown		n/a																				
aly1365.3	Unknown		n/a																				
aly1365.30	Unknown		n/a																				
aly1365.31	Unknown		n/a																				
aly1365.4	Unknown	GO:0005575,GO:0008150,GO:0003674	CG30380-PA																				
aly1365.5	Palmitoyltransferase ZDHHC3	GO:0005794,GO:0018345,GO:0016021,GO:0016020,GO:0000139,GO:0008270,GO:0019706,GO:0006605,GO:0016409	CG8314-PA						PF01529	PS50216													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1365.6	Transmembrane protein 208	GO:0006624,GO:0005773,GO:0006914,GO:0016021,GO:0005789	CG8320-PA						PF05620						156~174								
aly1365.7	Otoancorin	GO:0019226,GO:0016324,GO:0007160,GO:0007605,GO:0005578,GO:0031225	n/a																				
aly1365.8	Clavesin-2	GO:0005802,GO:0080025,GO:0005215,GO:0006810,GO:0005622,GO:0007040,GO:0030136,GO:0005768,GO:0031901,GO:0016918	CG10546-PA				SM00516,SM01100		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087,SSF46938									
aly1365.9	Peptidoglycan-recognition protein 1	GO:0045087,GO:0008745,GO:0016021,GO:0009253,GO:0005576,GO:0008270,GO:0005887,GO:0006955,GO:0042834	CG33717-PD				SM00701						G3DSA:3.40.80.10	SSF55846									
aly136793.1	Unknown		n/a																				
aly13682.1	Unknown		n/a																				
aly1370.1	Chondroitin proteoglycan 2	GO:0006030,GO:0000281,GO:0005576,GO:0008061,GO:0009790	CG33986-PB				SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00494		PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607	PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625										
aly1370.10	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 3	GO:0031418,GO:0016020,GO:0070062,GO:0016706,GO:0016021,GO:0016705,GO:0005506,GO:0055114	n/a				SM00702		PF13640	PS51471													
aly1370.11	Uncharacterized F-box/LRR-repeat protein C02F5.7	GO:0003676	CG4221-PA				SM00360,SM00367,SM00367,SM00367,SM00367,SM00367		PF00076,PF00646	PS50102			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:1.20.1280.50,G3DSA:3.30.70.330	SSF54928,SSF81383,SSF52047									
aly1370.12	Uncharacterized protein C19orf52		CG14270-PA						PF10171														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1370.13	Unknown		n/a																				
aly1370.14	Unknown	GO:0005575,GO:0003674,GO:0008150	CG13380-PB																				
aly1370.15	Probable 39S ribosomal protein L23, mitochondrial	GO:0005840,GO:0005739,GO:0000166,GO:0003735,GO:0005762,GO:0005622,GO:0006412	CG1320-PA						PF00276				G3DSA:3.30.70.330	SSF54189									
aly1370.16	Tyrosine-protein phosphatase non-receptor type 9	GO:0005737,GO:0006909,GO:0006470,GO:0004725,GO:0004726,GO:0035335,GO:0022008	CG32697-PA				SM00404,SM00194		PF00102,PF00650	PS50056,PS50055	PR00700,PR00700,PR00700,PR00700	PS00383	G3DSA:3.40.525.10,G3DSA:3.90.190.10	SSF52087,SSF52799									
aly1370.17	Bumetanide-sensitive sodium-(potassium)-chloride cotransporter	GO:0016021,GO:0006813,GO:0003333,GO:0006810,GO:0008511,GO:0015171,GO:0015377,GO:0006814,GO:0006811	CG31547-PB					TIGR00930	PF03522,PF00324		PR01207,PR01207,PR01207			SSF81665,SSF81665			REACT_15518						
aly1370.18	Unknown		n/a																				
aly1370.19	40S ribosomal protein S15	GO:0005737,GO:0022627,GO:0005730,GO:0006412,GO:0003735,GO:0007052,GO:0003723,GO:0000228,GO:0000022,GO:0015935	CG8332-PA	MF_00531		PIRSF002144		TIGR01025	PF00203		PR00975,PR00975,PR00975	PS00323	G3DSA:3.30.860.10	SSF54570									
aly1370.2	Voltage-dependent calcium channel subunit alpha-2/delta-3	GO:0051924,GO:0005262,GO:0070588,GO:0048786,GO:0005891,GO:0031629,GO:0007528,GO:0045886,GO:0045202,GO:0019233,GO:0005246,GO:0005245,GO:0046872,GO:0007274,GO:0048488,GO:0005244	CG12295-PC				SM00327		PF02743,PF13519	PS50234			G3DSA:3.30.450.20,G3DSA:3.40.50.410	SSF53300									
aly1370.20	DTW domain-containing protein 2	GO:0005575,GO:0003674,GO:1903955,GO:0008150	CG10050-PA						PF03942														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1370.21	Histone-lysine N-methyltransferase ash1	GO:0018024,GO:0042054,GO:0003677,GO:0046974,GO:0008270,GO:0051568,GO:0051567,GO:0001700,GO:0003727,GO:0005634,GO:0016571,GO:0048477,GO:0042802,GO:0006351,GO:0048096,GO:0034770,GO:0035327,GO:0018991,GO:0042800,GO:0006355,GO:0042799,GO:0000785,GO:0003682	CG8887-PB				SM00570,SM00439,SM00317,SM00297		PF01426,PF00856	PS51038,PS51215,PS50868,PS50280			G3DSA:1.20.920.10,G3DSA:2.170.270.10	SSF82199,SSF47370	1784~1811,2636~2663	00310+2.1.1.43							
aly1370.3	Integral membrane protein DGCR2/IDD	GO:0042493,GO:0016021,GO:0016020,GO:0050890,GO:0030246,GO:0005575,GO:0003674,GO:0007155,GO:0008150	CG42404-PD																				
aly1370.4	Solute carrier family 25 member 46	GO:0005743,GO:0016021,GO:0006810,GO:0005739	CG8931-PA						PF00153	PS50920			G3DSA:1.50.40.10	SSF103506,SSF103506									
aly1370.5	39S ribosomal protein L34, mitochondrial	GO:0005840,GO:0005739,GO:0005622,GO:0003735,GO:0005762,GO:0006412,GO:0032543	CG34147-PA						PF00468														
aly1370.6	Protein ENL	GO:0005737,GO:0006469,GO:0005674,GO:0005730,GO:0005634,GO:0032783,GO:0006366,GO:0005654,GO:0006355,GO:0008023,GO:0006367,GO:0003677,GO:0005669	CG4913-PB						PF03366	PS51037					613~639,347~372								
aly1370.7	Protein SMG5	GO:0005737,GO:0051721,GO:0000184,GO:0035195,GO:0005829,GO:0010467,GO:0016246,GO:0035303,GO:0005634,GO:0006406	CG8954-PA						PF10373,PF10374,PF13638				G3DSA:3.40.50.1010	SSF48452,SSF48452,SSF48452	841~861,379~399								
aly1370.8	Ubiquitin-like protein 7	GO:0005515	n/a				SM00213		PF00240	PS50053			G3DSA:3.10.20.90,G3DSA:1.10.8.10	SSF46934,SSF54236	21~41								
aly1370.9	Unknown		n/a												497~524,285~312								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly137036.1	Unknown		n/a						PF09808														
aly13777.1	Unknown		n/a																				
aly1379.1	Putative odorant receptor 85d	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG11742-PA						PF02949														
aly1379.10	C-myc promoter-binding protein	GO:0045175,GO:0008105,GO:0006351,GO:0045089,GO:0043547,GO:0031410,GO:0055037,GO:0005085,GO:0070831,GO:0017112,GO:0017137,GO:0032483,GO:0006355,GO:0005516,GO:0042998,GO:0003677,GO:0050829,GO:0005634,GO:0005938	CG12737-PA				SM00801,SM00800,SM00799		PF03455,PF02141,PF03456	PS50947,PS50211,PS51498,PS50946													
aly1379.11	Unknown		CG4553-PA						PF06413														
aly1379.12	Alpha-tocopherol transfer protein-like	GO:0016020,GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG3823-PA				SM00516		PF00650	PS50191	PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF46938,SSF52087									
aly1379.13	Alpha-tocopherol transfer protein-like	GO:0016020,GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG2663-PA						PF00650	PS50191			G3DSA:3.40.525.10	SSF46938,SSF52087									
aly1379.14	Alpha-tocopherol transfer protein-like	GO:0016020,GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG3823-PA						PF00650				G3DSA:3.40.525.10	SSF46938,SSF52087									
aly1379.15	Casein kinase I isoform gamma-3	GO:0005737,GO:0051126,GO:0006468,GO:0090175,GO:0016318,GO:0005634,GO:0016055,GO:0009612,GO:0004674,GO:0007283,GO:0007291,GO:0008347,GO:2001135,GO:0005886,GO:2000039,GO:0070864,GO:0005524,GO:0008355	CG6963-PL				SM00220		PF12605,PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1379.16	Cyclic AMP-responsive element-binding protein 3-like protein 3	GO:0001158,GO:0003677,GO:0043565,GO:0007435,GO:0007431,GO:0016021,GO:0006366,GO:0042803,GO:1990440,GO:0008363,GO:0045893,GO:0005789,GO:0035293,GO:0009953,GO:0030968,GO:0003700,GO:0001228,GO:0005700,GO:0006355,GO:0045944,GO:0000977,GO:0035497,GO:0005634	CG7450-PA				SM00338		PF00170	PS50217			G3DSA:1.20.5.170	SSF57959	418~459								
aly1379.2	Pancreatic lipase-related protein 2	GO:0009395,GO:0047714,GO:0004806,GO:0005615,GO:0008970,GO:0052689,GO:0016042,GO:0005575,GO:0005509,GO:0019376,GO:0004620,GO:0016298,GO:0047372	CG6271-PA						PF00151		PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly1379.3	Pancreatic lipase-related protein 2	GO:0009395,GO:0009791,GO:0047714,GO:0032094,GO:0005615,GO:0033993,GO:0008970,GO:0016042,GO:0005575,GO:0042589,GO:0051384,GO:0043434,GO:0005509,GO:0019376,GO:0004806,GO:0022008,GO:0016298,GO:0004620,GO:0047372	CG6277-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly1379.4	Pancreatic lipase-related protein 2	GO:0009395,GO:0047714,GO:0004806,GO:0005615,GO:0008970,GO:0052689,GO:0016042,GO:0005575,GO:0005509,GO:0019376,GO:0004620,GO:0016298,GO:0047372	CG6271-PA						PF00151		PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly1379.5	Pancreatic triacylglycerol lipase	GO:0061365,GO:0004806,GO:0008970,GO:0052689,GO:0016042,GO:0005575,GO:0030299,GO:0005576,GO:0022008,GO:0046872,GO:0016298	CG6277-PA						PF00151		PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly1379.6	Pancreatic lipase-related protein 2	GO:0009395,GO:0047714,GO:0004806,GO:0005615,GO:0008970,GO:0016042,GO:0005575,GO:0005509,GO:0019376,GO:0004620,GO:0016298,GO:0047372	CG6271-PA						PF00151		PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1379.7	Pancreatic lipase-related protein 2	GO:0009395,GO:0009791,GO:0047714,GO:0032094,GO:0005615,GO:0033993,GO:0008970,GO:0016042,GO:0005575,GO:0042589,GO:0051384,GO:0005509,GO:0019376,GO:0004806,GO:0004620,GO:0016298,GO:0043434,GO:0047372	CG6271-PA						PF00151		PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly1379.8	Mitochondrial inner membrane protein OXA1L	GO:0008565,GO:0033615,GO:0051205,GO:0032981,GO:0032780,GO:0097177,GO:0016021,GO:0051354,GO:0005739,GO:0008535,GO:0005743,GO:0005740,GO:0009060,GO:0051262,GO:0043234,GO:0031966,GO:0032592,GO:0097031,GO:0042803	CG6404-PB					TIGR03592	PF02096														
aly1379.9	U3 small nucleolar RNA-associated protein 15 homolog	GO:0005737,GO:0032040,GO:0005730,GO:0044822,GO:0034455,GO:0000462,GO:0045943,GO:0005515,GO:0030515,GO:0030054	CG3071-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF09384	PS50082,PS50082,PS50082,PS50294			G3DSA:2.130.10.10	SSF50978									
aly13793.1	Unknown		n/a																				
aly13793.2	Unknown	GO:0008150,GO:0003674,GO:0005887	CG15598-PC						PF07898,PF07841														
aly13793.3	Unknown		n/a											SSF50494									
aly13793.4	Unknown	GO:0003674,GO:0008150,GO:0005887	CG1169-PA						PF07898														
aly13793.5	Golgin subfamily A member 7	GO:0005795,GO:0018230,GO:0070062,GO:0031228,GO:0050821,GO:0043001,GO:0002178	CG5447-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly138.1	cGMP-specific 3',5'-cyclic phosphodiesterase	GO:0032240,GO:0004114,GO:0016020,GO:0016324,GO:0007165,GO:0005886,GO:0046068,GO:0046872,GO:0047555	CG8279-PC				SM00065,SM00065,SM00471		PF00233,PF01590,PF01590		PR00387,PR00387,PR00387,PR00387,PR00387,PR00387	PS00126	G3DSA:3.30.450.40,G3DSA:3.30.450.40,G3DSA:3.30.450.40,G3DSA:1.10.1300.10	SSF109604,SSF55781,SSF55781,SSF55781									
aly138.10	Serine/threonine-protein kinase pelle	GO:0019732,GO:0019221,GO:0007165,GO:0008063,GO:0048262,GO:0035556,GO:0046777,GO:0005737,GO:0005634,GO:0004674,GO:0004672,GO:0005524,GO:0006468,GO:0006606,GO:0045087,GO:0006915,GO:0035172,GO:0006952,GO:0030162,GO:0019904,GO:0005886,GO:0007352,GO:0009950,GO:0009620,GO:0005515,GO:0030097	CG5974-PA				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.20.20.70,G3DSA:2.60.120.200,G3DSA:1.10.533.10,G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112,SSF47986										
aly138.11	Wolframin	GO:0005783,GO:0017109,GO:0030425,GO:1902236,GO:0050821,GO:0042593,GO:0030176,GO:0043524,GO:0055074,GO:0045927,GO:0051247,GO:0000122,GO:0003091,GO:0045762,GO:0001822,GO:0032469,GO:0031398,GO:0050877,GO:0043069,GO:0007605,GO:0051117,GO:0007601,GO:0030433,GO:0043433,GO:0031625,GO:0030968,GO:0051928,GO:0004357,GO:0051726,GO:2000675,GO:1903892,GO:0034976	CG4917-PA								PR02060,PR02060,PR02060,PR02060,PR02060,PR02060,PR02060,PR02060,PR02060,PR02060,PR02060,PR02060											
aly138.12	Protein SHQ1 homolog	GO:0005654,GO:0005829,GO:0005575,GO:0022618,GO:0008150,GO:0003674	CG10055-PA						PF04925	PS51203													
aly138.13	Cytosolic beta-glucosidase	GO:0005975,GO:0005829,GO:0016139,GO:0008422,GO:0004565,GO:0006687,GO:0004553,GO:0017042,GO:0046477,GO:0006665,GO:0044281	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00572,PS00653	G3DSA:3.20.20.80	SSF51445									

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly138.14	Lactase-phlorizin hydrolase	GO:0017042,GO:0005903,GO:0044281,GO:0042594,GO:0010040,GO:0044245,GO:0010045,GO:0001666,GO:0016020,GO:0016740,GO:0010288,GO:0016324,GO:0007584,GO:0045471,GO:0005887,GO:0005886,GO:0043627,GO:0009744,GO:0000016,GO:0005975,GO:0042493,GO:0004553	CG9701-PA						PF00232,PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653,PS00572,PS00653,PS00572	G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF51445,SSF51445									
aly138.15	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly138.16	Thioredoxin-dependent peroxide reductase, mitochondrial	GO:0033673,GO:0008022,GO:0006909,GO:0042744,GO:0008379,GO:0032496,GO:0045454,GO:0007005,GO:0005737,GO:0070062,GO:0043209,GO:0005739,GO:0006979,GO:0043066,GO:0008385,GO:0042802,GO:0008284,GO:0018171,GO:0016209,GO:0006915,GO:0034614,GO:0019901,GO:0019900,GO:0008340,GO:0034599,GO:0001893,GO:0055114,GO:0051092,GO:0051881,GO:0042542,GO:0005829,GO:0004601,GO:0043154,GO:0043027,GO:0030099,GO:0005769	CG5826-PA			PIRSF000239			PF10417,PF00578	PS51352			G3DSA:3.40.30.10	SSF52833		00480+1.11.1.15							
aly138.17	Unknown		n/a																				
aly138.18	Unknown		n/a																				
aly138.19	Beta-glucosidase 11	GO:0005975,GO:0008422,GO:0004553	CG9701-PA						PF00232				G3DSA:3.20.20.80	SSF51445									
aly138.2	Cytochrome P450 4V2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016021,GO:0016020,GO:0005789,GO:0005506,GO:0010430,GO:0055114,GO:0009055	CG10842-PA						PF00067,PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463		G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264,SSF48264	847~849		REACT_13433						

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly138.20	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131		G3DSA:3.20.20.80	SSF51445									
aly138.3	Cytochrome P450 4V2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016021,GO:0016020,GO:0005789,GO:0005506,GO:0010430,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly138.4	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463		G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly138.5	MICOS complex subunit Mic60	GO:0070584,GO:0016021,GO:0005739,GO:0005743,GO:0003674,GO:0022008	CG6455-PE												330~354								
aly138.6	MICOS complex subunit Mic60	GO:0070584,GO:0016021,GO:0005739,GO:0005743,GO:0003674,GO:0022008	CG6455-PE						PF09731						254~274,494~514,411~460								
aly138.7	39S ribosomal protein L35, mitochondrial	GO:0005840,GO:0060429,GO:0005739,GO:0005622,GO:0003735,GO:0007293,GO:0005762,GO:0006412,GO:0032543	CG13410-PA						PF01632					SSF143034									
aly138.8	Fumarylacetoacetate hydrolase domain-containing protein 2	GO:0003824,GO:0046872,GO:0008152,GO:0016787	CG6028-PA						PF01557				G3DSA:3.90.850.10	SSF56529									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly138.9	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131		G3DSA:3.20.20.80	SSF51445									
aly138121.1	Putative nuclease HARBI1	GO:0005737,GO:0005813,GO:0005634,GO:0046872,GO:0004518	n/a						PF13359														
aly138281.1	Unknown		n/a																				
aly1383.1	Unknown	GO:0046872,GO:0003676	CG2052-PC																				
aly1383.2	Trypsin-7	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG9564-PC				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1383.3	Trypsin-7	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG9564-PC				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1383.4	Unknown		n/a																				
aly1383.5	Unknown		n/a																				
aly1383.6	Transcription factor IIIA	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG2052-PC				SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF13912,PF12874,PF00096	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667	18~38,461~481,495~515									
aly1383.7	Unknown		n/a																				
aly13879.1	Protein unc-13 homolog C	GO:0005737,GO:0001566,GO:0042734,GO:0019992,GO:0006887,GO:0007268,GO:0005886,GO:0035556,GO:0046872,GO:0030054	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly138866.1	Unknown	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0004984	CG10759-PA						PF02949														
aly13899.1	Pro-Pol polyprotein	GO:0006310,GO:0046718,GO:0075713,GO:0075732,GO:0004523,GO:0003887,GO:0015074,GO:0004190,GO:0003723,GO:0003676,GO:0042025,GO:0003964,GO:0030430,GO:0046872,GO:0019012	n/a							PS50994			G3DSA:3.30.420.10	SSF53098									
aly139.1	Unknown		CG13921-PB												795~815								
aly13906.1	Esterase E4	GO:0052689	CG1257-PA						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly139149.1	Unknown		n/a																				
aly13927.1	Neuropeptide F receptor	GO:0004930,GO:0030536,GO:0016021,GO:0007218,GO:0007217,GO:0004983,GO:0005887,GO:0008188,GO:0004995,GO:0042263,GO:0007186,GO:0007194	CG1147-PD						PF00001	PS50262	PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly139329.1	Protocadherin-19	GO:0007420,GO:0007224,GO:0016324,GO:0016339,GO:0016020,GO:0032529,GO:0007155,GO:0005902,GO:0048100,GO:0007304,GO:0005509,GO:0005887,GO:0005886,GO:0032533,GO:0007156,GO:0016021,GO:0007305	CG31009-PA				SM00112		PF00028	PS50268,PS50268	PR00205,PR00205,PR00205,PR00205		G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313									
aly139354.1	Unknown		n/a																				
aly1395.1	Unknown	GO:0005575,GO:0008150,GO:0003674,GO:0005515	CG10185-PA				SM00320,SM00320,SM00320,SM00320		PF00400	PS50294		PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50998									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1395.10	Zinc finger protein GLIS3	GO:0005737,GO:0005794,GO:0007517,GO:0000122,GO:0003700,GO:0005634,GO:0006366,GO:0007519,GO:0003705,GO:0005654,GO:0006355,GO:0001077,GO:0045944,GO:0003676,GO:0003677,GO:0007520,GO:0000978,GO:0046872,GO:0001078,GO:0007525	CG4677-PB				SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										
aly1395.11	Vitellogenin	GO:0005319,GO:0005576,GO:0045735,GO:0006869	n/a				SM00638,SM00216		PF01347,PF00094,PF09172	PS51233,PS51211			G3DSA:1.25.10.20,G3DSA:2.30.230.10,G3DSA:2.20.80.10	SSF56968,SSF56968,SSF48431			REACT_22258						
aly1395.12	Trehalase	GO:0015927,GO:0046658,GO:0016021,GO:0005991,GO:0003824,GO:0004555	CG9364-PF											SSF48208									
aly1395.13	Trehalase	GO:0015927,GO:0004555,GO:0016021,GO:0005991,GO:0046658	CG9364-PF						PF01204		PR00744,PR00744,PR00744,PR00744,PR00744,PR00744,PR00744	PS00927		SSF48208		00500+3.2.1.28							
aly1395.14	Cathepsin L	GO:0030154,GO:0007275,GO:0005764,GO:0004197,GO:0006508,GO:0008234	CG5367-PA				SM00645		PF00112			PS00139	G3DSA:3.90.70.10	SSF54001									
aly1395.15	Unknown	GO:0016021,GO:0055085,GO:0005353	CG15406-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly1395.16	Unknown		n/a																				
aly1395.2	Fibulin-1 (Fragment)	GO:0007155,GO:0016504,GO:0030198,GO:0005509,GO:0005578	CG31999-PA				SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179		PF12662,PF12662,PF12662,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645	PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026	PR01217,PR01217,PR01217,PR01217,PR01217	PS01187,PS01187,PS01186,PS00010,PS00010,PS01187,PS01187,PS01186,PS01187,PS01187,PS01187,PS01187,PS01186,PS01187,PS01186,PS00010,PS01186,PS00010,PS01187,PS00010	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57196,SSF57184,SSF57184,SSF57184,SSF57184,SSF57196,SSF57196									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1395.3	Sodium- and chloride-dependent GABA transporter 1	GO:0005328,GO:0005887,GO:0009636,GO:0005886,GO:0007612,GO:0030424,GO:0098779,GO:0014054,GO:0014074,GO:0051939,GO:0032355,GO:0016021,GO:0016020,GO:0051260,GO:0007268,GO:0005332,GO:0010288,GO:0009986,GO:0006810,GO:0051592,GO:0007269,GO:0006836,GO:0042210,GO:0055085,GO:0009744,GO:0032229	CG1732-PA						PF00209	PS50267	PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176	PS00610		SSF161070,SSF161070										
aly1395.4	Zinc finger protein 676	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG15269-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12171	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly1395.5	MAM and LDL-receptor class A domain-containing protein 1 (Fragment)	GO:0005044,GO:0016020,GO:0030247,GO:0006952,GO:0005576,GO:0005887,GO:0006955	CG8856-PA				SM00032,SM00032,SM00137,SM00201		PF00629,PF01033,PF00084	PS50958,PS50923,PS50060,PS50923		PS00524	G3DSA:2.10.70.10,G3DSA:2.10.70.10	SSF57535,SSF49899,SSF90188,SSF57535									
aly1395.6	Calcium-dependent secretion activator	GO:0008021,GO:0016192,GO:0045956,GO:0016079,GO:0008289,GO:0030659,GO:0045202,GO:0007269,GO:0015031,GO:0035249,GO:0030054,GO:0005509	CG18026-PA				SM00233		PF06292	PS51258,PS50003			G3DSA:2.30.29.30	SSF50729	316~336								
aly1395.7	LIM domain and actin-binding protein 1	GO:0005737,GO:0031529,GO:0015629,GO:0001725,GO:0030835,GO:0051017,GO:0032154,GO:0051015,GO:0005903,GO:0003785,GO:0005886,GO:0005925,GO:0008270	CG33521-PA				SM00132		PF00412	PS50023		PS00478	G3DSA:2.10.110.10	SSF57716,SSF57716									
aly1395.8	Round spermatid basic protein 1	GO:0005634	CG10600-PB												283~303,946~966								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1395.9	Forkhead box protein P1	GO:0033152,GO:0021517,GO:0030154,GO:0061470,GO:0008045,GO:0061140,GO:0009653,GO:0043565,GO:0001701,GO:0000122,GO:0005634,GO:0055007,GO:0007519,GO:0002329,GO:0006366,GO:0046872,GO:0000981,GO:2000727,GO:0072619,GO:0048745,GO:0045214,GO:0002639,GO:0060043,GO:1901250,GO:0050679,GO:0003700,GO:0003705,GO:0002053,GO:0006355,GO:0006357,GO:0045944,GO:0000978,GO:0003682	CG43067-PC				SM00339		PF00250,PF16159	PS50039	PR00053,PR00053,PR00053	PS00658	G3DSA:1.10.10.10	SSF46785	269~296,174~194								
aly13969.1	Histone acetyltransferase p300	GO:0032025,GO:0032922,GO:0014737,GO:0035066,GO:0000086,GO:0034605,GO:0050681,GO:0007613,GO:0045466,GO:0008270,GO:0044017,GO:0001745,GO:0007219,GO:0004402,GO:0003712,GO:0016746,GO:0071333,GO:0007088,GO:0006473,GO:0043966,GO:0043967,GO:0006475,GO:0065004,GO:0051592,GO:0001756,GO:0007519,GO:0043234,GO:0045793,GO:0071320,GO:0005667,GO:0032993,GO:0043974,GO:0048565,GO:0043971,GO:0060177,GO:0050821,GO:0000785,GO:0003677,GO:0043388,GO:0061418,GO:0040040,GO:0032092,GO:0005654,GO:0071456,GO:0045727,GO:0034612,GO:0018393,GO:0090043,GO:0009887,GO:0007623,GO:0035257,GO:0008013,GO:0032481,GO:0003823,GO:0045862,GO:0060765,GO:0035984,GO:0007224,GO:0043982,GO:0043983,GO:0043154,GO:0002223,GO:0000978,GO:0000979,GO:0043993,GO:0008022,GO:0001047,GO:0033613,GO:0003713,GO:0008140,GO:0031490,GO:0032967,GO:0034644,GO:0001666,GO:0007416,GO:0005737,GO:0000123,GO:0000122,GO:0010560,GO:0005634,GO:0016055,GO:0033160,GO:0008134,GO:0070301,GO:0018076,GO:0097157,GO:0001102,GO:0043923,GO:0060298,GO:0051091,GO:0006990,GO:1900034,GO:0070542,GO:0050714,GO:0001228,GO:0016407,GO:0045944,GO:0005515,GO:0043491,GO:8030097,GO:0003682,GO:0003684,GO:0071389,GO:1990090,GO:0030324,GO:0035690,GO:0001889,GO:0010942,GO:0006355,GO:0006325,GO:0043969,GO:0004468,GO:0048749,GO:0000278,GO:0045087,GO:0006915,GO:2000629,GO:0045471,GO:0045475,GO:0007269,GO:0043627,GO:0022008,GO:0008347,GO:0042771,GO:0007507,GO:0071549,GO:0000076,GO:0007399,GO:0051726,GO:0045773,GO:0007464,GO:0071300,GO:0016032,GO:0001934	CG15319-PC				SM00551		PF02135	PS50134			G3DSA:1.20.1020.10	SSF57933										
aly1398.1	Bleomycin hydrolase	GO:0005737,GO:0002474,GO:0070062,GO:0004177,GO:0009636,GO:0005829,GO:0004180,GO:0042493,GO:0000209,GO:0005654,GO:0004197,GO:0006508,GO:0005634,GO:0008234	CG1440-PD						PF03051				G3DSA:3.90.70.10	SSF54001									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1398.2	Uncharacterized protein F58A4.6		CG12123-PA						PF16065														
aly1398.3	Eukaryotic translation initiation factor 3 subunit A	GO:0006446,GO:0005852,GO:0016282,GO:0005829,GO:0007052,GO:0005515,GO:0033290,GO:0000022,GO:0006413,GO:0001731,GO:0003743	CG9805-PA				SM00088		PF01399														
aly13994.1	Unknown		n/a												38~58								
aly14.1	Hemicentin-2	GO:0005604,GO:0050896,GO:0007606,GO:0008039,GO:0005575,GO:0005576,GO:0003674,GO:0005509,GO:0030054,GO:0005938	CG34385-PC				SM00409,SM00409,SM00408,SM00408		PF13927,PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly14.2	Unknown		n/a																				
aly14.3	Unknown	GO:0003676	n/a										G3DSA:3.30.420.10	SSF53098									
aly14.4	Unknown		n/a						PF00536				G3DSA:1.10.150.50		76~96,421~443								
aly14.5	MD-2-related lipid-recognition protein	GO:0032934,GO:0015918,GO:0042381,GO:0007498,GO:0008289,GO:0005576	CG11314-PA				SM00737		PF02221				G3DSA:2.60.40.770	SSF81296									
aly14.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly140.1	WD repeat-containing protein 63	GO:0030286,GO:0007018,GO:0042623	CG14838-PA				SM00320,SM00320,SM00320						G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978	996~1017,919~957								
aly140.10	Cell surface glycoprotein 1	GO:0005618,GO:0005576,GO:0030246,GO:0030115,GO:0000272	CG30101-PA																				
aly140.11	Zinc finger protein 512B	GO:0006355,GO:0005634,GO:0046872,GO:0006351,GO:0003677	CG30101-PA																				
aly140.12	Angiotensin-converting enzyme	GO:0005737,GO:0004180,GO:0008241,GO:0016021,GO:0016020,GO:0005576,GO:0005886,GO:0006508,GO:0046872,GO:0008237	CG17988-PB						PF01401					SSF55486									
aly140.13	Cell death abnormality protein 1	GO:0006898,GO:0006909,GO:0030670,GO:0012501,GO:0031532,GO:0005044,GO:0016021,GO:0006915,GO:0043654,GO:0045184,GO:0043652,GO:0003674,GO:0034620,GO:0031260,GO:0005886,GO:0001891,GO:0001845,GO:0009986,GO:0042742	CG42282-PF						PF07546	PS51041		PS01186,PS00022	G3DSA:2.170.300.10										
aly140.14	von Willebrand factor D and EGF domain-containing protein	GO:0007498,GO:0005576,GO:0003674,GO:0042742,GO:0005515	CG31839-PA				SM00181,SM00181,SM00181,SM00181,SM00181,SM00181							SSF57184									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly140.15	Unknown		CG6329-PA											SSF57302									
aly140.2	Unknown		n/a																				
aly140.3	Unknown		n/a																				
aly140.4	Centaurin-gamma-1A	GO:0046872,GO:0043547,GO:0032312,GO:0005634,GO:0005096,GO:0005622,GO:0003924,GO:0008060,GO:0008270,GO:0008152,GO:0007264,GO:0043087,GO:0005525	CG31811-PB				SM00105,SM00175,SM00173,SM00233		PF01412,PF00071	PS50115,PS50003,PS51419	PR00405,PR00405,PR00405		G3DSA:2.30.29.30,G3DSA:2.30.29.30,G3DSA:3.40.50.300	SSF50729,SSF57863,SSF50729,SSF50729,SSF52540									
aly140.5	Centaurin-gamma-1A	GO:0046872,GO:0043547,GO:0032312,GO:0005634,GO:0005096,GO:0005622,GO:0003924,GO:0008060,GO:0008270,GO:0008152,GO:0007264,GO:0043087,GO:0005525	CG31811-PB																				
aly140.6	Angiotensin-converting enzyme	GO:0016020,GO:0005615,GO:0008241,GO:0009609,GO:0007552,GO:0004180,GO:0007291,GO:0008270,GO:0007289,GO:0006508,GO:0046872,GO:0008237,GO:0005576	CG8827-PA						PF01401		PR00791,PR00791,PR00791,PR00791,PR00791,PR00791,PR00791,PR00791			SSF55486									
aly140.7	Angiotensin-converting enzyme	GO:0016020,GO:0005615,GO:0008241,GO:0009609,GO:0007552,GO:0004180,GO:0007291,GO:0008270,GO:0007289,GO:0006508,GO:0046872,GO:0008237,GO:0005576	CG8827-PA						PF01401		PR00791,PR00791,PR00791,PR00791,PR00791,PR00791,PR00791,PR00791			SSF55486									
aly140.8	Angiotensin-converting enzyme (Fragment)	GO:0004180,GO:0008241,GO:0016021,GO:0016020,GO:0006508,GO:0046872,GO:0008237	CG17988-PB						PF01401		PR00791,PR00791,PR00791,PR00791,PR00791,PR00791,PR00791,PR00791			SSF55486									
aly140.9	Filamentous hemagglutinin	GO:0009986	CG16886-PA																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1402.1	Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase	GO:0005783,GO:0006486,GO:0016021,GO:0016020,GO:0005789,GO:0035010,GO:0004571,GO:0005509,GO:0030433,GO:1903561	CG11874-PA						PF01532		PR00747,PR00747,PR00747,PR00747,PR00747,PR00747		G3DSA:1.50.10.50,G3DSA:1.50.10.50	SSF48225									
aly1402.10	Glutamate receptor 1	GO:0045211,GO:0032281,GO:0008328,GO:0035235,GO:0006812,GO:0005230,GO:0015277,GO:0005234,GO:0034220,GO:0030054,GO:0005886,GO:0030425,GO:0035249,GO:0004970,GO:0004971	CG43743-PB				SM00079,SM00918		PF10613,PF01094				G3DSA:3.40.50.2300,G3DSA:1.10.287.70,G3DSA:3.40.190.10,G3DSA:3.40.50.2300	SSF53850,SSF53850,SSF53822									
aly1402.11	Unknown		n/a																				
aly1402.12	Glutamate receptor 1	GO:0045211,GO:0032281,GO:0008328,GO:0035235,GO:0006812,GO:0005230,GO:0015277,GO:0005234,GO:0034220,GO:0030054,GO:0005886,GO:0030425,GO:0035249,GO:0004970,GO:0004971	CG43743-PB										G3DSA:3.40.50.2300										
aly1402.13	Unknown		n/a																				
aly1402.14	Unknown		n/a																				
aly1402.2	Unknown		n/a																				
aly1402.3	Capon-like protein	GO:0005575,GO:0008150,GO:0003674	CG42673-PC				SM00462		PF00640	PS01179			G3DSA:2.30.29.30	SSF50729	337~357								
aly1402.4	ATP synthase subunit b, mitochondrial	GO:0015986,GO:0006909,GO:0046933,GO:0005811,GO:0005739,GO:0015992,GO:0008553,GO:0015078,GO:0000276	CG8189-PA						PF05405					SSF161060									
aly1402.5	Chitinase-like protein EN03	GO:0008084,GO:0005975,GO:0007444,GO:0005576,GO:0004568,GO:0006032	CG1780-PA				SM00636		PF00704				G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.10.50.10	SSF54556,SSF51445,SSF51445	428~436								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1402.6	Nucleobindin-2	GO:0005635,GO:0005783,GO:0070093,GO:0005164,GO:0046321,GO:0042594,GO:0003677,GO:0050829,GO:0044752,GO:0005737,GO:0005615,GO:0030818,GO:0032099,GO:0016020,GO:0005509,GO:1990680,GO:1901142,GO:0005794,GO:0005797,GO:0032504,GO:2000845,GO:0046627,GO:0003824,GO:0045599,GO:0005975,GO:0009749	CG32190-PA						PF13499	PS50222,PS50222		PS00018	G3DSA:1.10.238.10	SSF47473	143~170								
aly1402.7	Transcription initiation factor TFIID subunit 7	GO:0044212,GO:0051123,GO:0006355,GO:0003700,GO:0005634,GO:0003713,GO:0035035,GO:0001075,GO:0006357,GO:0006367,GO:0005669,GO:0008134	CG2670-PA						PF04658						346~380								
aly1402.8	Putative SERF like protein	GO:0005575,GO:0008150,GO:0005829,GO:0003674	CG17931-PA						PF04419						7~29								
aly1402.9	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	GO:0005737,GO:0003073,GO:0070062,GO:0007263,GO:0000052,GO:0006527,GO:0005739,GO:0003824,GO:0045429,GO:0045766,GO:0016403,GO:0046872,GO:0016597	CG1764-PB										G3DSA:3.75.10.10	SSF55909									
aly14023.1	PR domain zinc finger protein 5	GO:0031936,GO:0043565,GO:0000278,GO:0000122,GO:0005634,GO:0005700,GO:0008188,GO:0016575,GO:0044212,GO:0045892,GO:0006351,GO:0005515,GO:0003677,GO:0051567,GO:0000785,GO:0000978,GO:0046872,GO:0001078,GO:0070491,GO:0043035	CG8573-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly14023.2	Luciferin 4-monooxygenase	GO:0046872,GO:0006637,GO:0045289,GO:0004321,GO:0005777,GO:0004467,GO:0046949,GO:0001676,GO:0008218,GO:0047077,GO:0005524	CG6178-PA						PF00501			PS00455	G3DSA:3.40.50.980	SSF56801									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1405.1	TAR DNA-binding protein 43	GO:0035061,GO:0032024,GO:0008344,GO:0010629,GO:0045886,GO:0030264,GO:0003676,GO:0070935,GO:0007274,GO:0007417,GO:0005737,GO:0005634,GO:0000166,GO:0005654,GO:0003730,GO:0071765,GO:0006366,GO:0003690,GO:0008380,GO:0042802,GO:0016607,GO:0044822,GO:0007628,GO:0007528,GO:0043922,GO:0001205,GO:0008345,GO:0048471,GO:0034976,GO:0005726,GO:0051726,GO:0003700,GO:0048812,GO:0003723,GO:0001933,GO:0006397,GO:0003729	CG10327-PB				SM00360,SM00360		PF00076,PF14259	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									
aly1405.10	Tectonin beta-propeller repeat-containing protein	GO:0007031,GO:0000421,GO:0016021,GO:0000046,GO:0030246,GO:0032266,GO:0005765	CG32226-PA				SM00276,SM00693,SM00693,SM00706,SM00706,SM00706,SM00706,SM00706,SM00706,SM00706,SM00706,SM00706,SM00706,SM00694,SM00694,SM00908		PF06462,PF06462,PF06462,PF06462,PF06462,PF00337,PF06398,PF06398	PS51304			G3DSA:2.60.120.200	SSF49899									
aly1405.11	Splicing factor 3B subunit 1	GO:0071011,GO:0071013,GO:0000398,GO:0005686,GO:0008380,GO:0005681,GO:0006397	CG2807-PA						PF08920				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371	886~906								
aly1405.12	Vigilin	GO:0005737,GO:0000792,GO:0008203,GO:0031507,GO:0030529,GO:0006869,GO:0005634,GO:0005811,GO:0044822,GO:0005701,GO:0030261,GO:0003723,GO:0034364,GO:0007059,GO:0045727,GO:0003696,GO:0003697,GO:0003730	CG5170-PD				SM00322,SM00322,SM00322,SM00322,SM00322,SM00322,SM00322,SM00322,SM00322,SM00322,SM00322,SM00322,SM00322		PF00013,PF00013,PF00013,PF00013,PF00013,PF00013,PF00013,PF00013,PF00013,PF00013,PF00013,PF00013,PF00013,PF00013,PF00013,PF00013	PS50084,PS50084,PS50084,PS50084,PS50084,PS50084,PS50084,PS50084,PS50084,PS50084,PS50084,PS50084,PS50084,PS50084,PS50084,PS50084			G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10	SSF54791,SSF54791,SSF54791,SSF54791,SSF54791,SSF54791,SSF54791,SSF54791,SSF54791,SSF54791,SSF54791,SSF54791,SSF54791,SSF54791,SSF54791,SSF54791	624~644,1078~1098,1004~1024								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1405.13	UPF0505 protein C16orf62 homolog	GO:0008565,GO:0005575,GO:0030904,GO:0003674,GO:0042147,GO:0015031,GO:0008150,GO:0005769	CG8202-PA						PF03635														
aly1405.14	Unknown		n/a												270~290								
aly1405.15	Unknown		n/a																				
aly1405.16	Nipped-B protein	GO:0043234,GO:0032116,GO:0070193,GO:0034088,GO:0005634,GO:0071733,GO:0005700,GO:0005654,GO:0006355,GO:0010628,GO:0035327,GO:0045893,GO:0005515,GO:0000795,GO:0007064,GO:0003682,GO:0008278,GO:0006351	CG17704-PE						PF12765,PF12830				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371	514~534								
aly1405.17	Dehydrogenase/reductase SDR family protein 7-like	GO:0005575,GO:0016021,GO:0005778,GO:0008152,GO:0016491	CG7601-PA						PF00106				G3DSA:3.40.50.720	SSF51735									
aly1405.18	Dehydrogenase/reductase SDR family protein 7-like	GO:0005575,GO:0016021,GO:0005778,GO:0008152,GO:0016491	CG7601-PA						PF00106		PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly1405.19	Transmembrane protein 11 homolog, mitochondrial	GO:0070584,GO:0031305,GO:0005743,GO:0003674,GO:0042775,GO:0007007,GO:0007005	CG33718-PD						PF14972														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1405.2	Telomerase-binding protein EST1A	GO:0090502,GO:0005737,GO:0050808,GO:0000723,GO:0005730,GO:0043487,GO:0035195,GO:0005829,GO:0004540,GO:0004521,GO:0000781,GO:0010467,GO:0000184,GO:0042162,GO:0016246,GO:0035303,GO:0046872,GO:0007274,GO:0005634,GO:0006406,GO:0005697	CG6369-PA						PF10373,PF10374				G3DSA:1.25.40.10	SSF48452	1351~1378								
aly1405.20	Neurogenic locus Notch protein	GO:0007616,GO:0030720,GO:0008587,GO:0005788,GO:0045466,GO:0045465,GO:0045463,GO:0007297,GO:0007298,GO:0001745,GO:0061382,GO:0045468,GO:0007219,GO:0016021,GO:0005770,GO:0007450,GO:0007451,GO:0042688,GO:0042689,GO:0007400,GO:0042686,GO:0005796,GO:0035172,GO:0060250,GO:0035170,GO:0035171,GO:0008362,GO:0046331,GO:0007521,GO:0045316,GO:0043234,GO:0007440,GO:0007447,GO:0007446,GO:0007293,GO:0005829,GO:0009608,GO:0046843,GO:0048749,GO:0035165,GO:0035167,GO:0035162,GO:0035003,GO:0010629,GO:0046329,GO:0048190,GO:0007346,GO:0008407,GO:0005654,GO:0048803,GO:0048477,GO:0035153,GO:0035155,GO:0035157,GO:0042067,GO:0060288,GO:0048863,GO:0046666,GO:0046667,GO:0007424,GO:0009952,GO:0007423,GO:0007422,GO:0007314,GO:0006351,GO:0005634,GO:0007498,GO:0007519,GO:0005886,GO:0035222,GO:0031012,GO:0007419,GO:0010001,GO:0007411,GO:0005737,GO:0050767,GO:0030708,GO:0007252,GO:0000122,GO:0001708,GO:0030707,GO:0050768,GO:0045747,GO:0005509,GO:0008284,GO:0051489,GO:0050877,GO:0009986,GO:0060429,GO:0045595,GO:0005912,GO:0007403,GO:0051539,GO:0036335,GO:0030718,GO:2000048,GO:0030713,GO:0005622,GO:0045944,GO:0005515,GO:0048542,GO:0003682,GO:0016333,GO:0005201,GO:0016330,GO:0007464,GO:0030139,GO:0004872,GO:0008045,GO:0008356,GO:0007478,GO:0040005,GO:0007473,GO:0040008,GO:0007476,GO:0007474,GO:0007475,GO:1900087,GO:0061331,GO:0035214,GO:0048666,GO:0016348,GO:0042676,GO:0022416,GO:0048052,GO:0007155,GO:0008340,GO:0007157,GO:0036099,GO:0008347,GO:0007015,GO:0007398,GO:0007460,GO:0036011,GO:0007391,GO:0004888,GO:0005768,GO:0005578	CG33196-PQ				SM00289,SM00289,SM00289,SM00289,SM00289,SM00289,SM00289,SM00289,SM00289,SM00289,SM00289,SM00289,SM00289,SM00289,SM00289,SM00289,SM00181,SM00274,SM00179,SM00286		PF07645,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645	PS50026,PS50026		PS01186,PS01186,PS01187,PS01187,PS01186,PS01187,PS00010,PS01187,PS00010,PS01186,PS00010,PS01187,PS01187,PS01187,PS00010,PS01187,PS01186,PS01187,PS01186,PS01187,PS01186,PS01186,PS01186,PS01186,PS00010,PS00010,PS01186,PS01186,PS00010,PS00010,PS01186,PS00010,PS01186,PS01186,PS01186,PS01187,PS01187,PS01186,PS01186,PS01187,PS01186,PS01186,PS01186,PS00022,PS01186,PS00010,PS01187,PS01187,PS01186,PS01186,PS01187,PS01186,PS01186,PS00010,PS00010,PS00010,PS00010,PS00010,PS00010,PS01186,PS01186,PS01186	G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57196,SSF57184,SSF57196,SSF57196,SSF57184,SSF57196,SSF90148,SSF57196,SSF57196,SSF57184,SSF57184,SSF57196,SSF90148,SSF57184,SSF57184,SSF57196,SSF57196									
aly1405.21	Neurogenic locus notch homolog protein 1	GO:0055016,GO:0005201,GO:0016021,GO:0021531,GO:0021514,GO:0031017,GO:0031016,GO:0031012,GO:0021523,GO:0042663,GO:0004872,GO:0001525,GO:0021986,GO:0007219,GO:0040005,GO:0007368,GO:0050768,GO:0007475,GO:0002244,GO:0005509,GO:0001840,GO:0061314,GO:0048337,GO:0060271,GO:0048936,G	CG33196-PQ				SM00274,SM00274,SM00274,SM00274,SM00274,SM00274,SM00274,SM00274,SM00274,SM00274,SM00274,SM00181,SM0			PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS51034,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026		PS01186,PS01186	G3DSA:2.10.25.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF90148,SSF90148,SSF90148,SSF90148,SSF90148,SSF90148,SSF90148,SSF90148	3261~3261								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1405.22	Sodium- and chloride-dependent GABA transporter ine	GO:0019226,GO:0042065,GO:0005328,GO:0047484,GO:0042066,GO:0016021,GO:0005886,GO:0050891,GO:0016323,GO:0005034,GO:0007165,GO:0009414,GO:0006836,GO:0009881	CG15444-PC						PF00209	PS50267	PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR01205	PS00610		SSF161070										
aly1405.23	Unknown		n/a																				
aly1405.24	Putative glycerol kinase 3	GO:0004370,GO:0005975,GO:0019563,GO:0005575,GO:0046167,GO:0005741,GO:0006072,GO:0005524	CG18374-PA						PF00370,PF00370,PF02782			PS00445,PS00933	G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.30.420.40	SSF53067,SSF53067		00561+2.7.1.30		PWY-4261	UPA00618				
aly1405.25	tRNA-splicing ligase RtcB homolog	GO:0072669,GO:0008452,GO:0003972,GO:0005524,GO:0006388,GO:0022008,GO:0046872,GO:0006396	CG9987-PA	MF_03144					PF01139			PS01288		SSF103365									
aly1405.26	NADH dehydrogenase [ubiqui] 1 beta subcomplex subunit 11, mitochondrial	GO:0016021,GO:0005739,GO:0003674,GO:0005747,GO:0022904,GO:0055114	CG6008-PA						PF10183														
aly1405.27	Unknown		CG14285-PA				SM00320,SM00320,SM00320						G3DSA:2.130.10.10	SSF50998									
aly1405.28	Unknown	GO:0005214,GO:0040003,GO:0005578	CG14534-PA				SM00690		PF03103		PR01217,PR01217,PR01217,PR01217,PR01217,PR01217												
aly1405.29	Sodium-coupled monocarboxylate transporter 1	GO:0006810,GO:0008507,GO:0070062,GO:0015293,GO:0016324,GO:0005215,GO:0016021,GO:0016020,GO:0006814,GO:0005886,GO:0006811,GO:0055085,GO:0006915	CG5687-PA					TIGR00813	PF00474	PS50283													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1405.3	Unknown		n/a																				
aly1405.30	Golgi reassembly-stacking protein 2	GO:0005795,GO:0016333,GO:0007030,GO:0005783,GO:0005794,GO:0007472,GO:0005798,GO:0000139,GO:0005797,GO:0006996,GO:0005886,GO:0032580	CG7809-PA						PF04495				G3DSA:2.30.42.10	SSF50156,SSF50156									
aly1405.31	Hyccin	GO:0005737,GO:0007165,GO:0004871,GO:0005886	CG6406-PB						PF09790,PF15868														
aly1405.32	Unknown		n/a																				
aly1405.33	F-box only protein 21	GO:0005515,GO:0003677	n/a				SM00256		PF13369,PF12937	PS50181			G3DSA:1.20.1280.50	SSF81383									
aly1405.34	Fat-like cadherin-related tumor suppressor homolog	GO:0005201,GO:0016339,GO:0031012,GO:0007293,GO:0004872,GO:0007295,GO:0050829,GO:0005925,GO:0007431,GO:0007156,GO:0030950,GO:0007475,GO:0005509,GO:0009925,GO:0048477,GO:0045089,GO:0007442,GO:0060429,GO:0008362,GO:0046331,GO:0005887,GO:0005886,GO:0044331,GO:0050839,GO:0007424,GO:0007440,GO:0051539,GO:0040005,GO:0042247,GO:0045571,GO:0005578	CG33196-PQ				SM00181,SM00181,SM00181			PS50026,PS50026,PS50026			G3DSA:2.10.25.10	SSF57184									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1405.4	Neurofilament heavy polypeptide	GO:0005201,GO:0019894,GO:0015643,GO:0030031,GO:0048619,GO:0021510,GO:0031012,GO:0021766,GO:0005200,GO:0000226,GO:0001552,GO:0061564,GO:0021987,GO:0005737,GO:0005615,GO:0007472,GO:0045502,GO:0007476,GO:0005739,GO:0005198,GO:0048803,GO:0060562,GO:1902513,GO:0097418,GO:0005178,GO:0031103,GO:0071392,GO:0008017,GO:0019901,GO:0005883,GO:0007409,GO:0042220,GO:0035296,GO:0034599,GO:0030424,GO:0043204,GO:0097481,GO:0030674,GO:1903935,GO:0033693,GO:0043209,GO:0048936,GO:0005515,GO:0005634	CG13648-PC				SM00214,SM00214,SM00214,SM00214			PS50184				SSF57603,SSF57603,SSF57603,SSF57603,SSF57603,SSF57603										
aly1405.5	TOX high mobility group box family member 3	GO:0034056,GO:0006351,GO:0006338,GO:0005634,GO:0006915,GO:0051219,GO:0043524,GO:0005575,GO:0003674,GO:0045893,GO:0008150,GO:0003682,GO:0042803	CG12104-PA				SM00398		PF00505	PS50118	PR00886,PR00886,PR00886		G3DSA:1.10.30.10	SSF47095									
aly1405.6	Protein RER1	GO:0006890,GO:0016192,GO:0005793,GO:0016021,GO:0071340,GO:0030173,GO:0090004,GO:0009986	CG11857-PA			PIRSF016013			PF03248														
aly1405.7	Serine/threonine-protein phosphatase 2B catalytic subunit 3	GO:0033192,GO:0006470,GO:0004722,GO:0051533,GO:0005575,GO:0030431,GO:0046872	CG9819-PA				SM00156		PF00149		PR00114,PR00114,PR00114,PR00114,PR00114,PR00114,PR00114	PS00125	G3DSA:3.60.21.10	SSF56300									
aly1405.8	Phosphatidylinositol N-acetylglucosaminyltransferase subunit P	GO:0017176,GO:0016021,GO:0005783,GO:0000506,GO:0006506	CG42498-PA						PF08510,PF09341							00563+2.4.1.198			UPA00196				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1405.9	PXMP2/4 family protein 4	GO:0016021,GO:0005778	CG14778-PA						PF04117														
aly14063.1	Putative glucosylceramidase 3	GO:0006665,GO:0005975,GO:0034620,GO:0004348	CG31148-PA						PF02055				G3DSA:2.60.40.1180,G3DSA:3.20.20.80	SSF51445									
aly14063.2	Glucosylceramidase	GO:0034620,GO:0005765,GO:0005975,GO:0004348,GO:0006665	CG31414-PB						PF02055		PR00843,PR00843,PR00843		G3DSA:3.20.20.80,G3DSA:2.60.40.1180	SSF51445									
aly14063.3	Glucosylceramidase	GO:0051384,GO:0043407,GO:0034620,GO:0043202,GO:0004348,GO:0097066,GO:0071356,GO:0033561,GO:0006680,GO:0006665,GO:0043589,GO:1903052,GO:0023021,GO:0043627,GO:0009268,GO:0035307,GO:0070062,GO:0005975,GO:0033574,GO:0005765,GO:0032715,GO:0005102,GO:0046512,GO:0046513	CG31148-PA						PF02055		PR00843,PR00843,PR00843,PR00843		G3DSA:3.20.20.80,G3DSA:2.60.40.1180	SSF51445									
aly14063.4	Glucosylceramidase	GO:0005765,GO:0005975,GO:0004348,GO:0006665	n/a						PF02055		PR00843,PR00843		G3DSA:3.20.20.80	SSF51011									
aly1407.1	Cholecystokinin receptor	GO:0004930,GO:0043195,GO:0043025,GO:0016021,GO:0015054,GO:0008345,GO:0007218,GO:0007204,GO:0007528,GO:0004951,GO:0006950,GO:0005887,GO:0008188,GO:0005886,GO:0007186,GO:0008344	CG42301-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR01822,PR01822	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1407.10	Unknown		n/a																				
aly1407.11	Zinc finger protein jing	GO:0007424,GO:0007479,GO:0006351,GO:0000122,GO:0003700,GO:0042246,GO:0007382,GO:0035098,GO:0007476,GO:0007474,GO:0007418,GO:0006355,GO:0045944,GO:0016568,GO:0003676,GO:0007411,GO:0007298,GO:0046872,GO:0005634,GO:0008347,GO:0007417	CG9397-PI				SM00355,SM00355,SM00355			PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667										
aly1407.2	Cholecystokinin receptor	GO:0004930,GO:0007186,GO:0043195,GO:0008345,GO:0016021,GO:0015054,GO:0007218,GO:0007204,GO:0007528,GO:0004951,GO:0006950,GO:0005887,GO:0008188,GO:0005886,GO:0043025,GO:0008344	CG42301-PA						PF00001	PS50262	PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1407.3	Unknown		n/a																				
aly1407.4	Proton-coupled amino acid transporter 4	GO:0015293,GO:0003333,GO:0015171,GO:0015827,GO:0015824,GO:0005774,GO:0015808,GO:0016021	CG8785-PB						PF01490														
aly1407.5	Unknown		CG14186-PA						PF15383														
aly1407.6	DNA-binding protein D-ETS 4	GO:0043565,GO:0003700,GO:0005634,GO:0030154,GO:0006355,GO:0006357,GO:0000981,GO:0003677,GO:0008354	CG5583-PA				SM00251,SM00413		PF00178,PF02198	PS51433,PS50061	PR00454,PR00454,PR00454,PR00454	PS00345,PS00346	G3DSA:1.10.10.10,G3DSA:1.10.150.50	SSF46785,SSF47769									
aly1407.7	Unknown		n/a												2026~2046								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1407.8	Phospholipase D1	GO:0006654,GO:0005789,GO:0010004,GO:0009395,GO:0031985,GO:0031982,GO:0031410,GO:0007349,GO:0004630,GO:0048471,GO:0031902,GO:0030335,GO:0030027,GO:0048215,GO:0050764,GO:0007602,GO:0008152,GO:0043434,GO:0048017,GO:0007030,GO:0043231,GO:0008654,GO:0035091,GO:0000139,GO:0070290	CG12110-PF			PIRSF009376	SM00155,SM00155,SM00312		PF00787,PF13091,PF00614	PS50035,PS50195,PS50035			G3DSA:3.30.870.10,G3DSA:3.30.870.10,G3DSA:3.30.870.10,G3DSA:3.30.1520.10,G3DSA:3.30.1520.10,G3DSA:2.30.29.30	SSF56024,SSF64268,SSF64268,SSF56024,SSF56024		00564+3.1.4.4,00565+3.1.4.4		PWY-3561,PWY-7039					
aly1407.9	Unknown		n/a																				
aly1409.1	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0006631,GO:0016021,GO:0006629,GO:0017105,GO:0006723,GO:0046872,GO:0042811,GO:0004768,GO:0016717,GO:0055114	CG5925-PA						PF00487		PR00075,PR00075,PR00075,PR00075,PR00075,PR00075,PR00075	PS00476						PWY-5987,PWY-5996					
aly1409.10	Unknown		CG34205-PA																				
aly1409.11	Prominin-1-A	GO:0031528,GO:0035996,GO:0005783,GO:0005793,GO:0016324,GO:0016021,GO:0003674,GO:0005886,GO:0042052	CG42310-PD						PF05478						209~229,549~569								
aly1409.12	Protein takeout	GO:0007631,GO:0007623,GO:0005615,GO:0007617,GO:0005576,GO:0042594,GO:0042595,GO:0008343,GO:0008049,GO:0007622	CG11854-PB				SM00700		PF06585														
aly1409.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1409.3	Cyclin-dependent kinase 8	GO:0008353,GO:0006468,GO:0016592,GO:0000278,GO:0034472,GO:0006355,GO:0000082,GO:0005634,GO:0007411,GO:0036011,GO:0001104,GO:0004674,GO:0045498,GO:0022416,GO:0006351,GO:0006367,GO:0004672,GO:0004693,GO:0007095,GO:0005524	CG10572-PA				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly1409.4	NEDD4-binding protein 2-like 1	GO:0005575,GO:0008150,GO:0003674	CG7139-PA						PF13671				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	1088~1108								
aly1409.5	Unknown	GO:0005575,GO:0003674,GO:0008150	CG32603-PA																				
aly1409.6	Unknown	GO:0005575,GO:0003674,GO:0008150	CG32603-PA																				
aly1409.7	Unknown	GO:0005575,GO:0003674,GO:0008150	CG32603-PA																				
aly1409.8	Unknown	GO:0005575,GO:0003674,GO:0008150	CG32603-PA																				
aly1409.9	Unknown		n/a																				
aly140990.1	Unknown		n/a																				
aly141.1	Receptor expression-enhancing protein 2	GO:0005881,GO:0016021	CG42678-PI						PF03134														
aly141.2	Testis-expressed sequence 10 protein homolog	GO:0016021,GO:0031965,GO:0071339,GO:0005730	CG1575-PA						PF12333				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371									
aly141.3	Nucleolar protein 16	GO:0042273,GO:0044822,GO:0005730	CG11563-PA						PF09420,PF09420						180~200								
aly141.4	Protein DPCD	GO:0030317,GO:0007283,GO:0060972,GO:0021678,GO:0005634,GO:0021670,GO:0007368,GO:0003351	CG13901-PA						PF14913		PR02065,PR02065,PR02065,PR02065												

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly141.5	Putative tyrosine-protein phosphatase 1	GO:0006470,GO:0004725,GO:0008138	CG13197-PA						PF00782	PS50056		PS00383	G3DSA:3.90.190.10	SSF52799									
aly141.6	Unknown		n/a																				
aly141.7	Unknown		n/a						PF00167				G3DSA:2.80.10.50	SSF50353									
aly141.8	Unknown		n/a																				
aly14101.1	Phosphatidylinositol 3-kinase catalytic subunit type 3	GO:0046934,GO:0000910,GO:0033227,GO:0006897,GO:0035004,GO:0036092,GO:0016303,GO:0006914,GO:0035005,GO:0030496,GO:0035032,GO:0000045,GO:0048015,GO:0009267,GO:0046854,GO:0005622,GO:0010506,GO:0005524	CG5373-PA										G3DSA:1.25.40.70	SSF48371									
aly141017.1	4-hydroxyphenylpyruvate dioxygenase	GO:0006572,GO:0006559,GO:0003868,GO:0055114,GO:0046872,GO:0009072	CG11796-PA										G3DSA:3.10.180.10	SSF54593									
aly1411.1	Unknown		n/a										G3DSA:3.30.40.10	SSF57903									
aly1411.2	3-oxoacyl-[acyl-carrier-protein] reductase FabG	GO:0050661,GO:0051287,GO:0030497,GO:0004316,GO:0008152,GO:0016491	CG31548-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735	35~55								
aly1411.3	3-oxoacyl-[acyl-carrier-protein] reductase FabG	GO:0050661,GO:0051287,GO:0030497,GO:0004316,GO:0008152,GO:0016491	CG31548-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735	64~84,35~55								
aly14110.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1412.1	Neural/ectodermal development factor IMP-L2	GO:0046628,GO:0005615,GO:0046627,GO:0005576,GO:0005515,GO:0007155,GO:0008340,GO:0005520	CG15009-PC				SM00408,SM00408,SM00409,SM00409		PF13927,PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly1412.10	Unknown	GO:0003824,GO:0008152	CG6236-PB						PF02995														
aly1412.2	Pro-resilin	GO:0040003,GO:0032992,GO:0005214,GO:0030023,GO:0008010,GO:0031012,GO:0005576,GO:0008061,GO:0042302	CG9036-PA						PF00379	PS51155		PS00233											
aly1412.3	Unknown	GO:0003824,GO:0008152	CG6236-PB						PF02995														
aly1412.4	Ommochrome-binding protein	GO:0003824,GO:0008152	CG6236-PB						PF02995				G3DSA:3.40.720.10,G3DSA:2.120.10.30	SSF53649,SSF63829									
aly1412.5	Putative serine protease F56F10.1	GO:0006508,GO:0045087,GO:0045121,GO:0008236	CG18493-PA						PF05577				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474									
aly1412.6	Tetraspanin-6	GO:0039532,GO:0070062,GO:0016021,GO:0008150,GO:0003674,GO:0004871,GO:1901223,GO:0043123	CG9033-PB			PIRSF002419			PF00335		PR00259,PR00259,PR00259,PR00259			SSF48652									
aly1412.7	CD63 antigen	GO:0042470,GO:2001046,GO:0016021,GO:0048757,GO:0007160,GO:0005765,GO:0003674,GO:0002092,GO:0035646,GO:0097487,GO:0015031,GO:0008150,GO:0016477,GO:0031226,GO:0031902,GO:1900746	CG9033-PB			PIRSF002419			PF00335		PR00259,PR00259,PR00259			SSF48652									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1412.8	CD63 antigen	GO:0048757,GO:0007160,GO:0003674,GO:0031226,GO:0005737,GO:0045785,GO:0016021,GO:0035646,GO:0030855,GO:0032403,GO:0016477,GO:0031902,GO:2001046,GO:0030658,GO:0008150,GO:0002092,GO:0005886,GO:0097487,GO:0043234,GO:0042470,GO:0010633,GO:0005764,GO:0005765,GO:1900746,GO:0015031,GO:0045807	CG9033-PB			PIRSF002419			PF00335		PR00259,PR00259,PR00259,PR00259			SSF48652									
aly1412.9	Unknown		n/a																				
aly14131.1	Synaptic vesicle glycoprotein 2A	GO:0030672,GO:0005783,GO:0006874,GO:0016021,GO:0048786,GO:0005215,GO:0031594,GO:0022857,GO:0004872,GO:0005911,GO:0006836,GO:0043195,GO:0055085,GO:0045202	CG31106-PB						PF07690,PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473									
aly14131.2	Unknown	GO:0006310,GO:0015074,GO:0003677	n/a						PF00589				G3DSA:1.10.443.10	SSF56349	268~288								
aly14131.3	Unknown		n/a																				
aly14145.1	Unknown		n/a												317~337,1373~1376								
aly14145.2	Cyclin-dependent kinase 1	GO:0055059,GO:0000086,GO:0000082,GO:0048142,GO:0008315,GO:0004693,GO:0008353,GO:0007067,GO:0044818,GO:0007140,GO:0007141,GO:0005634,GO:0005875,GO:0004674,GO:0004672,GO:0032880,GO:0005524,GO:0006468,GO:0000278,GO:0009987,GO:0006974,GO:0007283,GO:0007284,GO:0022008,GO:0051726,GO:0070816,GO:0005515,GO:0007095	CG5363-PA				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly14145.3	Glucosylceramidase	GO:0006665,GO:0005765,GO:0005975,GO:0034620,GO:0004348	CG31148-PA						PF02055,PF02055				G3DSA:3.20.20.80,G3DSA:2.60.40.1180	SSF51445									
aly141455.1	Unknown	GO:0005575,GO:0003924,GO:0005622,GO:0035011,GO:0007264,GO:0005525	CG5701-PB																				
aly14155.1	Peptidyl-prolyl cis-trans isomerase CWC27 homolog	GO:0071011,GO:0071013,GO:0006457,GO:0003755,GO:0000398	CG10907-PA						PF00160				G3DSA:2.40.100.10	SSF50891									
aly14161.1	Cytochrome P450 6B6	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0042742,GO:0005506,GO:0055114,GO:0009055	CG2397-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly14173.1	Microcephalin	GO:0005737,GO:0021987,GO:0005815	n/a				SM00292,SM00292,SM00292			PS50172			G3DSA:3.40.50.10190,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190	SSF52113,SSF52113,SSF52113,SSF52113,SSF52113,SSF52113	347~367								
aly14173.2	Bardet-Biedl syndrome 5 protein homolog	GO:0036064,GO:0042384,GO:0046907,GO:0060170,GO:0032266,GO:0005622,GO:0001103,GO:0015031,GO:0005930,GO:0034464	CG1126-PA			PIRSF010072	SM00683,SM00683		PF07289														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly14175.1	Probable NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 12	GO:0008137,GO:0005739,GO:0006120,GO:0005743,GO:0005747,GO:0070469,GO:0003954,GO:0009055	CG3214-PC						PF05071														
aly14175.2	Unknown		n/a																				
aly14175.3	Putative gamma-glutamylcyclotransferase CG2811	GO:0005575,GO:0008150,GO:0003674,GO:0016746	CG2811-PA						PF06094				G3DSA:3.10.490.10	SSF110857									
aly14196.1	Unknown	GO:0007443,GO:0002009,GO:0007440,GO:0007510,GO:0008258,GO:0042250,GO:0007431,GO:0007391,GO:0007435	CG17716-PB				SM00408,SM00408,SM00408,SM00409,SM00409,SM00409		PF08205	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726									
aly142.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly142.2	Ras-related protein Rab-21	GO:0012506,GO:0055037,GO:0009898,GO:0005789,GO:0045202,GO:0048260,GO:0005925,GO:0098559,GO:0070062,GO:0030100,GO:0006886,GO:0008089,GO:0043005,GO:2000643,GO:0005525,GO:0003924,GO:0030659,GO:0008152,GO:0030516,GO:0032580,GO:0036313,GO:0031982,GO:0050775,GO:0016192,GO:0032482,GO:0005802,GO:0030866,GO:0019003,GO:0005515,GO:0015031,GO:0017157,GO:0005768,GO:0005769	CG17515-PD				SM00176,SM00173,SM00174,SM00175	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly142.3	ATPase family AAA domain-containing protein 3-A	GO:0005737,GO:0016021,GO:0017111,GO:0005743,GO:0042645,GO:0005524	CG6815-PA				SM00382		PF12037,PF00004				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	197~217,136~160,56~76,84~104,107~127								
aly142.4	Lipopolysaccharide-induced tumor necrosis factor-alpha factor homolog	GO:0005737,GO:0005125,GO:0005575,GO:0006355,GO:0003674,GO:0006351,GO:0008150	CG32280-PA				SM00714		PF10601														
aly142.5	Beta-parvin	GO:0016203,GO:0005856,GO:0031532,GO:0030031,GO:0005829,GO:0030032,GO:0007475,GO:0003779,GO:0030027,GO:0071963,GO:0005515,GO:0005886,GO:0007155,GO:0005925,GO:0034329,GO:0030018	CG32528-PA			PIRSF039131	SM00033,SM00033		PF00307,PF00307	PS50021,PS50021			G3DSA:1.10.418.10,G3DSA:1.10.418.10	SSF47576,SSF47576									
aly142.6	Ecotropic viral integration site 5 ortholog	GO:0005737,GO:0030334,GO:0031982,GO:0032313,GO:0043087,GO:0005096,GO:0005097,GO:0017137,GO:0007298,GO:0032880,GO:0005768,GO:0043547	CG11727-PA				SM00164		PF00566	PS50086			G3DSA:1.10.8.270	SSF47923,SSF47923	36~56,698~734,502~541,633~681,436~470,769~789,740~767,387~414								
aly1420.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1420.2	Unknown		n/a																				
aly1420.3	Unknown		n/a																				
aly1420.4	Unknown		n/a																				
aly1420.5	Unknown		n/a																				
aly142140.1	Unknown	GO:0006464	CG4089-PA						PF03133	PS51221			G3DSA:3.30.470.20										
aly1422.1	Insulin-like growth factor-binding protein complex acid labile subunit	GO:0048749,GO:0005615,GO:0005515,GO:0005886,GO:0007155,GO:0002121,GO:0007185	CG5820-PD				SM00365,SM00365,SM00365,SM00365,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058	648~675								
aly1422.2	Probable hydroxyacid-oxoacid transhydrogenase, mitochondrial	GO:0015993,GO:0005739,GO:0055114,GO:0046872,GO:0047988,GO:0016491	CG3425-PA						PF00465				G3DSA:1.20.1090.10,G3DSA:3.40.50.1970	SSF56796									
aly1422.3	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1	GO:0005737,GO:0046872,GO:0060271,GO:0032312,GO:0016020,GO:0005096,GO:0008060,GO:0008270,GO:0007264,GO:0005912	CG30372-PB				SM00248,SM00248,SM00248,SM00233,SM00326,SM00105		PF16746,PF01412,PF12796,PF00169,PF00018	PS50297,PS50115,PS50114,PS50002,PS50088,PS50003	PR00405,PR00405,PR00405,PR00452,PR00452,PR00452		G3DSA:2.30.30.40,G3DSA:2.30.29.30,G3DSA:1.25.40.20,G3DSA:1.20.1270.60	SSF57863,SSF48403,SSF103657,SSF103657,SSF50729,SSF50044	246~273								
aly1422.4	Biogenesis of lysosome-related organelles complex 1 subunit 5	GO:0031083,GO:0031175,GO:0050942,GO:0008089,GO:0003674,GO:0048490,GO:0035646,GO:0032402,GO:0008150,GO:0030133	CG34131-PA						PF14942						125~145								
aly1422.5	Transmembrane protein 199	GO:0016021	CG7071-PA						PF11712														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1422.6	Sequestosome-1	GO:0016239,GO:0005783,GO:0005080,GO:0030154,GO:0016236,GO:0016235,GO:0098779,GO:0008270,GO:0006511,GO:0007005,GO:0005737,GO:0005764,GO:0016605,GO:0030382,GO:0070062,GO:0031410,GO:0005634,GO:0005770,GO:0005776,GO:0019058,GO:0044130,GO:0043122,GO:0042803,GO:0042169,GO:0006914,GO:0006915,GO:0051291,GO:0000407,GO:0000932,GO:0002376,GO:0043130,GO:0001934	CG10360-PA				SM00291		PF16577,PF00569	PS50135		PS01357	G3DSA:3.10.20.240,G3DSA:1.10.8.10	SSF54277,SSF46934,SSF57850									
aly1422.7	Unknown		n/a						PF03725					SSF55666			REACT_21257						
aly14247.1	Unknown	GO:0008270,GO:0005515	n/a				SM00249		PF14529			PS01359	G3DSA:3.60.10.10,G3DSA:3.30.40.10	SSF57903,SSF56219									
aly1426.1	Stabilizer of axonemal microtubules 2		CG7131-PA																				
aly1426.10	Unknown		n/a																				
aly1426.11	Unknown		n/a																				
aly1426.12	Viral cathepsin	GO:0008234	n/a				SM00848		PF08246				G3DSA:3.90.70.10	SSF54001									
aly1426.13	Viral cathepsin	GO:0008234	n/a				SM00848		PF08246				G3DSA:3.90.70.10	SSF54001									
aly1426.14	Unknown		n/a																				
aly1426.15	Regulation of nuclear pre-mRNA domain-containing protein 2	GO:0016591	CG15160-PC				SM00582		PF04818	PS51391			G3DSA:1.25.40.90	SSF48464									
aly1426.16	Unknown		n/a						PF13358														
aly1426.17	Protein lifeguard 3	GO:1902042,GO:0005794,GO:0005123,GO:1902045,GO:0070062,GO:0016021,GO:0048553,GO:2000504,GO:0005575,GO:0005765,GO:0008150,GO:0003674,GO:0090005,GO:0010008	CG33673-PB						PF01027														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1426.18	Unknown		n/a																				
aly1426.2	NSFL1 cofactor p47	GO:0005795,GO:0061025,GO:0007030,GO:0042052,GO:0008599,GO:0043161,GO:0005829,GO:0050790,GO:0008289,GO:0000045,GO:0031468,GO:0043130,GO:0005634	CG11139-PA				SM00553,SM00166		PF14555,PF08059,PF00789	PS51399,PS50033			G3DSA:3.10.20.90,G3DSA:1.10.8.10	SSF102848,SSF54236,SSF46934									
aly1426.3	Unknown		CG11127-PA																				
aly1426.4	Unknown		n/a																				
aly1426.5	A-kinase anchor protein 13	GO:0005089,GO:0051168,GO:0097190,GO:0035025,GO:0004871,GO:0035023,GO:0004691,GO:0005737,GO:0005634,GO:0016020,GO:0043065,GO:0048471,GO:0046872,GO:0051056,GO:0006468,GO:0045859,GO:0048011,GO:0007264,GO:0010611,GO:1900169,GO:0005829,GO:0005575	CG10188-PC				SM00325,SM00233		PF00621	PS50003,PS50010,PS50081			G3DSA:1.20.900.10,G3DSA:2.30.29.30	SSF48065,SSF50729	1015~1056								
aly1426.6	Unknown	GO:0000242,GO:0003674,GO:0051297	CG11175-PA																				
aly1426.7	Unknown	GO:0005515	CG4911-PA				SM00256		PF00646	PS50181			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF81383									
aly1426.8	Anoctamin-8	GO:0005229,GO:1902476,GO:0016021,GO:0005622,GO:0006821,GO:0005886	CG15270-PA						PF04547,PF04547														
aly1426.9	Unknown		CG15270-PA																				
aly142700.1	Unknown		n/a											SSF82895									
aly14271.1	Unknown		n/a																				
aly14286.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly14292.1	Unknown		n/a																				
aly1432.1	Unknown	GO:0005575,GO:0003674,GO:0008150	CG12994-PA																				
aly1432.10	Protein chibby homolog 1	GO:0008013,GO:0035869,GO:0042384,GO:0007367,GO:0055007,GO:0035082,GO:0005634,GO:0045444,GO:0005739,GO:0008104,GO:0090090,GO:0005814,GO:0016607,GO:0007286,GO:0045892,GO:0036064,GO:0030425,GO:0030178,GO:0042802,GO:0005802	CG13415-PC						PF14645						66~100								
aly1432.11	Major facilitator superfamily domain-containing protein 10	GO:0051119,GO:0005215,GO:0016021,GO:0006915,GO:0048477,GO:0055085	CG5760-PA										G3DSA:1.20.1250.20	SSF103473									
aly1432.12	Major facilitator superfamily domain-containing protein 10	GO:0006810,GO:0051119,GO:0015904,GO:0016021,GO:0006915,GO:0008493,GO:0048477,GO:0055085	CG5760-PA						PF07690	PS50850			G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1432.13	28S ribosomal protein S23, mitochondrial	GO:0045111,GO:0044822,GO:0031965,GO:0005739,GO:0032543,GO:0003735,GO:0005761,GO:0005763,GO:0006412	CG31842-PA						PF04803,PF10484						97~124,143~163								
aly1432.14	Splicing factor U2AF 50 kDa subunit	GO:0051168,GO:0000381,GO:0000245,GO:0005515,GO:0071011,GO:0005634,GO:0003998,GO:0000166,GO:0005654,GO:0007052,GO:0003723,GO:0046833,GO:0008187,GO:0005686,GO:0022008,GO:0046982,GO:0008380,GO:0005681,GO:0003729	CG9998-PB				SM00360,SM00360,SM00360	TIGR01642	PF14259,PF00076,PF00076	PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1432.15	Histone deacetylase complex subunit SAP130	GO:0070822,GO:0043966,GO:0000122,GO:0006325,GO:0003713,GO:0010467,GO:0030914,GO:0005654,GO:0007052,GO:0006351,GO:0045814,GO:0040029	CG11006-PC						PF16014														
aly1432.16	BTB/POZ domain-containing protein KCTD5	GO:0005829,GO:0006811,GO:0051260,GO:0017022,GO:0045187,GO:0030431,GO:0032403,GO:0005216,GO:0042803	CG32810-PB						PF02214				G3DSA:3.30.710.10	SSF54695									
aly1432.17	Serine/threonine-protein kinase N	GO:0007165,GO:0090303,GO:0004697,GO:0046777,GO:0051301,GO:0005737,GO:0006355,GO:0007472,GO:0005634,GO:0016020,GO:0004674,GO:0007049,GO:0004672,GO:0005524,GO:0005856,GO:0006468,GO:0030027,GO:0030054,GO:0032154,GO:0007155,GO:0005829,GO:0030496,GO:0007391,GO:0031532,GO:0006351,GO:0005515	CG2049-PG				SM00742,SM00742,SM00742		PF02185,PF02185,PF02185				G3DSA:1.10.287.160,G3DSA:1.10.287.160,G3DSA:1.10.287.160,G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF46585,SSF46585,SSF46585,SSF49562,SSF49562	116~143,207~227,291~311									
aly1432.18	Glucose-induced degradation protein 4 homolog		n/a						PF09783														
aly1432.19	Unknown		n/a						PF15888														
aly1432.2	Lipase 3	GO:0004806,GO:0006629,GO:0016788,GO:0016042	CG6113-PC			PIRSF000862			PF04083				G3DSA:3.40.50.1820	SSF53474									
aly1432.20	Unknown		n/a																				
aly1432.21	Pupal cuticle protein 20	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG8634-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly1432.22	Pupal cuticle protein 20	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG13214-PC						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1432.23	Unknown		CG15449-PA																				
aly1432.24	Unknown		CG15449-PA																				
aly1432.25	Extracellular serine/threonine protein CG31145	GO:0005794,GO:0006468,GO:0005576,GO:0007476,GO:0004672	CG31145-PC						PF06702														
aly1432.26	Zinc finger protein 84	GO:0045931,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178,GO:0008270	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF12874,PF12874,PF12874,PF12874,PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667								
aly1432.27	Charged multivesicular body protein 6	GO:0007034,GO:0000815,GO:0043162,GO:0042059,GO:0003674,GO:0008593,GO:0015031,GO:0031902	CG4071-PA						PF03357						122~142,18~89								
aly1432.28	Luc7-like protein 3	GO:0016607,GO:0005634,GO:0000398,GO:0006376,GO:0003677,GO:0005685,GO:0008380,GO:0003729	CG3198-PA						PF03194						133~156,204~235								
aly1432.29	Unknown	GO:0032797	n/a						PF11095														
aly1432.3	Lipase 3	GO:0004806,GO:0006629,GO:0016788,GO:0016042	CG6113-PC						PF04083				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1432.30	Tigger transposable element-derived protein 6	GO:0005634,GO:0003677	n/a				SM00249		PF03221,PF03184	PS50960,PS51253		PS01359	G3DSA:1.10.10.60,G3DSA:3.30.40.10	SSF46689,SSF46689,SSF57903									
aly1432.4	Lipase 3	GO:0004806,GO:0006629,GO:0016788,GO:0016042	CG6113-PC			PIRSF000862			PF00561				G3DSA:3.40.50.1820	SSF53474									
aly1432.5	Serine hydroxymethyl transferase, cytosolic	GO:0005737,GO:0004372,GO:0006564,GO:0006563,GO:0048149,GO:0006544,GO:0035999,GO:0005739,GO:0030170	CG3011-PA	MF_00051		PIRSF000412			PF00464			PS00096	G3DSA:3.40.640.10,G3DSA:3.90.1150.10	SSF53383	429~456	00460+2.1.2.1,00630+2.1.2.1,00260+2.1.2.1,00680+2.1.2.1,00670+2.1.2.1		PWY-2161,PWY-181,PWY-3841,PWY-3661,PWY-5497,PWY-2201,PWY-1622,PWY-3661-1	UPA00193,UPA00288				
aly1432.6	Ras-related protein Rab-40C	GO:0072659,GO:0031982,GO:0016567,GO:0006886,GO:0005886,GO:0003924,GO:0010008,GO:0032482,GO:0008360,GO:0019003,GO:0015031,GO:0048471,GO:0007264,GO:0016192,GO:0005525	CG1900-PB				SM00174,SM00969,SM00173,SM00175,SM00253	TIGR00231	PF00071,PF07525	PS50225,PS51419	PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF158235,SSF52540			REACT_11044		UPA00143				
aly1432.7	Unknown	GO:0008150,GO:0016021,GO:0003674	CG1079-PA																				
aly1432.8	rRNA methyltransferase 2, mitochondrial	GO:0008650,GO:0005739,GO:0006364,GO:0001510,GO:0008168,GO:0032259	CG11447-PA	MF_01547		PIRSF005461			PF01728				G3DSA:3.40.50.150	SSF53335									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1432.9	DNA topoisomerase 3-alpha	GO:0016605,GO:0000002,GO:0048589,GO:0000724,GO:0005634,GO:0042246,GO:0005739,GO:0005654,GO:0006265,GO:0003917,GO:0003916,GO:0008270,GO:0003677,GO:0005694	CG10123-PA				SM00437,SM00493,SM00436		PF01396,PF06839,PF06839,PF01131,PF01751	PS50880	PR00417,PR00417,PR00417,PR00417,PR00417	PS00396	G3DSA:3.30.65.10,G3DSA:1.10.460.10,G3DSA:1.10.460.10,G3DSA:1.10.290.10,G3DSA:3.40.50.140	SSF56712,SSF56712,SSF56712										
aly14321.1	Furostanol glycoside 26-O-beta-glucosidase	GO:0009507,GO:0005975,GO:0004553	CG9701-PA						PF00232			PS00653	G3DSA:3.20.20.80	SSF51445									
aly14321.2	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA						PF00011	PS01031	PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly14321.3	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA			PIRSF036514			PF00011	PS01031	PR00299,PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly14321.4	Unknown		n/a											SSF49764									
aly14321.5	Unknown		n/a																				
aly14321.6	Unknown		n/a																				
aly1433.1	Neurotrimin	GO:0050767,GO:0043005,GO:0016337,GO:0005911,GO:0048149,GO:0009986,GO:0007606,GO:0005575,GO:0003674,GO:0005515,GO:0005886,GO:0043025,GO:0031225	CG33485-PA				SM00409,SM00409,SM00408,SM00408,SM00406,SM00406		PF13895,PF07686	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly1433.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1433.3	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0016491,GO:0005737,GO:0030728,GO:0070062,GO:0007179,GO:0004022,GO:0016323,GO:0003824,GO:0008152,GO:0045786,GO:0055114,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106,PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735,SSF51735									
aly1433.4	Unknown		n/a																				
aly1433.5	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG3106-PA				SM00703		PF01757														
aly14332.1	Unknown		n/a																				
aly14337.1	Dynactin subunit 1	GO:0016330,GO:0051383,GO:0042052,GO:0042051,GO:0035371,GO:0007349,GO:0045198,GO:0030286,GO:0031616,GO:0007067,GO:0051028,GO:0005876,GO:0034501,GO:0005737,GO:0005818,GO:0005813,GO:0045502,GO:0001709,GO:0007018,GO:0005739,GO:0051225,GO:0048477,GO:0003774,GO:0003777,GO:0051299,GO:0047497,GO:0035011,GO:0007052,GO:0048491,GO:0005869,GO:0001754,GO:0022008,GO:0001751,GO:0000776,GO:0051642,GO:0008090,GO:0005828,GO:0030496,GO:0051256,GO:0006886	CG9206-PA										G3DSA:1.20.5.340	SSF90257	30~50,58~144								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly14337.2	Dynactin subunit 1	GO:0016330,GO:0051383,GO:0042052,GO:0042051,GO:0035371,GO:0007349,GO:0045198,GO:0030286,GO:0031616,GO:0007067,GO:0051028,GO:0005876,GO:0034501,GO:0005737,GO:0005818,GO:0005813,GO:0045502,GO:0001709,GO:0007018,GO:0005739,GO:0051225,GO:0048477,GO:0003774,GO:0003777,GO:0051299,GO:0047497,GO:0035011,GO:0007052,GO:0048491,GO:0005869,GO:0001754,GO:0022008,GO:0001751,GO:0000776,GO:0051642,GO:0008090,GO:0005828,GO:0030496,GO:0051256,GO:0006886	CG9206-PA												1~42,46~110								
aly14353.1	Eukaryotic translation initiation factor 2-alpha kinase 4	GO:0006446,GO:0004686,GO:0022626,GO:0045793,GO:0030968,GO:0071011,GO:0005829,GO:0017148,GO:0006468,GO:0000398,GO:0004674,GO:0010998,GO:0009267,GO:0004672,GO:0006417,GO:0071013,GO:0005524,GO:0004694	CG1609-PC																				
aly14353.2	Unknown		n/a																				
aly143641.1	Unknown	GO:0015149,GO:0016021,GO:0006909,GO:0022857,GO:0055085	CG14606-PA						PF00083				G3DSA:1.20.1250.20	SSF103473									
aly14372.1	Lipase 3	GO:0006629,GO:0016788,GO:0016042	CG18301-PA										G3DSA:3.40.50.1820	SSF53474									
aly1439.1	Unknown		n/a																				
aly1439.10	Apyrase	GO:0016787,GO:0008253,GO:0017110,GO:0017111,GO:0016788,GO:0000166,GO:0009166,GO:0005576,GO:0046872,GO:0005524	CG42249-PC						PF00149		PR01607,PR01607,PR01607	PS00786	G3DSA:3.60.21.10	SSF56300									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1439.11	Unknown		n/a																				
aly1439.2	Alstrom syndrome protein 1	GO:0005737,GO:0016197,GO:0000278,GO:0000086,GO:0005813,GO:0005829,GO:0051492,GO:0000922,GO:0005654,GO:0006996,GO:0005929,GO:0005634	n/a						PF15309														
aly1439.3	Luciferin 4-monooxygenase	GO:0046872,GO:0006637,GO:0045289,GO:0004321,GO:0005777,GO:0004467,GO:0046949,GO:0001676,GO:0008218,GO:0047077,GO:0005524	CG6178-PA						PF00501,PF13193				G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.30.300.30	SSF56801										
aly1439.4	Luciferin 4-monooxygenase	GO:0046872,GO:0006637,GO:0045289,GO:0004321,GO:0005777,GO:0004467,GO:0046949,GO:0001676,GO:0008218,GO:0047077,GO:0005524	CG6178-PA						PF13193,PF00501				G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.30.300.30,G3DSA:3.40.50.980	SSF56801										
aly1439.5	Luciferin 4-monooxygenase	GO:0046872,GO:0006637,GO:0045289,GO:0004321,GO:0005777,GO:0004467,GO:0046949,GO:0001676,GO:0008218,GO:0047077,GO:0005524	CG6178-PA						PF00501,PF00501,PF13193,PF13193			PS00455	G3DSA:3.40.50.980,G3DSA:3.40.50.980,G3DSA:3.30.300.30,G3DSA:3.30.300.30,G3DSA:2.30.38.10,G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.40.50.980	SSF56801,SSF56801										
aly1439.6	Fatty acid-binding protein, muscle	GO:0005737,GO:0007616,GO:0005215,GO:0006810,GO:0008289,GO:0005504,GO:0005875	CG6783-PC						PF00061		PR00178,PR00178	PS00214	G3DSA:2.40.128.20	SSF50814										
aly1439.7	Fatty acid-binding protein 2	GO:0005737,GO:0005215,GO:0008289	n/a										G3DSA:2.40.128.20	SSF50814										
aly1439.8	Unknown	GO:0005515	n/a						PF12657				G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1439.9	Probable ATP-dependent RNA helicase kurz	GO:0005737,GO:0008026,GO:0005730,GO:0005634,GO:0004004,GO:0004386,GO:0006396,GO:0003676,GO:0022008,GO:0044822,GO:0005524	CG3228-PA				SM00847,SM00490,SM00487		PF07717,PF04408,PF00271	PS51194,PS51192		PS00690	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	500~524								
aly143987.1	Unknown		n/a																				
aly144.1	Histone H4	GO:0005634,GO:0000786,GO:0006333,GO:0003677,GO:0046982,GO:0006334	CG33909-PA				SM00417		PF15511		PR00623,PR00623,PR00623,PR00623,PR00623,PR00623	PS00047	G3DSA:1.10.20.10	SSF47113									
aly144.10	Selenide, water dikinase	GO:0008284,GO:2000378,GO:0016301,GO:0016260,GO:0007444,GO:0007049,GO:0008283,GO:0006541,GO:0005524,GO:0022008,GO:0004756,GO:0007005	CG8553-PB			PIRSF036407		TIGR00476	PF00586,PF02769				G3DSA:3.90.650.10,G3DSA:3.30.1330.10	SSF56042,SSF55326		00450+2.7.9.3		PWY-6281					
aly144.11	DET1- and DDB1-associated protein 1		CG31855-PA						PF10172														
aly144.12	Unknown	GO:0005488	n/a											SSF48371,SSF48371,SSF48371									
aly144.13	Unknown		n/a												1237~1243								
aly144.14	Activating signal cointegrator 1	GO:0005737,GO:0044389,GO:0030520,GO:0030331,GO:0005634,GO:0003713,GO:0035035,GO:0005815,GO:0005654,GO:0006355,GO:1901998,GO:0008270,GO:0002020,GO:0006366,GO:0016922,GO:0005829,GO:0045893	CG11710-PB				SM01022		PF06221,PF04266				G3DSA:2.30.130.30,G3DSA:2.30.130.30	SSF88697,SSF88697									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly144.15	NADH dehydrogenase [ubiqui] iron-sulfur protein 5	GO:0032981,GO:0006120,GO:0005743,GO:0005747,GO:0005758,GO:0070469,GO:0003954,GO:0055114	CG11455-PA						PF10200				G3DSA:1.10.810.10	SSF47072									
aly144.16	Fibroblast growth factor receptor	GO:0008284,GO:0006468,GO:0045792,GO:0016021,GO:0005007,GO:0016339,GO:0016020,GO:0045177,GO:0042060,GO:0004714,GO:0090303,GO:0004713,GO:0005887,GO:0004672,GO:0007156,GO:0007030,GO:0005524,GO:0005509	CG10244-PA				SM00219		PF07714	PS50011	PR00109,PR00109	PS00109,PS00107	G3DSA:1.10.510.10,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF56112,SSF49265									
aly144.17	DnaJ homolog subfamily C member 13	GO:0007032,GO:0016020,GO:0006897,GO:0070062,GO:0001649,GO:1902954,GO:0006898,GO:0005875,GO:0005765,GO:0005488,GO:0015031,GO:0007298,GO:2000641,GO:0031201,GO:0031901,GO:0010008	CG8014-PA				SM00271		PF14237,PF00226	PS50076			G3DSA:1.10.287.110,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF46565,SSF48371,SSF48371									
aly144.18	Serine--tRNA ligase, cytoplasmic	GO:0005737,GO:0006434,GO:0097056,GO:0004828,GO:0005524	CG17259-PA					TIGR00414	PF02403,PF00587	PS50862	PR00981,PR00981,PR00981,PR00981,PR00981,PR00981		G3DSA:3.30.930.10,G3DSA:1.10.287.40	SSF55681,SSF46589		00970+6.1.1.11	REACT_71	PWY-6281	UPA00906				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly144.19	Tumor susceptibility gene 101 protein	GO:0003714,GO:0045926,GO:0048306,GO:0060439,GO:0019082,GO:0008333,GO:1903772,GO:0061024,GO:0043405,GO:1902188,GO:0003677,GO:0046755,GO:0019068,GO:0043162,GO:0051301,GO:0010008,GO:0005737,GO:0070062,GO:0007430,GO:0005730,GO:0005771,GO:0005770,GO:0075733,GO:0019058,GO:0044130,GO:0031902,GO:0042803,GO:0008285,GO:1903774,GO:0016032,GO:0036258,GO:0046425,GO:0032509,GO:0030216,GO:0006464,GO:0030374,GO:0007050,GO:0045571,GO:0001558,GO:0045892,GO:0005886,GO:1903543,GO:0016197,GO:0031625,GO:0035090,GO:2000397,GO:1903551,GO:0000813,GO:0046790,GO:0006513,GO:0043130,GO:0005515,GO:0015031,GO:0048524,GO:0005768,GO:0005769	CG9712-PA						PF05743,PF09454	PS51322,PS51312			G3DSA:3.10.110.10	SSF140111,SSF54495	250~319								
aly144.2	Limbic system associated membrane protein	GO:0050767,GO:0016337,GO:0043005,GO:0007399,GO:0009986,GO:0007606,GO:0008039,GO:0005575,GO:0035641,GO:0003674,GO:0005911,GO:0005886,GO:0043025,GO:0031225	CG34385-PC				SM00408,SM00408,SM00409,SM00409		PF07686,PF13927	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly144.20	60S ribosomal protein L12	GO:0044267,GO:0000184,GO:0006415,GO:0005840,GO:0022625,GO:0005829,GO:0016020,GO:0044822,GO:0006614,GO:0003735,GO:0010467,GO:0019058,GO:0019083,GO:0006414,GO:0016032,GO:0000022,GO:0005925,GO:0006413,GO:0006412,GO:0070062	CG3195-PA	MF_00736			SM00649		PF00298,PF03946			PS00359	G3DSA:1.10.10.250,G3DSA:3.30.1550.10	SSF54747,SSF46906									

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly144.21	MAU2 chromatid cohesion factor homolog	GO:0032116,GO:0034088,GO:0005634,GO:0005654,GO:0000785,GO:0005515,GO:0007411,GO:0051301	CG4203-PA						PF10345				G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452									
aly144.22	Unknown		n/a																				
aly144.23	WD repeat-containing protein 91	GO:0042060	CG6005-PA																				
aly144.24	GTP-binding protein Rit2	GO:0007165,GO:0008152,GO:0005634,GO:0007268,GO:0003924,GO:0048011,GO:0006970,GO:0005516,GO:0042594,GO:0005886,GO:0015031,GO:0009408,GO:0006184,GO:0007264,GO:0006979,GO:0005525	CG8418-PA				SM00175,SM00174,SM00173	TIGR00231	PF00071	PS51421	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540	168~188		REACT_11044						
aly144.25	Atrial natriuretic peptide receptor 1	GO:0017046,GO:0019901,GO:0006468,GO:0050880,GO:0048662,GO:0016941,GO:0030828,GO:0043235,GO:0016021,GO:0005886,GO:0005622,GO:0042417,GO:0004872,GO:0007166,GO:0004672,GO:0007168,GO:0035556,GO:0005525,GO:0004383,GO:0005524,GO:0006182	CG3216-PC						PF07714,PF01094	PS50011	PR00255,PR00255,PR00255		G3DSA:1.10.510.10,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.30.200.20,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300	SSF53822,SSF56112									
aly144.26	Atrial natriuretic peptide receptor 1	GO:0017046,GO:0043235,GO:0006468,GO:0005622,GO:0048662,GO:0016941,GO:0030828,GO:0004383,GO:0005886,GO:0042562,GO:0042417,GO:0050880,GO:0004872,GO:0004672,GO:0007168,GO:0035556,GO:0005525,GO:0016021,GO:0005524,GO:0006182	CG3216-PC				SM00044		PF07701,PF00211	PS50125		PS00452	G3DSA:3.30.70.1230	SSF55073	18~49	00230+4.6.1.2							

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly144.27	Unknown	GO:0009593,GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0004970	CG15324-PA										G3DSA:1.10.287.70	SSF53850,SSF53850									
aly144.28	Unknown		n/a											SSF57184									
aly144.29	Unknown	GO:0036038,GO:0010826,GO:0042384	n/a						PF09773,PF09773														
aly144.3	ATP-binding cassette sub-family B member 8, mitochondrial	GO:0042626,GO:0005215,GO:0016021,GO:0006810,GO:0005743,GO:0055085,GO:0005524	CG1824-PA				SM00382		PF00664,PF00005	PS50929,PS50893		PS00211	G3DSA:3.40.50.300,G3DSA:1.20.1560.10	SSF90123,SSF52540	293~313								
aly144.30	Unknown		n/a																				
aly144.31	Transitional endoplasmic reticulum ATPase TER94	GO:0008104,GO:0008103,GO:0005783,GO:0005886,GO:0007279,GO:0043523,GO:0000226,GO:0043525,GO:0016887,GO:0032436,GO:0005875,GO:0046598,GO:0042052,GO:0005737,GO:0043186,GO:0007029,GO:0005634,GO:0005811,GO:0006200,GO:0006508,GO:0048477,GO:0005524,GO:0016787,GO:0098586,GO:0031965,GO:0006810,GO:0016320,GO:0017111,GO:0007317,GO:0030433,GO:0000502,GO:0045451,GO:0007030,GO:0045169,GO:0048813,GO:0006511,GO:0005515	CG2331-PC				SM01073,SM01072,SM00382,SM00382	TIGR01243	PF00004,PF00004,PF02359,PF02933,PF09336			PS00674,PS00674	G3DSA:3.40.50.300,G3DSA:1.10.8.60,G3DSA:3.10.330.10,G3DSA:2.40.40.20,G3DSA:3.40.50.300	SSF54585,SSF52540,SSF50692,SSF52540									
aly144.32	Unknown		n/a												177~197,278~298								
aly144.33	Unknown	GO:0006355,GO:0022008,GO:0035363,GO:0046716,GO:0003677	CG33456-PA							PS50090,PS51477,PS51477			G3DSA:1.10.10.60,G3DSA:1.20.1160.11	SSF46689,SSF47762									

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly144.34	Ninjurin-2	GO:0007155,GO:0016021,GO:0042246	CG14394-PD						PF04923														
aly144.35	Dihydropteridine reductase	GO:0010288,GO:0006729,GO:0043005,GO:0070062,GO:0006559,GO:0005829,GO:0033762,GO:0005739,GO:0070404,GO:0035690,GO:0001889,GO:0008152,GO:0070402,GO:0010044,GO:0004155,GO:0042803	CG4665-PC						PF00106				G3DSA:3.40.50.720	SSF51735									
aly144.36	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly144.37	Malate dehydrogenase	GO:0005737,GO:0006099,GO:0030060,GO:0008152,GO:0055114,GO:0016491	CG10512-PA						PF02615				G3DSA:1.10.1530.10,G3DSA:3.30.1370.60	SSF89733									
aly144.38	Malate dehydrogenase	GO:0005737,GO:0006099,GO:0030060,GO:0055114,GO:0016491	CG10512-PA						PF02615				G3DSA:3.30.1370.60,G3DSA:1.10.1530.10	SSF89733									
aly144.39	Unknown		n/a										G3DSA:3.90.10.10										
aly144.4	Fork head domain-containing protein FD3	GO:0030154,GO:0009790,GO:0048484,GO:0048485,GO:0009653,GO:0007275,GO:0043565,GO:0000122,GO:0048846,GO:0005634,GO:0003690,GO:0000981,GO:0006351,GO:0007389,GO:0008134,GO:0009888,GO:0008301,GO:0051090,GO:0007422,GO:0003700,GO:0003705,GO:0006355,GO:0006357,GO:0045944,GO:0048937,GO:0005667	CG3668-PA				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00658,PS00657	G3DSA:1.10.10.10	SSF46785									
aly144.40	Probable beta-hexosaminidase fdl	GO:0005794,GO:0005770,GO:0016063,GO:0007420,GO:0006491,GO:0032428,GO:0016231,GO:0004563,GO:0006517,GO:0005886,GO:0006032,GO:0005783	CG8824-PB			PIRSF001093			PF14845,PF00728		PR00738,PR00738,PR00738,PR00738,PR00738,PR00738		G3DSA:3.30.379.10,G3DSA:3.20.20.80	SSF51445,SSF55545	135~155	00604+3.2.1.52,00520+3.2.1.52,00511+3.2.1.52,00603+3.2.1.52,00513+3.2.1.52,00531+3.2.1.52		PWY-6902					

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly144.41	Unknown	GO:0016319,GO:0055059,GO:0005819,GO:0000132,GO:0034454,GO:0005813,GO:0045179,GO:0045180,GO:0005938,GO:0005515,GO:0003677,GO:0007058,GO:0051233,GO:0005875,GO:0040040	CG12047-PH												421~455,990~1024,1836~1916,2066~2086,1191~1232,2368~2388,548~575,905~939,958~985,601~635,2091~2118,368~388,481~522,1722~1817,1602~1657,721~762,243~284,1078~1112,195~229,2394~2432,841~868,661~695,1662~1703,1032~1052,1542~1583,1								
aly144.42	Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]	GO:0016787,GO:0008803,GO:0006139,GO:0006915,GO:0005739,GO:0005575,GO:0004081,GO:0008150,GO:0005525	CG31713-PA						PF00293	PS51462	PR01405,PR01405,PR01405,PR01405,PR01405	PS00893	G3DSA:3.90.79.10	SSF55811		00240+3.6.1.17,00230+3.6.1.17							
aly144.43	GON-4-like protein	GO:0005634,GO:0035363,GO:0046716,GO:0006355,GO:0003677,GO:0022008,GO:0003682	CG34415-PC																				
aly144.44	Phosphorylated adapter RNA export protein	GO:0005737,GO:0005654,GO:0043231,GO:0007399,GO:0005730,GO:0005634,GO:0006408,GO:0003723,GO:0015031,GO:0015030,GO:0043025,GO:0015643	CG8069-PA						PF10258						285~305								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly144.45	Probable beta-hexosaminidase fdl	GO:0005794,GO:0016231,GO:0016063,GO:0007420,GO:0006491,GO:0032428,GO:0005770,GO:0004563,GO:0006517,GO:0005886,GO:0006032,GO:0005783	CG8824-PB			PIRSF001093			PF14845,PF00728		PR00738,PR00738,PR00738,PR00738,PR00738,PR00738,PR00738,PR00738		G3DSA:3.30.379.10,G3DSA:3.20.20.80	SSF55545,SSF51445		00604+3.2.1.52,00520+3.2.1.52,00511+3.2.1.52,00603+3.2.1.52,00513+3.2.1.52,00531+3.2.1.52		PWY-6902					
aly144.46	E3 SUMO-protein ligase PIAS3	GO:0008022,GO:0030425,GO:0030261,GO:0042176,GO:0010628,GO:0008270,GO:0003676,GO:0003677,GO:0050829,GO:0046426,GO:0005737,GO:0005634,GO:0019789,GO:0005654,GO:0005652,GO:0045838,GO:0017151,GO:0033235,GO:0048749,GO:0045089,GO:0046425,GO:0015459,GO:0035012,GO:0019899,GO:0030097,GO:0022008,GO:0016925,GO:0016874,GO:0007446,GO:0051276,GO:0009725,GO:0005700,GO:0006355,GO:0006351,GO:0007095,GO:0045202	CG8068-PI						PF14324,PF02891	PS51466,PS51044									UPA00886				
aly144.47	Zinc finger protein 609	GO:0042461,GO:0048190,GO:0000122,GO:0003700,GO:0005634,GO:0003714,GO:0007476,GO:0045879,GO:0007411,GO:0045570,GO:0007412,GO:0046872,GO:0008345	CG5580-PJ							PS50157		PS00028											
aly144.48	Ankyrin repeat and LEM domain-containing protein 1		CG8679-PA				SM00540		PF03020	PS50954			G3DSA:1.10.720.40	SSF63451									
aly144.49	Unknown		n/a										G3DSA:1.25.40.20	SSF48403									
aly144.5	Putative phosphatidate phosphatase	GO:0007424,GO:0045177,GO:0016020,GO:0016791,GO:0009880,GO:0016311,GO:0035234,GO:0016021,GO:0019991,GO:0035233,GO:0007280,GO:0045824,GO:0005886,GO:0050829,GO:0042803,GO:0008195,GO:0008354,GO:0005918	CG8804-PB				SM00014		PF01569				G3DSA:1.20.144.10	SSF48317									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly144.50	Probable methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	GO:0006567,GO:0004485,GO:0006574,GO:0004658,GO:0006552,GO:0016421,GO:0006551,GO:0009062,GO:0006550,GO:0005759,GO:0009087,GO:0007563,GO:0005524	CG3267-PA						PF01039	PS50980,PS50989			G3DSA:3.90.226.10,G3DSA:3.90.226.10	SSF52096,SSF52096	35~55	00253+6.4.1.2,00620+6.4.1.2,00640+6.4.1.2,00061+6.4.1.2,00254+6.4.1.2,00720+6.4.1.2		PWY-7388,PWY-5789,PWY-5743,PWY-5744,PWY-6722,PWY-6679,PWY-4381	UPA00655				
aly144.6	Putative phosphatidate phosphatase	GO:0007424,GO:0045177,GO:0016020,GO:0016791,GO:0009880,GO:0016311,GO:0035234,GO:0019991,GO:0035233,GO:0007280,GO:0045824,GO:0005886,GO:0050829,GO:0042803,GO:0008195,GO:0008354,GO:0005918	CG8804-PB				SM00014		PF01569				G3DSA:1.20.144.10	SSF48317									
aly144.7	Putative phosphatidate phosphatase	GO:0007424,GO:0045177,GO:0016020,GO:0016791,GO:0009880,GO:0016311,GO:0035234,GO:0016021,GO:0019991,GO:0035233,GO:0007280,GO:0045824,GO:0005886,GO:0050829,GO:0042803,GO:0008195,GO:0008354,GO:0005918	CG8804-PB				SM00014		PF01569				G3DSA:1.20.144.10	SSF48317									
aly144.8	Kyphoscoliosis peptidase	GO:0005856,GO:0007517,GO:0007528,GO:0008270,GO:0008233,GO:0030018	CG30147-PB				SM00460,SM00132		PF00412	PS50023		PS00478	G3DSA:2.10.110.10	SSF54001	209~236								
aly144.9	Dystrophin, isoform B	GO:0005200,GO:0008586,GO:0046716,GO:0045202,GO:0030010,GO:0007274,GO:0005856,GO:0007517,GO:0007474,GO:0005198,GO:0003779,GO:0005509,GO:0005737,GO:0042383,GO:0050699,GO:0008307,GO:0046928,GO:0048172,GO:0005938,GO:0008092,GO:0016010,GO:0008270	CG31175-PH						PF09068				G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF57850,SSF47473	392~422								

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1441.1	von Willebrand factor D and EGF domain-containing protein	GO:0006909,GO:0005044,GO:0016021,GO:0006910,GO:0046331,GO:0042742,GO:0005515,GO:0009986,GO:0042834,GO:0005576	CG6124-PC				SM00181,SM00181,SM00181,SM00181,SM00181,SM00181		PF02363,PF02363,PF02363,PF02363,PF02363,PF02363,PF02363,PF02363														
aly14415.1	Unknown		n/a												132~152								
aly14415.2	Unknown		n/a																				
aly14419.1	Unknown		n/a				SM00249,SM00249						G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57903,SSF57903	350~398,142~169								
aly14419.2	Unknown		n/a						PF14529				G3DSA:3.60.10.10	SSF56219									
aly1442.1	Esterase FE4	GO:0052689	CG1121-PA						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly1442.2	Neuropeptide FF receptor 2	GO:0004930,GO:0042277,GO:0005887,GO:2000479,GO:0045761,GO:0016021,GO:0007268,GO:0007218,GO:0004983,GO:0032870,GO:0001653,GO:1901652,GO:0007166,GO:0008188,GO:0043408,GO:0007186,GO:0015629	CG5811-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1442.3	Pyroglutamylated RFamide peptide receptor	GO:0004930,GO:0042277,GO:0005887,GO:0016021,GO:0005886,GO:0004983,GO:0032870,GO:0001653,GO:1901652,GO:0007166,GO:0008188,GO:0007186	CG5811-PB						PF00001	PS50262	PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1443.1	Calexcitin-1	GO:0016529,GO:0003924,GO:0005509	CG14904-PA						PF13202	PS50222,PS50222,PS50222		PS00018,PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1443.2	CDK5 regulatory subunit-associated protein 3	GO:0005737,GO:1900182,GO:0044389,GO:1903363,GO:0000079,GO:0032088,GO:0005575,GO:0003674,GO:0031398,GO:1901798,GO:0005634	CG30291-PA						PF05600														
aly1443.3	Neutral phospholipase A2 3	GO:0006644,GO:0047498,GO:0016042,GO:0005576,GO:0005509,GO:0004623	CG14507-PC				SM00085		PF00068		PR00389,PR00389,PR00389,PR00389	PS00118,PS00119	G3DSA:1.20.90.10	SSF48619		00564+3.1.1.4,00590+3.1.1.4,00592+3.1.1.4,00		PWY-7409,PWY-7417,PWY-6803,PWY-7416					
aly1443.4	Unknown		n/a																				
aly1443.5	Unknown		n/a																				
aly1443.6	Unknown		n/a																				
aly1443.7	Unknown	GO:0007218,GO:0005184,GO:0005615	CG14358-PB																				
aly1443.8	Unknown		n/a						PF13843														
aly1444.1	Tachykinin-like peptides receptor 99D	GO:0007218,GO:0042048,GO:0016021,GO:0008188,GO:0007217,GO:0050805,GO:0050911,GO:0005887,GO:0005886,GO:0004995,GO:0007186	CG7887-PC						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00244,PR00244,PR00244,PR00244	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1444.2	Unknown		n/a																				
aly1445.1	Beta-1-syntrophin	GO:0005737,GO:0005856,GO:0042383,GO:0008092,GO:0008582,GO:0016013,GO:0008307,GO:0045202,GO:0005515,GO:0043234,GO:0005925	CG7152-PB				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156,SSF50729									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1445.2	Zinc finger protein 133	GO:0003700,GO:0005634,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667									
aly1445.3	Tyrosine-protein kinase transmembrane receptor Ror	GO:0006468,GO:0016021,GO:0016020,GO:0018108,GO:0004714,GO:0005030,GO:0007165,GO:0005886,GO:0007169,GO:0007417,GO:0005524,GO:0004713	CG4926-PA				SM00130,SM00409		PF00051,PF07714,PF07679	PS50070,PS50038,PS50835		PS00021	G3DSA:2.40.20.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:1.10.510.10,G3DSA:2.60.40.10	SSF57440,SSF56112,SSF48726									
aly1445.4	Glycoprotein hormone beta-5	GO:0005179,GO:0009755,GO:0002155,GO:0005615,GO:0005576,GO:0001664,GO:0046982	CG40041-PC						PF00007				G3DSA:2.10.90.10	SSF57501									
aly1445.5	Irregular chiasm C-roughest protein	GO:0048749,GO:0016202,GO:0016201,GO:0046667,GO:0046331,GO:0016021,GO:0005886,GO:0045177,GO:0007156,GO:0030165,GO:0005576,GO:0003674,GO:0008045,GO:0007520,GO:0005913,GO:0007157,GO:0001745,GO:0046666,GO:0042802	CG15138-PA						PF08205,PF13927	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly1445.6	ATP-binding cassette sub-family G member 4	GO:0043190,GO:0042626,GO:0005215,GO:0016021,GO:0017127,GO:0033344,GO:0016887,GO:0005886,GO:0046982,GO:0055085,GO:0005524,GO:0042803	CG31689-PH						PF00005,PF01061	PS50893		PS00211	G3DSA:3.40.50.300	SSF52540									
aly144546.1	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	GO:0004174,GO:0046872,GO:0051539,GO:0006635,GO:0051536,GO:0005811,GO:0005739,GO:0031966,GO:0005743,GO:0006979,GO:0009055,GO:0005875,GO:0006119	CG12140-PB						PF05187					SSF54862									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1448.1	Dynactin subunit 1	GO:0016330,GO:0051383,GO:0042052,GO:0042051,GO:0035371,GO:0007349,GO:0045198,GO:0030286,GO:0031616,GO:0007067,GO:0051028,GO:0005876,GO:0034501,GO:0005737,GO:0005818,GO:0005813,GO:0045502,GO:0001709,GO:0007018,GO:0005739,GO:0051225,GO:0048477,GO:0003774,GO:0003777,GO:0051299,GO:0047497,GO:0035011,GO:0007052,GO:0048491,GO:0005869,GO:0001754,GO:0022008,GO:0001751,GO:0000776,GO:0051642,GO:0008090,GO:0005828,GO:0030496,GO:0051256,GO:0006886	CG9206-PA						PF12455						398~432,183~288									
aly1448.2	Unknown		n/a																				
aly1449.1	ERC protein 2	GO:0005737,GO:0005856,GO:0048786,GO:0048789,GO:0048788,GO:0042734,GO:0005262,GO:0007614,GO:0007615,GO:0030426,GO:0048790,GO:0031594,GO:0048167,GO:0007269,GO:0007268,GO:0007274,GO:0008344,GO:0030054	CG42344-PJ						PF10174						130~157,180~200									
aly1449.2	Probable 28S ribosomal protein S16, mitochondrial	GO:0005840,GO:0005622,GO:0003735,GO:0005763,GO:0006412,GO:0032543	CG8338-PA					TIGR00002	PF00886				G3DSA:3.30.1320.10	SSF54565									
aly1449.3	Receptor expression-enhancing protein 5	GO:0016021,GO:0070062	CG8331-PA						PF03134						162~189								
aly1449.4	Multiple C2 and transmembrane domain-containing protein 1	GO:0016021,GO:0005622,GO:0008150,GO:0005509,GO:0019722	CG33146-PA				SM00239,SM00239		PF08372,PF00168,PF00168	PS50004,PS50004			G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562,SSF49562	463~483								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1449.5	Unknown		n/a												1~39								
aly145.1	Heterogeneous nuclear ribonucleoprotein L	GO:0005737,GO:0045120,GO:0070062,GO:0044212,GO:0005634,GO:0016020,GO:0044822,GO:0000398,GO:0030529,GO:0005654,GO:0010467,GO:0003723,GO:0003676,GO:0007411,GO:0008340,GO:0008343,GO:0000166,GO:0008380,GO:0006396,GO:0003729	CG9218-PT				SM00360		PF13893,PF13893	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928										
aly145.10	Zinc finger protein 778	GO:0005737,GO:0005819,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0005876,GO:0006351	CG8474-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF13912,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly145.11	Unknown		n/a												459~479								
aly145.12	Dynamin-like 120 kDa protein, mitochondrial	GO:0070584,GO:0010636,GO:0035073,GO:0016021,GO:0006915,GO:0003924,GO:0005739,GO:0005743,GO:0008053,GO:0005758,GO:0043009,GO:0001745,GO:0007005,GO:0005525	CG8479-PA				SM00053		PF00350	PS51718	PR00195,PR00195,PR00195		G3DSA:3.40.50.300	SSF52540	667~687,928~953,2000~252									
aly145.13	EH domain-binding protein 1	GO:0005737,GO:0031941,GO:0003779,GO:0045747,GO:0005938,GO:0005515,GO:0005886,GO:0045035,GO:0005509	CG15609-PF						PF10358,PF00307	PS50021			G3DSA:1.10.418.10	SSF47576										
aly145.14	EH domain-binding protein 1	GO:0005737,GO:0031941,GO:0003779,GO:0045747,GO:0005938,GO:0005886,GO:0045035,GO:0005509	CG15609-PF						PF12130						517~537,231~272									
aly145.15	Protein stum	GO:0042330,GO:0071683,GO:0050954,GO:0016021,GO:0030425,GO:0019230	CG30263-PC						PF15795						688~708,111~145									
aly145.16	Unknown		n/a																					

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly145.17	Thyroid receptor-interacting protein 11	GO:0005795,GO:0000137,GO:0007030,GO:0016192,GO:0005794,GO:0000042,GO:0003281,GO:0005634,GO:0005856,GO:0003713,GO:0017137,GO:0002081,GO:0000139,GO:0002079,GO:0005801,GO:1903506,GO:0006996,GO:0006366	CG33206-PA							PS50913				SSF90257	496~530,1254~1292,786~855,427~468,44~71,133~206,1296~1330,1194~1235,325~345,100~127,953~1008,553~66										
aly145.18	Zinc finger protein 26	GO:0051726,GO:0003700,GO:0005634,GO:0006355,GO:0003676,GO:0003677,GO:0046872	CG11247-PB				SM00868,SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776,PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly145.19	Adult-specific cuticular protein ACP-20	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG6305-PA						PF00379	PS51155		PS00233											
aly145.2	Zinc finger protein 560	GO:0031935,GO:0003700,GO:0005634,GO:0006355,GO:0048813,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG11352-PF				SM00355,SM00355,SM00355			PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60	SSF57667									
aly145.20	Unknown	GO:0008670,GO:0016614,GO:0006635,GO:0008152,GO:0016491	CG3699-PA						PF00106				G3DSA:3.40.50.720	SSF51735									
aly145.21	Uncharacterized oxidoreductase YciK	GO:0008152,GO:0016491	CG31548-PA						PF00106				G3DSA:3.40.50.720	SSF51735	67~71								
aly145.22	3-oxoacyl-[acyl-carrier-protein] reductase FabG	GO:0050661,GO:0051287,GO:0030497,GO:0004316,GO:0008152,GO:0016491	CG31548-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,P		G3DSA:3.40.50.720	SSF51735									
aly145.23	Unknown		n/a																				
aly145.3	Zinc finger protein 100	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG1832-PB				SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF13912,PF13912	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly145.4	Protein-glutamate O-methyltransferase	GO:0006479,GO:0008757,GO:0005575,GO:0008150,GO:0051998,GO:2001020,GO:0003674,GO:0032259	CG11474-PA						PF01937					SSF111321,SSF111321,SSF111321									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly145.5	Nanos homolog 2	GO:0042078,GO:0008270,GO:0035282,GO:0007275,GO:0008354,GO:0005737,GO:0005634,GO:0001709,GO:0043066,GO:0045835,GO:0006402,GO:0048477,GO:1900153,GO:0016321,GO:0007281,GO:0008595,GO:0007283,GO:0007314,GO:0045892,GO:0048471,GO:0048134,GO:0030718,GO:0007280,GO:0000932,GO:0048813,GO:0003723,GO:0005515,GO:0017148,GO:0006378,GO:0003729,GO:0045495	CG5637-PA						PF05741	PS51522													
aly145.6	Ommochrome-binding protein		n/a										G3DSA:2.120.10.30	SSF50969									
aly145.7	Ommochrome-binding protein		n/a										G3DSA:2.120.10.30	SSF101898									
aly145.8	Rho guanine nucleotide exchange factor 11	GO:0005089,GO:0016331,GO:0016020,GO:0035277,GO:0030589,GO:0007349,GO:0035025,GO:0001505,GO:0035556,GO:0007277,GO:0005737,GO:0045177,GO:0019992,GO:0007369,GO:0045179,GO:0045178,GO:0016324,GO:0016476,GO:0038032,GO:0016328,GO:0007370,GO:0030478,GO:0005096,GO:0008360,GO:0090254,GO:0005826,GO:0007015,GO:0007375,GO:0050770,GO:0007377,GO:0031532,GO:0070252,GO:0007374	CG9635-PA				SM00325,SM00228,SM00109		PF00595,PF16652,PF09128,PF00621	PS50081,PS50010,PS50106			G3DSA:1.20.900.10,G3DSA:2.30.42.10,G3DSA:3.30.60.20,G3DSA:2.30.29.30	SSF57889,SSF50156,SSF48097,SSF48065,SSF50729			REACT_14797,REACT_11061						
aly145.9	Zinc finger protein 791	GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG6654-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF13912,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly1450.1	Adenine phosphoribosyltransferase	GO:0005737,GO:0044209,GO:0003999,GO:0006166,GO:0006168,GO:0009116	CG18315-PA						PF00156				G3DSA:3.40.50.2020	SSF53271									
aly1450.10	F-box/LRR-repeat protein 14	GO:0005737,GO:0005794,GO:0000152,GO:0005654,GO:0006511,GO:0042787,GO:0019005,GO:0004842	CG9952-PB				SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00256,SM00368,SM00368,SM		PF00646	PS50181			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047,SSF81383									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1450.11	Unknown		n/a																				
aly1450.12	Unknown	GO:0005549,GO:0016020,GO:0007608,GO:0004984	n/a						PF02949						94~114								
aly1450.13	YY1-associated factor 2	GO:0005737,GO:0006351,GO:0016604,GO:0005634,GO:0003714,GO:0003713,GO:0005654,GO:0045892,GO:0008270,GO:0003677,GO:0010623,GO:0045893	CG12190-PA				SM00547		PF00641	PS50199		PS01358		SSF90209									
aly1450.14	ERC protein 2	GO:0005737,GO:0005856,GO:0048786,GO:0048789,GO:0048788,GO:0042734,GO:0005262,GO:0007614,GO:0007615,GO:0030426,GO:0048790,GO:0031594,GO:0048167,GO:0045202,GO:0007269,GO:0007268,GO:0007274,GO:0008344,GO:0030054	CG42344-PJ						PF10174,PF10174					SSF57997	1191~1267,21~80,1099~1168,935~1049,635~655,572~599,667~872,242~336,1331~1365,876~927,1810~1830,1506~1540,109~143,1701~1721,1548~1589,1604~1631,151~178,537~557,193~234,383~529,344~371,1269~1317,607~627,1370~1495,1057~1084,1838~1865,1902~1929								
aly1450.15	Unknown		n/a																				
aly1450.2	Unknown		n/a						PF15868														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1450.3	Unknown		n/a												151~171,177~211,25~52,374~394,240~267								
aly1450.4	Probable ribonuclease ZC3H12D	GO:0005737,GO:0042130,GO:2000134,GO:0030308,GO:0004519,GO:0005634,GO:0009932,GO:0006402,GO:0046872	CG42360-PA						PF11977														
aly1450.5	Protein Wnt-5b	GO:0048675,GO:0005788,GO:0009798,GO:0045444,GO:0007275,GO:0071300,GO:0007517,GO:0070062,GO:0000122,GO:0045600,GO:0002062,GO:0090090,GO:0030335,GO:0005796,GO:0030182,GO:0009986,GO:0070307,GO:0060070,GO:0005886,GO:0005615,GO:0007424,GO:0045165,GO:0009952,GO:0016055,GO:0005109,GO:0005576,GO:0005102,GO:0005578	CG1916-PA				SM00097		PF00110		PR01349,PR01349,PR01349,PR01349,PR01349	PS00246					REACT_14797							
aly1450.6	Probable salivary secreted peptide	GO:0005575,GO:0003674,GO:0005576,GO:0008150	CG33998-PA						PF15868														
aly1450.7	Unknown		n/a						PF15868														
aly1450.8	Unknown		n/a						PF15868														
aly1450.9	Unknown		n/a						PF15868														
aly145218.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly14528.1	Putative serine/threonine-protein kinase C05D10.2	GO:0005737,GO:0006468,GO:0045792,GO:0050709,GO:0005635,GO:0007030,GO:0005789,GO:0004674,GO:0004707,GO:0034389,GO:0034198,GO:0005622,GO:0005524	CG32703-PA						PF00069	PS50011	PR01771,PR01771,PR01771	PS01351,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly14528.2	Unknown		n/a																				
aly1454.1	Transcription elongation factor B polypeptide 2	GO:0008023,GO:0030891,GO:0003713,GO:0007474,GO:0070449,GO:0016567,GO:0045944,GO:0005667,GO:0032403,GO:0006368,GO:0005875	CG4204-PA				SM00213		PF00240	PS50053			G3DSA:3.10.20.90	SSF54236									
aly1454.10	Phosphopantothenate--cysteine ligase	GO:0030708,GO:0006766,GO:0070328,GO:0070062,GO:0015937,GO:0015939,GO:0030713,GO:0007476,GO:0006767,GO:0030036,GO:0044281,GO:0022416,GO:0009108,GO:0007297,GO:0004632,GO:0007303,GO:0005829,GO:0055091,GO:0046843	CG5629-PA						PF04127,PF04127				G3DSA:3.40.50.10300	SSF102645		00770+6.3.2.5			UPA00241				
aly1454.11	Putative transporter ZK637.1	GO:0030672,GO:0006629,GO:0005215,GO:0016021,GO:0006810,GO:0015075,GO:0016298,GO:0055085	CG31272-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1454.12	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0030672,GO:0016021,GO:0016020,GO:0008513,GO:0022857,GO:0001669,GO:0005886,GO:0006836,GO:0055085,GO:0030054	CG15221-PB						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1454.13	Synaptic vesicle glycoprotein 2C	GO:0008021,GO:0030672,GO:0006629,GO:0005215,GO:0016021,GO:0006810,GO:0022857,GO:0006836,GO:0016298,GO:0055085,GO:0030054	CG31272-PA						PF07690	PS50850			G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1454.2	Suppressor of SWI4 1 homolog	GO:0001560,GO:0007444,GO:0005634,GO:0005730,GO:0005575,GO:0002164,GO:0003674,GO:0022008,GO:0048477,GO:0044822	CG5786-PA				SM00879		PF04427	PS50833				SSF52954,SSF52954	271~331								
aly1454.3	DNA replication licensing factor Mcm3	GO:0003682,GO:0042555,GO:0032508,GO:0006270,GO:0005656,GO:0006267,GO:0003677,GO:0003678,GO:0007095,GO:0022008,GO:0043138,GO:0005634,GO:0005524	CG4206-PA				SM00350		PF14551,PF00493,PF00493	PS50051	PR01657,PR01657,PR01657,PR01657,PR01657,PR01659,PR01659,PR01659,PR01659,PR01659	PS00847	G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:3.40.50.300,G3DSA:3.30.1640.10	SSF50249,SSF52540,SSF52540			REACT_152,REACT_383,REACT_1538						
aly1454.4	UPF0483 protein AAEL000016	GO:0005575,GO:0008150,GO:0003674	CG5412-PA						PF03959				G3DSA:3.40.50.1820	SSF53474									
aly1454.5	tRNA (guanine(10)-N2)-methyltransferase homolog	GO:0008168,GO:0032259,GO:0008033,GO:0000049,GO:0003676	CG1074-PA						PF01170	PS51627	PR00507,PR00507	PS00092	G3DSA:3.40.50.150	SSF53335									
aly1454.6	ER membrane protein complex subunit 2	GO:0005737,GO:0005783,GO:0005634,GO:0072546,GO:0005515,GO:0005875	CG17556-PA							PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1454.7	Zinc finger protein 264	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG31224-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	817~837									
aly1454.8	Unknown		n/a										G3DSA:1.25.10.10	SSF48371									
aly1454.9	Unknown		n/a																				
aly145475.1	Multidrug resistance protein homolog 49	GO:0015893,GO:0042626,GO:0042623,GO:0016021,GO:0031427,GO:0006855,GO:0015238,GO:0008559,GO:0005524,GO:0005887,GO:0005886,GO:0001666,GO:0055085,GO:0008354	CG3879-PA						PF00664	PS50929			G3DSA:1.20.1560.10	SSF90123									
aly14552.1	Unknown		n/a																				
aly1456.1	Coatomer subunit delta	GO:0007436,GO:0043473,GO:0006890,GO:0006909,GO:0005783,GO:0009306,GO:0006886,GO:0044822,GO:0035158,GO:0010883,GO:0030131,GO:0030126,GO:0008344,GO:0021691	CG14813-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1456.10	Pleckstrin homology domain-containing family G member 2	GO:0005089,GO:0017160,GO:0007480,GO:0005085,GO:0007474,GO:0005575,GO:0035023,GO:0032489	CG30115-PE						PF00621	PS50010			G3DSA:1.20.900.10	SSF48065									
aly1456.2	UPF0488 protein CG14286	GO:0005575,GO:0003674,GO:0008150	CG14286-PA						PF15393						47~67								
aly1456.3	Mitochondrial import inner membrane translocase subunit Tim10	GO:0008565,GO:0015450,GO:0005743,GO:0006626,GO:0042719,GO:0045039,GO:0045824,GO:0015031,GO:0005744,GO:0050829,GO:0046872	CG9878-PA						PF15932,PF02953				G3DSA:1.10.287.810	SSF144122									
aly1456.4	GPI mannosyltransferase 1	GO:0016758,GO:0016021,GO:0005789,GO:0006506	CG9865-PA						PF05007										UPA00196				
aly1456.5	Vacuolar protein sorting associated protein 26	GO:0008565,GO:0007034,GO:0006886,GO:0016055,GO:0030906,GO:0006605,GO:0030904,GO:0030111,GO:0042147,GO:0007040,GO:0005768	CG14804-PA						PF03643														
aly1456.6	Mitochondrial import receptor subunit TOM20 homolog	GO:0015450,GO:0016021,GO:0006886,GO:0005739,GO:0006605,GO:0005742,GO:0044233,GO:0005741,GO:0051082,GO:0006626	CG7654-PA			PIRSF037707			PF02064		PR00351,PR00351,PR00351,PR01989,PR01989,PR01989,PR01989,PR01989,PR01989		G3DSA:1.20.960.10	SSF47157	37~57,148~154								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1456.7	Porphobilinogen deaminase	GO:0032025,GO:0042493,GO:0018160,GO:0006778,GO:0030424,GO:0044281,GO:0010043,GO:0001666,GO:0004852,GO:0050662,GO:0032355,GO:0071418,GO:0006783,GO:0006782,GO:0005634,GO:0033014,GO:0033273,GO:0071236,GO:0031100,GO:0048708,GO:0000793,GO:0051597,GO:0071243,GO:0009743,GO:0071549,G	CG9165-PA						PF01379,PF03900		PR00151,PR00151,PR00151	PS00533	G3DSA:3.40.190.10,G3DSA:3.30.160.40,G3DSA:3.30.160.40,G3DSA:3.40.190.10	SSF53850,SSF54782		00860+2.5.1.61		PWY-5189,PWY-5188	UPA00251				
aly1456.8	Coatomer subunit zeta-1	GO:0006891,GO:0006890,GO:0006909,GO:0005215,GO:0006886,GO:0006810,GO:0005198,GO:0010883,GO:0030126,GO:1901998,GO:0055114,GO:0016491	CG3948-PA						PF01217				G3DSA:3.30.450.60	SSF64356									
aly1456.9	Nucleosomal histone kinase 1	GO:0018107,GO:0016055,GO:0018105,GO:0000785,GO:0007143,GO:0051301,GO:0005737,GO:0007126,GO:0005730,GO:0005634,GO:0004674,GO:0004672,GO:0005524,GO:0006468,GO:0016572,GO:0007052,GO:0035405,GO:2001020,GO:0022008,GO:0007130,GO:0036098,GO:0036099,GO:0097150,GO:0000070,GO:0006897,G	CG8878-PA				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10	SSF56112,SSF56112	766~786,930~930								
aly1457.1	Unknown		n/a																				
aly145756.1	Unknown		n/a																				
aly14581.1	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005886,GO:0006508	CG34350-PB						PF00089	PS50240			G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly14581.2	Transmembrane protease serine 11E	GO:0004252,GO:0050890,GO:0005576,GO:0005887,GO:0006508,GO:0008236	CG34350-PB						PF00089	PS50240			G3DSA:2.40.10.10	SSF50494									
aly14581.3	60S ribosomal protein L23	GO:0005840,GO:0022625,GO:0017022,GO:0003735,GO:0007052,GO:0000022,GO:0022008,GO:0006412	CG3661-PA	MF_01367					PF00238			PS00049	G3DSA:2.40.150.20	SSF50193									
aly14581.4	Proteasome subunit beta type-4 (Fragment)	GO:0005737,GO:0051603,GO:0004175,GO:0005839,GO:0008283,GO:0043161,GO:0005634,GO:0009987,GO:0004298,GO:0006974,GO:0007052,GO:0006511,GO:0051297,GO:0006508,GO:0022008,GO:0000022	CG12000-PB			PIRSF001213			PF00227	PS51476		PS00854	G3DSA:3.60.20.10	SSF56235			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_110						
aly14581.5	RNA-binding protein 8A	GO:0035145,GO:0007294,GO:0046595,GO:0000226,GO:0003676,GO:0005737,GO:0005634,GO:0000166,GO:0008380,GO:0006406,GO:0000335,GO:0071013,GO:0007317,GO:0007314,GO:0007173,GO:0007312,GO:0007310,GO:0045451,GO:0000398,GO:0005515,GO:0006396,GO:0003729	CG8781-PA				SM00360		PF00076	PS50102	PR01738,PR01738,PR01738,PR01738		G3DSA:3.30.70.330	SSF54928									
aly14581.6	Metaxin-2	GO:0006626,GO:0005741	CG8004-PA						PF14497					SSF47616,SSF47616									
aly14608.1	Unknown		n/a							PS50292			G3DSA:1.10.640.10										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly14625.1	Ras-related protein Rab-24	GO:0016020,GO:0050803,GO:0035220,GO:0005776,GO:0030139,GO:0048227,GO:0045202,GO:0007298,GO:0007067,GO:0048488,GO:0035088,GO:0031982,GO:0006325,GO:0016189,GO:0006886,GO:0005811,GO:0007349,GO:0005739,GO:0048803,GO:0048477,GO:0005525,GO:0008285,GO:0006914,GO:0003924,GO:0016321,GO:0016348,GO:0032482,GO:0007409,GO:0046664,GO:0030100,GO:0034058,GO:0007220,GO:0006897,GO:0016192,GO:0043025,GO:0005829,GO:0048813,GO:0005515,GO:0015031,GO:0005768,GO:0005769	CG3664-PI				SM00173,SM00174,SM00176,SM00175	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540	177~200		REACT_11044						
aly14625.2	Protein toll	GO:0009897,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0035007,GO:0008063,GO:0006955,GO:0007416,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0002229,GO:0006952,GO:0042802,GO:0016201,GO:0009880,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005887,GO:0005886,GO:0007155,GO:0007352,GO:0043234,GO:0007507,GO:0009950,GO:0009620,GO:0004888,GO:0045944,GO:0005515,GO:0030097,GO:0045610,GO:0005769,GO:0007165	CG5490-PC				SM00082,SM00082,SM00255,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF01582,PF13306	PS51450,PS50104,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR01537,PR01537		G3DSA:3.40.50.10140,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047,SSF52200	922~925								
aly146252.1	Unknown		n/a						PF13873														
aly14673.1	Unknown		n/a						PF03372				G3DSA:3.60.10.10	SSF56219									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly14673.2	Unknown		n/a				SM00249			PS50081		PS01359	G3DSA:3.30.40.10,G3DSA:1.20.5.340	SSF57903,SSF57997	114~155								
aly1468.1	Cytosolic beta-glucosidase	GO:0005975,GO:0005829,GO:0016139,GO:0008422,GO:0004565,GO:0006687,GO:0004553,GO:0017042,GO:0046477,GO:0006665,GO:0044281	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131	PS00572	G3DSA:3.20.20.80	SSF51445									
aly1468.10	Putative nuclease HARBI1	GO:0005737,GO:0004518,GO:0005634,GO:0046872	CG43088-PA						PF13359														
aly1468.11	Unknown		n/a						PF13873						230~250								
aly1468.12	General transcription factor 3C polypeptide 5	GO:0000127,GO:0006909,GO:0005654,GO:0010467,GO:0006351,GO:0003677,GO:0035914,GO:0042797,GO:0006383,GO:0042791	CG10563-PA						PF09734														
aly1468.13	Clavesin-1	GO:0006892,GO:0005811,GO:0080025,GO:0005215,GO:0006810,GO:0030669,GO:0098779,GO:0061024,GO:0032588,GO:0007040,GO:0005802,GO:0030136,GO:0005768,GO:0031901,GO:0016918	CG5958-PA				SM00516,SM01100		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087,SSF46938	26~46								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1468.14	Alpha-tocopherol transfer protein-like	GO:0006810,GO:0005215,GO:0016020,GO:0005622,GO:0005885,GO:0016918	CG5973-PA				SM00516,SM01100		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF46938,SSF52087									
aly1468.15	Clavesin-1	GO:0006892,GO:0008431,GO:0005802,GO:0080025,GO:0005215,GO:0006810,GO:0030669,GO:0005622,GO:0098779,GO:0061024,GO:0032588,GO:0007040,GO:0030136,GO:0005768,GO:0031901,GO:0016918	CG10237-PB				SM01100,SM00516		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF46938,SSF52087									
aly1468.16	Clavesin-1	GO:0008431,GO:0005802,GO:0080025,GO:0005215,GO:0006810,GO:0005622,GO:0007040,GO:0030136,GO:0005768,GO:0031901,GO:0016918	CG10026-PB				SM01100,SM00516		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087,SSF46938									
aly1468.17	Ras-like protein family member 11B	GO:0048382,GO:0016020,GO:0003924,GO:0005622,GO:0005575,GO:0008150,GO:0007165,GO:0006184,GO:0007264,GO:0005525	CG8519-PA				SM00173,SM00175		PF00071	PS51421	PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540									
aly1468.18	Class E basic helix-loop-helix protein 22	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0008045,GO:0046983	CG5545-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459	89~109								
aly1468.19	Cysteine/serine-rich nuclear protein 2	GO:0008285,GO:0010923,GO:0043565,GO:0003700,GO:0005634,GO:0006915,GO:0001228,GO:0019902,GO:0045944,GO:0006366	CG4272-PB						PF16019		PR02031,PR02031,PR02031				259~279								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1468.2	Rab3 GTPase-activating protein catalytic subunit	GO:0061646,GO:0060325,GO:0043087,GO:0071782,GO:0005737,GO:0043547,GO:0021854,GO:0005096,GO:0005097,GO:0017137,GO:0048172,GO:0032851,GO:0060079,GO:0070062,GO:0043234,GO:0034389,GO:0007420,GO:0097051,GO:0010628,GO:1903373,GO:0043010,GO:1903233	CG31935-PA						PF13890						571~591								
aly1468.20	Protein FAN	GO:0005737,GO:0048749,GO:0019898,GO:0007041,GO:0016197,GO:0048786,GO:0050807,GO:0030424,GO:0031594,GO:0022416,GO:0005543,GO:0012505,GO:0007409,GO:0005057,GO:0031396,GO:0008340,GO:0035556,GO:0046872,GO:0006672,GO:0007165	CG14001-PA				SM01026,SM00320,SM00320,SM00320,SM00320,SM00320		PF02138,PF00400,PF00400	PS50082,PS50082,PS50294,PS50197		PS00678	G3DSA:1.10.1540.10,G3DSA:2.130.10.10,G3DSA:2.30.29.40	SSF81837,SSF50978,SSF50729									
aly1468.21	Heat shock factor protein 5	GO:0003700,GO:0006355,GO:0005634,GO:0006351,GO:0043565	n/a				SM00415		PF00447				G3DSA:1.10.10.10	SSF46785									
aly1468.22	Proteasome subunit alpha type-7-1	GO:0005737,GO:0004175,GO:0005839,GO:0019773,GO:0005634,GO:0010499,GO:0004298,GO:0006974,GO:0006511,GO:0005875,GO:0043161,GO:0000502,GO:0006508	CG3422-PA				SM00948		PF10584,PF00227	PS51475		PS00388	G3DSA:3.60.20.10	SSF56235			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_110						
aly1468.23	Coiled-coil domain-containing protein 43		CG9586-PC												153~175								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1468.24	Secretion-regulating guanine nucleotide exchange factor	GO:0005737,GO:0045111,GO:0050709,GO:0005730,GO:0005634,GO:0005087,GO:0043547	CG7420-PB						PF00415,PF00415,PF00415,PF00415,PF00415,PF00415	PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012	PR00633,PR00633,PR00633,PR00633,PR00633,PR00633,PR00633	PS00626	G3DSA:2.130.10.30,G3DSA:2.130.10.30	SSF50985,SSF50985									
aly1468.25	Unknown	GO:0030246,GO:0007399	CG15765-PA						PF00059	PS50041			G3DSA:3.10.100.10	SSF56436									
aly1468.26	Unknown		n/a																				
aly1468.27	Leucine-rich repeats and immunoglobulin-like domains protein 3	GO:0005615,GO:0016021,GO:0005886,GO:0030659,GO:0005515,GO:0008045,GO:0032474	CG14351-PC				SM00369,SM00369,SM00369,SM00369,SM00369		PF13855	PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly1468.3	Protein FAM92A1		CG6405-PA						PF06730					SSF103657									
aly1468.4	Heat shock factor-binding protein 1	GO:0005634,GO:0035987,GO:0035220	CG5446-PA						PF06825				G3DSA:1.20.1250.10		49~76								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1468.5	Cell division cycle protein 23 homolog	GO:0007113,GO:0045842,GO:0006909,GO:0005515,GO:0070979,GO:0007080,GO:0090302,GO:0022008,GO:0004842,GO:0030071,GO:0051301,GO:0005680	CG2508-PA				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF00515,PF00515,PF13414,PF04049	PS50005,PS50293,PS50005,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452					UPA00143				
aly1468.6	Arf-GAP domain and FG repeat-containing protein 1	GO:0042995,GO:0045109,GO:0016023,GO:0032312,GO:0005634,GO:0006810,GO:0005096,GO:0005575,GO:0046872,GO:0008060,GO:0008270,GO:0003677,GO:0007289,GO:0001675,GO:0043025,GO:0007275,GO:0043231	CG3365-PF				SM00105		PF01412	PS50115	PR00405,PR00405,PR00405			SSF57863									
aly1468.7	Regulator of nonsense transcripts 2	GO:0005737,GO:0035145,GO:0050808,GO:0031100,GO:0035195,GO:0005829,GO:0010467,GO:0000184,GO:0001889,GO:0003723,GO:0016246,GO:0048471,GO:0007274,GO:0005634,GO:0006406	CG2253-PA				SM00543,SM00543,SM00543		PF04050,PF02854,PF02854,PF02854				G3DSA:1.25.40.180,G3DSA:1.25.40.180	SSF48371,SSF48371,SSF48371	1035~1055								
aly1468.8	Asparagine synthetase domain-containing protein CG17486	GO:0005575,GO:0006529,GO:0006541,GO:0004066	CG17486-PB						PF13537,PF00733	PS51278			G3DSA:3.40.50.620,G3DSA:3.60.20.10	SSF56235,SSF52402									
aly1468.9	Nuclear pore complex protein Nup93	GO:0034399,GO:1903146,GO:0016973,GO:0017056,GO:0005643,GO:0006606,GO:0044615,GO:0006810,GO:0031965,GO:0006607,GO:0006999,GO:0007184,GO:0051292,GO:0034613	CG11092-PA						PF04097,PF04097														
aly14688.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1469.1	Orexin receptor type 2	GO:0007268,GO:0008528,GO:0004930,GO:0042277,GO:0007631,GO:0007200,GO:0016021,GO:0016499,GO:0007218,GO:0004983,GO:0032870,GO:0045187,GO:1901652,GO:0022410,GO:0005887,GO:0008188,GO:0008340,GO:0007186	CG10823-PA						PF00001	PS50262	PR01012,PR01012,PR01012,PR01012,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797							
aly1469.2	Unknown		n/a						PF00089				G3DSA:2.40.10.10	SSF50494									
aly1469.3	Trypsin-3	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG17571-PA						PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly146902.1	Unknown	GO:0045475	CG18437-PF																				
aly14709.1	Ornithine decarboxylase antizyme 2	GO:0008073,GO:0005829,GO:0030154,GO:0006596,GO:0090316	CG16747-PC						PF02100					SSF55729			REACT_13						
aly14709.2	Dihydrofolate reductase	GO:0006139,GO:0050661,GO:0006760,GO:0006545,GO:0006730,GO:0009165,GO:0006189,GO:0005515,GO:0015955,GO:0004146,GO:0046654,GO:0055114	CG14887-PA						PF00186	PS51330	PR00070,PR00070,PR00070,PR00070	PS00075	G3DSA:3.40.430.10	SSF53597		00790+1.5.1.3,00670+1.5.1.3		PWY-6614,PWY-3841	UPA00077				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1471.1	Alpha-N-acetylgalactosaminidase	GO:0005737,GO:0008456,GO:0005975,GO:0016139,GO:0009311,GO:0005764,GO:0004557,GO:0046477	CG5731-PA						PF16499		PR00740,PR00740,PR00740,PR00740,PR00740,PR00740	PS00512	G3DSA:2.60.40.1180,G3DSA:3.20.20.70	SSF51011,SSF51445		00052+3.2.1.22,00600+3.2.1.22,00603+3.2.1.22,00561+3.2.1.22		PWY-6527					
aly1471.2	Unknown	GO:0016787,GO:0046872,GO:0003676	CG3819-PA				SM00892		PF01223				G3DSA:3.40.570.10	SSF54060									
aly1471.3	Unknown		n/a																				
aly1471.4	Unknown		n/a												55~78								
aly1471.5	WD repeat domain phosphoinositide-interacting protein 4	GO:0005737,GO:0006497,GO:0006995,GO:0080025,GO:0000422,GO:0006914,GO:0032266,GO:0000045,GO:0034045,GO:0034497,GO:0044804,GO:0005515,GO:0019898,GO:0005829	CG11975-PA				SM00320,SM00320			PS50294			G3DSA:2.130.10.10	SSF50978,SSF50978									
aly14729.1	Unknown		n/a																				
aly14729.2	Unknown		n/a																				
aly14729.3	Unknown		n/a																				
aly1475.1	Probable C-5 sterol desaturase	GO:0006633,GO:0000254,GO:0000248,GO:0016021,GO:0005788,GO:0005789,GO:0006696,GO:0005506,GO:0055114,GO:0016491	CG11162-PA						PF04116														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1475.10	Fatty-acid amide hydrolase 2-A	GO:0016787,GO:0016021,GO:0050567,GO:0016884	CG5191-PB						PF01425,PF01425			PS00571	G3DSA:3.90.1300.10,G3DSA:3.90.1300.10,G3DSA:3.90.1300.10,G3DSA:3.90.1300.10	SSF75304,SSF75304		00970+6.3.5.7		PWY-5921					
aly1475.11	Unknown		n/a				SM00540,SM00540,SM00540		PF03020,PF03020,PF03020	PS50954,PS50954,PS50954			G3DSA:1.10.720.40,G3DSA:1.10.720.40,G3DSA:1.10.720.40	SSF63451,SSF63451,SSF63451									
aly1475.12	Inner nuclear membrane protein Man1	GO:0006997,GO:0032926,GO:0005639,GO:0005637,GO:0016021,GO:0016020,GO:0000166,GO:0035914,GO:0051726,GO:0003677,GO:0002044,GO:0030514,GO:0030512,GO:1903053	CG3167-PA				SM00540		PF03020,PF09402	PS50954			G3DSA:3.30.70.330,G3DSA:1.10.720.40	SSF63451,SSF54928									
aly1475.13	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	GO:0005947,GO:0007584,GO:0005739,GO:0051591,GO:0017086,GO:0032403,GO:0046949,GO:0003863,GO:0051384,GO:0009083	CG17691-PC				SM00861		PF02779,PF02780				G3DSA:3.40.50.970,G3DSA:3.40.50.920	SSF52518,SSF52922									
aly1475.14	Unknown		n/a																				
aly1475.15	Protein FAM46C		CG30497-PA						PF07984														
aly1475.16	Unknown		n/a																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1475.17	Protein GDAP2 homolog	GO:0005575,GO:0008150,GO:0003674	CG18812-PC				SM00516,SM00506		PF01661,PF13716	PS50191,PS51154			G3DSA:3.40.220.10,G3DSA:3.40.525.10	SSF52949,SSF52087									
aly1475.18	Phosphatidylinositol-glycan biosynthesis class F protein	GO:0044267,GO:0016021,GO:0005789,GO:0006501,GO:0004307,GO:0006506,GO:0016254,GO:0043687	CG9376-PA						PF06699										UPA00196				
aly1475.19	5-aminolevulinate synthase, erythroid-specific, mitochondrial	GO:0040003,GO:0006879,GO:0005743,GO:0006783,GO:0006782,GO:0005739,GO:0030218,GO:0030170,GO:0005759,GO:0042541,GO:0003870,GO:0001666	CG3017-PA					TIGR01821	PF00155				G3DSA:3.40.640.10,G3DSA:3.90.1150.10	SSF53383		00260+2.3.1.37,00860+2.3.1.37	REACT_9431	PWY-5189,PWY-7536	UPA00251				
aly1475.2	Zinc finger protein Noc	GO:0007424,GO:0035214,GO:0007420,GO:0007219,GO:0008283,GO:0005634,GO:0003677,GO:0035220,GO:0035218,GO:0010629,GO:0006357,GO:0005515,GO:0008056,GO:0007430,GO:0002121,GO:0046872,GO:0003676,GO:0001752	CG4491-PA							PS50157			G3DSA:3.30.160.60										
aly1475.20	Pre-mRNA-processing factor 17	GO:0071011,GO:0071013,GO:0044822,GO:0000398,GO:0005515,GO:0008380,GO:0005681,GO:0006397	CG6015-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50082,PS50294		PS00678	G3DSA:2.130.10.10	SSF50978									
aly1475.21	V-type proton ATPase subunit F	GO:0015992,GO:0015991,GO:0033181,GO:0033180,GO:0000221,GO:0046961,GO:0005886	CG8210-PA			PIRSF015945		TIGR01101	PF01990				G3DSA:3.40.50.10580	SSF159468									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1475.22	Putative carbonic anhydrase 3	GO:0006730,GO:0004089,GO:0008270	CG6074-PA				SM01057		PF00194,PF00194	PS51144			G3DSA:3.10.200.10,G3DSA:3.10.200.10,G3DSA:3.10.200.10	SSF51069,SSF51069	246~258								
aly1475.23	Unknown		n/a																				
aly1475.24	Zinc finger protein 98	GO:0006697,GO:0007616,GO:0045938,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0008340,GO:0046872,GO:0006351	CG34100-PD				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00354,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667	2470~2479								
aly1475.25	Vacuolar protein sorting associated protein 51 homolog	GO:0005575,GO:0003674,GO:0008150	CG15087-PA						PF15469						73~93								
aly1475.26	TBC1 domain family member 5	GO:0030904,GO:0042147,GO:0032313,GO:0031410,GO:0006914,GO:0005096,GO:0005097,GO:0005776,GO:0098779,GO:0010508,GO:0002092,GO:0042594,GO:0015031,GO:0035612,GO:0010008	CG8449-PA				SM00164		PF00566	PS50086			G3DSA:1.10.8.270,G3DSA:1.10.8.270	SSF47923,SSF47923									
aly1475.27	Unknown	GO:0046872	CG5694-PA						PF10491	PS50157					331~351								
aly1475.28	Transmembrane protein 181	GO:0016021,GO:0009405,GO:0015643	CG13409-PA						PF06664														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1475.3	Zinc finger protein Elbow	GO:0007424,GO:0035214,GO:0003676,GO:0008283,GO:0005634,GO:0035220,GO:0035218,GO:0010629,GO:0007219,GO:0001752,GO:0005515,GO:0000228,GO:0046872,GO:0048737	CG4220-PD							PS50157			G3DSA:3.30.160.60										
aly1475.4	Solute carrier family 22 member 13	GO:0090416,GO:0070062,GO:0016324,GO:0016021,GO:0015695,GO:0008513,GO:2001142,GO:0005887,GO:0015747,GO:0015101,GO:0055085	CG8654-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1475.5	Solute carrier family 22 member 3	GO:0015651,GO:0019534,GO:0051615,GO:0005329,GO:0032098,GO:0016021,GO:1901998,GO:0072488,GO:0015101,GO:0015697,GO:0008513,GO:0015872,GO:0015695,GO:0098655,GO:0055085,GO:1903146	CG8654-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1475.6	Solute carrier family 22 member 3	GO:0015651,GO:0019534,GO:0006855,GO:0051615,GO:0005329,GO:0015697,GO:0032098,GO:0005215,GO:0016021,GO:0016020,GO:0008513,GO:0098779,GO:0015101,GO:0044281,GO:0005887,GO:0005886,GO:0015695,GO:0015872,GO:0055085	CG8654-PA						PF00083	PS50850		PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly1475.7	IQ and AAA domain-containing protein 1-like	GO:0005524	CG14183-PA						PF00004				G3DSA:3.40.50.300	SSF52540	320~349								
aly1475.8	Meiosis-specific nuclear structural protein 1	GO:0051321,GO:0036126,GO:0005635,GO:0070986,GO:0007283,GO:0005882,GO:0045724,GO:0044782,GO:0005930	n/a						PF13868						206~226,357~384,156~183								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1475.9	Amphiphysin	GO:0005737,GO:0005856,GO:0048488,GO:0008104,GO:0006897,GO:0042052,GO:0006937,GO:0031256,GO:0030054,GO:0005543,GO:0007612,GO:0032154,GO:0008021,GO:0006887,GO:0007269,GO:0005886,GO:0030672,GO:0045313,GO:0045202	CG8604-PA				SM00326,SM00721		PF03114,PF14604	PS50002,PS51021	PR01251,PR01251,PR01251,PR01251,PR01251,PR01251,PR01251		G3DSA:2.30.30.40,G3DSA:1.20.1270.60	SSF50044,SSF103657	168~192,249~269								
aly1478.1	Unknown	GO:0005230,GO:0006811,GO:0005231,GO:0016021	CG6698-PA						PF12248,PF02931				G3DSA:2.70.170.10	SSF63712									
aly1478.10	Structural maintenance of chromosomes protein 4	GO:0005829,GO:0005524,GO:0007076,GO:0046982,GO:0005694,GO:0005634,GO:0051301	n/a											SSF90257	2~88								
aly1478.2	Probable chitinase 2	GO:0005975,GO:0000272,GO:0005576,GO:0008061,GO:0004553,GO:0004568,GO:0006032	CG9357-PA				SM00636,SM00494		PF00704,PF01607	PS50940		PS01095	G3DSA:3.10.50.10,G3DSA:2.170.140.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF54556,SSF57625,SSF51445,SSF51445		00520+3.2.1.14		PWY-6902					
aly1478.3	Vacuolar fusion protein MON1 homolog A	GO:0032510,GO:0006879,GO:0016192,GO:0009306,GO:0005829,GO:0005085,GO:0005623,GO:0015031,GO:0035658	CG11926-PA						PF03164		PR01546,PR01546,PR01546,PR01546,PR01546,PR01546,PR01546,PR01546,PR01546,PR01546,PR01546,PR01546,PR01546,PR01546			SSF64356									
aly1478.4	Pre-mRNA-splicing factor 38A	GO:0043234,GO:0071011,GO:0071013,GO:0000398,GO:0008380,GO:0005515,GO:0010389,GO:0005681,GO:0006397	CG30342-PA						PF03371														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1478.5	Structural maintenance of chromosomes protein 4	GO:0005737,GO:0000070,GO:0000819,GO:0007422,GO:0005634,GO:0000166,GO:0007052,GO:0000796,GO:0051301,GO:0003677,GO:0007076,GO:0000785,GO:0007067,GO:0046982,GO:0005694,GO:0005829,GO:0005524	CG11397-PA				SM00968		PF02463,PF06470				G3DSA:3.40.50.300,G3DSA:1.20.1170.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF75553,SSF52540,SSF52540,SSF57997	323~385,400~420,428~448,502~564,841~875,256~283,891~918,768~802,460~494,810~837								
aly1478.6	UBX domain-containing protein 6	GO:0005737,GO:0070062,GO:0005730,GO:0005634,GO:0005815,GO:0005515	CG5469-PD				SM00166,SM00580		PF09409,PF00789	PS50033			G3DSA:3.10.20.90	SSF54236,SSF143503	87~107								
aly1478.7	Unknown		CG42306-PC																				
aly1478.8	Unknown		n/a																				
aly1478.9	Laccase-4	GO:0052716,GO:0004322,GO:0009986,GO:0045178,GO:0055072,GO:0046274,GO:0005381,GO:0031233,GO:0005507,GO:0055114,GO:0005576	CG3759-PA						PF00394,PF07731,PF07732			PS00092,PS00080,PS00079	G3DSA:2.60.40.420,G3DSA:2.60.40.420,G3DSA:2.60.40.420	SSF49503,SSF49503,SSF49503									
aly1480.1	Ankyrin repeat and SAM domain-containing protein 1A	GO:0005737,GO:0016322,GO:0005654,GO:0006929,GO:0043005,GO:0048013	CG4393-PB				SM00462,SM00454,SM00454		PF07647,PF00536,PF00640	PS01179,PS50105			G3DSA:2.30.29.30,G3DSA:1.10.150.50,G3DSA:1.10.150.50	SSF50729,SSF47769,SSF47769	294~318								
aly1480.2	Unknown		n/a																				
aly14812.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1482.1	Unknown		n/a																				
aly1482.10	Zinc finger protein 397	GO:0005737,GO:0003700,GO:0005634,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG3407-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										
aly1482.11	Unknown		n/a																				
aly1482.12	Unknown		n/a																				
aly1482.13	Unknown		n/a																				
aly1482.14	Unknown	GO:0005575,GO:0046982,GO:0008150	CG43980-PC										G3DSA:1.25.40.20,G3DSA:1.25.40.20										
aly1482.2	Ankyrin repeat and BTB/POZ domain-containing protein 2	GO:0005654,GO:0097237,GO:0005575,GO:0008150,GO:0046982,GO:0005634	CG43980-PC				SM00225		PF00651	PS50097			G3DSA:1.10.20.10,G3DSA:1.10.20.10,G3DSA:3.30.710.10	SSF47113,SSF54695									
aly1482.3	Unknown		n/a																				
aly1482.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1482.5	ADP-ribosylation factor-like protein 1	GO:0033227,GO:0006471,GO:0035220,GO:0048488,GO:0007431,GO:0000042,GO:0034067,GO:0070861,GO:0005525,GO:0060628,GO:0005794,GO:0030334,GO:0003924,GO:0019904,GO:0007269,GO:0007264,GO:0016197,GO:0090158,GO:0007030,GO:0005802,GO:0005515,GO:0015031,GO:0033363	CG6025-PA				SM00175,SM00177,SM00178	TIGR00231	PF00025	PS51417	PR00328,PR00328,PR00328,PR00328		G3DSA:3.40.50.300	SSF52540									
aly1482.6	Unknown		n/a																				
aly1482.7	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG9447-PC												648~648								
aly1482.8	Unknown		n/a						PF03128,PF00341	PS50278			G3DSA:2.10.90.10	SSF57501									
aly1482.9	Lipoyl synthase, mitochondrial	GO:0009249,GO:0009107,GO:0051539,GO:0016992,GO:0005739,GO:0046872	CG5231-PC	MF_00206		PIRSF005963	SM00729	TIGR00510	PF16881,PF04055				G3DSA:3.20.20.70	SSF102114		00785+2.8.1.8		PWY-6987,PWY-7382,PWY-7381	UPA00538				
aly14849.1	Unknown		n/a						PF14214														
aly14849.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1486.1	Phosphatidylinositide phosphatase SAC1	GO:0052866,GO:0012505,GO:0016791,GO:0071683,GO:0016311,GO:0016021,GO:0016199,GO:0030424,GO:0042578,GO:0046329,GO:0060074,GO:0046488,GO:0052744,GO:0046664,GO:0005789,GO:0046856,GO:0031122,GO:0043025,GO:0008088	CG9128-PB						PF02383	PS50275													
aly1486.2	Phosphatidylinositide phosphatase SAC1-A	GO:0052866,GO:0016791,GO:0071683,GO:0016311,GO:0016021,GO:0016199,GO:0030424,GO:0046329,GO:0060074,GO:0046488,GO:0052744,GO:0046664,GO:0005789,GO:0046856,GO:0031122,GO:0043025,GO:0008088	CG9128-PB																				
aly1486.3	Probable ATP-dependent RNA helicase DDX27	GO:0005634,GO:0042254,GO:0004004,GO:0003724,GO:0003676,GO:0010501,GO:0044822,GO:0005524	CG2173-PA				SM00487,SM00490		PF00270,PF00271	PS51192,PS51194,PS51195		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	576~596,130~153,672~692								
aly1486.4	Unknown	GO:0005634,GO:0042742	CG2247-PA				SM00391		PF12937,PF01429	PS50982			G3DSA:3.80.10.10,G3DSA:3.30.890.10	SSF52047,SSF54171	128~148								
aly1487.1	Ryanodine receptor	GO:0072347,GO:0005219,GO:0006936,GO:0006874,GO:0016021,GO:0070588,GO:0006816,GO:0005789,GO:0033017,GO:0060047,GO:0005509,GO:0035206,GO:0007275,GO:0005875	CG10844-PI				SM00472,SM00472,SM00472,SM00449,SM00449,SM00449		PF08709,PF00622,PF00622,PF00622,PF01365,PF01365,PF02815,PF02026,PF02026,PF02026,PF02026	PS50919,PS50188,PS50919,PS50188,PS50919,PS50919,PS50919	PR00795,PR00795,PR00795,PR00795,PR00795,PR00795,PR00795,PR00795		G3DSA:2.80.10.50,G3DSA:2.80.10.50	SSF49899,SSF82109,SSF49899,SSF49899,SSF82109	461~481								
aly1487.2	Ryanodine receptor	GO:0072347,GO:0016021,GO:0005219,GO:0006936,GO:0006874,GO:0005216,GO:0016020,GO:0070588,GO:0006816,GO:0055085,GO:0033017,GO:0060047,GO:0005875,GO:0005509,GO:0035206,GO:0007275,GO:0005789,GO:0006811	CG10844-PI						PF00520,PF06459,PF08454				G3DSA:1.10.238.10	SSF47473	523~543								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1487.3	Golgi pH regulator	GO:0004175,GO:0008258,GO:0048102,GO:0007291,GO:0010623,GO:0010941,GO:0007417,GO:0005737,GO:0001700,GO:0007516,GO:0016021,GO:0007552,GO:0031638,GO:0005739,GO:0006508,GO:0010506,GO:0042803,GO:0048749,GO:0008285,GO:0035071,GO:0006919,GO:0035234,GO:0006915,GO:0016322,GO:0012501,GO:0046668,GO:0045476,GO:0008340,GO:0035070,GO:0007423,GO:0046672,GO:0016540,GO:0000139,GO:0048813,GO:0004197,GO:0015031,GO:0005244	CG8090-PA				SM00258		PF01342,PF12537,PF01753,PF12430	PS50864,PS50865		PS01360	G3DSA:3.10.390.10	SSF63763,SSF144232										
aly1487.4	Zinc finger protein 689	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0035914,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly1487.5	Putative glycerol kinase 3	GO:0004370,GO:0005975,GO:0046167,GO:0005575,GO:0019563,GO:0005741,GO:0006072,GO:0005524	CG7995-PC						PF02782,PF00370			PS00933	G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.30.420.40	SSF53067,SSF53067		00561+2.7.1.30		PWY-4261	UPA00618				
aly1487.6	Unknown		n/a																				
aly1487.7	Unknown		n/a																				
aly148849.1	Unknown		n/a												40~66								
aly1489.1	Pinopsin	GO:0008020,GO:0004930,GO:0009881,GO:0016021,GO:0007601,GO:0018298,GO:0007602,GO:0007186	CG5638-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1489.10	Unknown	GO:0008080	CG13759-PA																				
aly1489.11	Zinc finger protein 300	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG6654-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12874,PF07776,PF00096,PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.40.10,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57716,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly1489.12	Inhibitor of nuclear factor kappa-B kinase subunit alpha	GO:0018105,GO:0019730,GO:0019731,GO:0006963,GO:0033598,GO:0008063,GO:0005737,GO:0004674,GO:0071356,GO:0005654,GO:0007595,GO:0004672,GO:0008385,GO:0008384,GO:0005524,GO:0043123,GO:0035994,GO:0006468,GO:0045088,GO:0030316,GO:0042803,GO:0030163,GO:0060749,GO:0042475,GO:0051607,GO:0009950,GO:0002011,GO:0002230,GO:0045944,GO:0005515,GO:0046982	CG4201-PB				SM00220		PF00069	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly1489.13	MCM domain containing protein 2	GO:0005737,GO:0016321,GO:0006260,GO:0003677,GO:0007131,GO:0007143,GO:0005524	CG8923-PB																				
aly1489.14	Helix-loop-helix protein delilah	GO:0016203,GO:0006355,GO:0007498,GO:0005634,GO:0007474,GO:0003700,GO:0006357,GO:0006351,GO:0003677,GO:0043425,GO:0070888,GO:0046983,GO:0046982,GO:0007525,GO:0000981,GO:0033627	CG5441-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459									
aly1489.15	Nuclear nucleic acid-binding protein C1D	GO:0005737,GO:0000178,GO:0005730,GO:0003723,GO:0003677,GO:0010468,GO:0006364	CG8928-PA						PF04000														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1489.16	ADP-dependent glucokinase	GO:0043843,GO:0005783,GO:0016773,GO:0016020,GO:0005576,GO:0005975,GO:0046872,GO:0006096	CG6650-PA						PF04587	PS51255			G3DSA:3.40.1190.20	SSF53613					UPA00109				
aly1489.17	26S proteasome non-ATPase regulatory subunit 1	GO:0004175,GO:0005838,GO:0043161,GO:0030234,GO:0006974,GO:0042176,GO:0008270,GO:0000502,GO:0006508,GO:0008540	CG11888-PB			PIRSF015947			PF13646,PF01851,PF01851,PF01851				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371	312~332		REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_110						
aly1489.18	Signal recognition particle receptor subunit alpha	GO:0016020,GO:0005785,GO:0050708,GO:0070062,GO:0005047,GO:0005811,GO:0003924,GO:0006614,GO:0005789,GO:0007409,GO:0006184,GO:0003729,GO:0044822,GO:0005525	CG2522-PA				SM00382,SM00963,SM00962		PF00448,PF04086,PF02881			PS00300	G3DSA:1.20.120.140,G3DSA:3.40.50.300	SSF52540,SSF47364,SSF64356			REACT_15380						
aly1489.19	Unknown		n/a																				
aly1489.2	Dishevelled-associated activator of morphogenesis 1	GO:0005737,GO:0007424,GO:0035152,GO:0050770,GO:0051489,GO:0016020,GO:0051017,GO:0051491,GO:0003779,GO:0001725,GO:0030036,GO:0017048,GO:0005886,GO:0035017,GO:0044295,GO:0042802	CG14622-PD				SM00498		PF02181,PF02181,PF06367,PF06371	PS51232,PS51231,PS51444				SSF101447,SSF48371	845~872,491~560,757~777								
aly1489.20	Protein maelstrom homolog	GO:0008104,GO:0030154,GO:0003677,GO:0007275,GO:0005737,GO:0043565,GO:0043186,GO:0005634,GO:0010529,GO:0048477,GO:0031023,GO:0016325,GO:0019094,GO:0048600,GO:0007317,GO:0007283,GO:0007314,GO:0045892,GO:0031047,GO:0051321,GO:0007010,GO:0009950,GO:0008298,GO:0007312	CG11254-PC						PF13017,PF09011	PS50118			G3DSA:1.10.30.10	SSF47095	78~101								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1489.21	Alpha-(1,6)-fucosyltransferase	GO:0046368,GO:0006486,GO:0036071,GO:0008424,GO:0016021,GO:0006487,GO:0046702,GO:0008417,GO:0018279,GO:0030173,GO:0046921,GO:0033578,GO:0032580	CG2448-PA							PS51659			G3DSA:2.30.30.40	SSF50044	15~42								
aly1489.22	Protein jagged 1	GO:0042127,GO:0007219,GO:0031100,GO:0016021,GO:0016020,GO:0001709,GO:0042491,GO:0045596,GO:0005509,GO:0005886,GO:0007154,GO:0005112	CG1567-PA				SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00179		PF12661,PF12661,PF00008,PF00053	PS50026,PS50026,PS50026,PS50026		PS00022,PS00022,PS00022,PS00022,PS00022,PS00022,PS00022,PS00022	G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.10.25.10	SSF57196								
aly1489.23	Zinc finger protein 512B	GO:0006355,GO:0005634,GO:0046872,GO:0006351,GO:0003677	CG16885-PA																				
aly1489.24	Neprilysin	GO:0008021,GO:0030425,GO:0030424,GO:0005903,GO:0045202,GO:0050435,GO:0005737,GO:0044306,GO:0042277,GO:0016021,GO:0001822,GO:0019233,GO:0046449,GO:0004222,GO:0071493,GO:0071492,GO:0005886,GO:0006508,GO:0071345,GO:0090399,GO:0006518,GO:0008270	CG6265-PD						PF05649,PF01431		PR00786,PR00786,PR00786,PR00786		G3DSA:3.40.390.10,G3DSA:3.40.390.10	SSF55486,SSF55486									
aly1489.25	Unknown		n/a																				
aly1489.26	Unknown		CG16885-PA																				
aly1489.27	Unknown		CG16885-PA																				
aly1489.28	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1489.29	Unknown		n/a																				
aly1489.3	Unknown	GO:0010972,GO:0005634,GO:0003674,GO:0005829	CG15727-PA												216~236								
aly1489.30	Unknown		n/a																				
aly1489.4	Unknown		n/a																				
aly1489.5	Unknown	GO:0005515	n/a				SM00240		PF00498	PS50006			G3DSA:2.60.200.20	SSF49879	718~738								
aly1489.6	GDP-mannose 4,6 dehydratase	GO:0008446,GO:0050662,GO:0007219,GO:0042350,GO:0042351,GO:0005622,GO:2000035,GO:0048477,GO:0019673	CG8890-PA	MF_00955				TIGR01472	PF16363				G3DSA:3.40.50.720,G3DSA:3.90.25.10,G3DSA:3.90.25.10	SSF51735		00520+4.2.1.47,00051+4.2.1.47		PWY-5740,PWY-7573,PWY-5738,PWY-5739,PWY-66	UPA00128				
aly1489.7	Integrator complex subunit 11	GO:0016180,GO:0016787,GO:0005847,GO:0034472,GO:0032039,GO:0006378,GO:0006379,GO:0022008	CG1972-PA				SM00849,SM01027		PF10996,PF07521,PF16661				G3DSA:3.60.15.10	SSF56281									
aly1489.8	Tubulin polyglutamylase TTLL6	GO:0005737,GO:0036064,GO:0015631,GO:0018095,GO:0051013,GO:0001578,GO:0006464,GO:0003353,GO:0016874	CG4089-PA						PF03133	PS51221				SSF56059,SSF56059									
aly1489.9	Unknown	GO:0008080	CG13759-PA						PF00583	PS51186			G3DSA:3.40.630.30	SSF55729									
aly148908.1	Unknown		n/a																				
aly14896.1	Cyclin-G1	GO:0000711,GO:2000134,GO:0006302,GO:0051726,GO:0005634,GO:0060429,GO:0005700,GO:0016538,GO:0007067,GO:0007143,GO:0051301	CG11525-PD						PF00134				G3DSA:1.10.472.10	SSF47954									
aly14896.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly14896.3	Unknown		n/a																				
aly14896.4	Unknown		n/a																				
aly1491.1	Neurotrimin	GO:0032355,GO:0016337,GO:0005615,GO:0009986,GO:0005886,GO:0030424,GO:0010977,GO:0005911,GO:0060076,GO:0048471,GO:0021549,GO:0043025,GO:0031225	CG42596-PC				SM00409,SM00409,SM00408,SM00408		PF13927,PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly14927.1	Unknown		n/a												249~269,191~211								
aly14927.2	Caspase activity and apoptosis inhibitor 1	GO:0006915	CG32176-PA						PF15335						165~185,430~450,837~857								
aly14927.3	RNA pseudouridylate synthase domain-containing protein 1	GO:0045089,GO:0043723,GO:0009982,GO:0009451,GO:0003723,GO:0050829,GO:0001522	CG6187-PA						PF00849					SSF55120									
aly1493.1	Elongation of very long chain fatty acids protein 4	GO:0007111,GO:0007110,GO:0007112,GO:0000915,GO:0000212,GO:0016021,GO:0030497,GO:0009922,GO:0016740,GO:0030176,GO:0019367,GO:0042761,GO:0051225,GO:0005783	CG6921-PB						PF01151			PS01188				00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598						
aly1493.2	Elongation of very long chain fatty acids protein 7	GO:0006633,GO:0009922,GO:0016021,GO:0030497,GO:0005789,GO:0005575,GO:0016740	CG33110-PA						PF01151							00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1493.3	Unknown	GO:0006909,GO:0005515	CG16791-PA							PS50835													
aly1493.4	Dual specificity testis-specific protein kinase 2	GO:0005737,GO:0007015,GO:0001700,GO:0045873,GO:0005634,GO:0045177,GO:0006468,GO:0030036,GO:0005654,GO:0004674,GO:0007283,GO:0048041,GO:0004713,GO:0004672,GO:0004712,GO:0046872,GO:0005524	CG6027-PA						PF07714	PS50011	PR00109,PR00109,PR00109,PR00109	PS00109	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly1493.5	Unknown		n/a																				
aly1493.6	Unknown		n/a																				
aly1493.7	Unknown		n/a												1~25								
aly1493.8	Unknown		n/a																				
aly1494.1	Alaserpin	GO:0060570,GO:0005783,GO:0005576,GO:0030162,GO:0004867,GO:0010951,GO:0004869,GO:0010955,GO:0005615	CG9453-PB				SM00093		PF00079				G3DSA:2.30.39.10,G3DSA:3.30.497.10	SSF56574										
aly1494.2	Serine protease inhibitor 3/4 (Fragment)	GO:0060570,GO:0005783,GO:0005576,GO:0030162,GO:0004867,GO:0010951,GO:0004869,GO:0010955,GO:0005615	CG9453-PB				SM00093		PF00079				G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:2.30.39.10,G3DSA:2.30.39.10	SSF56574										
aly1494.3	Unknown		n/a																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1494.4	Serine protease inhibitor 3/4 (Fragment)	GO:0005615,GO:0005575,GO:0030162,GO:0004867,GO:0010951,GO:0045861	CG10913-PA				SM00093		PF00079				G3DSA:2.30.39.10,G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574									
aly1494.5	Serine protease inhibitor 3/4 (Fragment)	GO:0060570,GO:0005783,GO:0005576,GO:0030162,GO:0004867,GO:0010951,GO:0004869,GO:0010955,GO:0005615	CG9453-PB				SM00093		PF00079,PF00079				G3DSA:3.30.497.10	SSF56574									
aly1497.1	Unknown	GO:0016021,GO:0005272,GO:0006814	CG13278-PA						PF00858				G3DSA:2.60.470.10,G3DSA:2.60.470.10,G3DSA:2.60.470.10										
aly1497.10	Catalase	GO:0007568,GO:0035206,GO:0020037,GO:0042542,GO:0038001,GO:0016209,GO:0005886,GO:0005777,GO:0016339,GO:0003007,GO:0045471,GO:0042744,GO:0072593,GO:0004096,GO:0008340,GO:0046872,GO:0006979,GO:0055114	CG6871-PA			PIRSF038928	SM01060		PF00199,PF06628	PS51402	PR00067,PR00067,PR00067,PR00067,PR00067,PR00067		G3DSA:2.40.180.10	SSF56634		00630+1.11.1.6,00380+1.11.1.6		PWY-5506					
aly1497.11	UDP-xylose and UDP-N-acetylglucosamine transporter	GO:0005783,GO:0036084,GO:1990569,GO:0036066,GO:0016021,GO:0008643,GO:0005462,GO:0005461,GO:0005460,GO:0015790,GO:0005464,GO:0005794,GO:0005338,GO:0005789,GO:0055085,GO:0015788,GO:0015783,GO:0015782,GO:0015787,GO:0015786,GO:0015784,GO:0015012,GO:0005458,GO:0005456,GO:0005457	CG3774-PA						PF08449	PS51257													
aly1497.12	Calmodulin-binding transcription activator 2	GO:0006351,GO:0016059,GO:0003700,GO:0042826,GO:0005634,GO:0006357,GO:0001077,GO:0045944,GO:0005516,GO:0045893,GO:0003677,GO:0009416,GO:0003682,GO:0014898,GO:0008134,GO:0042803	CG42332-PF				SM01076,SM00015,SM00015,SM00015		PF03859,PF01833	PS51437			G3DSA:2.60.40.10,G3DSA:1.25.40.20	SSF81296,SSF48403	1142~1142								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1497.13	Unknown		n/a												1~21								
aly1497.2	Protein yellow	GO:0060179,GO:0016853,GO:0048067,GO:0005576,GO:0042438,GO:0007275	CG17914-PA						PF03022		PR01366,PR01366,PR01366		G3DSA:2.120.10.30	SSF101898,SSF101898									
aly1497.3	Phosphatidylinositol-glycan biosynthesis class X protein	GO:0016021,GO:0005789,GO:0006506	CG16711-PC				SM00780		PF08320						1081~1101				UPA00196				
aly1497.4	Ankyrin repeat domain-containing protein 13D	GO:0005770,GO:0005886	CG15118-PA				SM00248,SM00248		PF11904,PF12796	PS50297,PS50088			G3DSA:1.25.40.20	SSF48403									
aly1497.5	DnaJ homolog subfamily C member 28	GO:0005575,GO:0008150,GO:0003674	CG43322-PA				SM00271		PF09350,PF00226	PS50076			G3DSA:1.10.287.110	SSF46565	239~259								
aly1497.6	Trifunctional purine biosynthetic protein adenosine-3	GO:0005737,GO:0004641,GO:0004644,GO:0009113,GO:0006189,GO:0005524,GO:0008168,GO:0046872,GO:0004637	CG31628-PA	MF_00138,MF_01930,MF_00741				TIGR00639,TIGR00877,TIGR00878,TIGR00878	PF00586,PF00586,PF00551,PF02769,PF02769,PF02844,PF01071,PF02843	PS50975		PS00184,PS00373	G3DSA:3.90.600.10,G3DSA:3.40.50.170,G3DSA:3.30.470.20,G3DSA:3.40.50.20,G3DSA:3.30.1330.10,G3DSA:3.30.1330.10,G3DSA:3.30.1490.20,G3DSA:3.90.650.10,G3DSA:3.90.650.10,G3DSA:3.90.650.10	SSF55326,SSF56059,SSF53328,SSF56042,SSF51246,SSF52440,SSF55326,SSF56042		00230+6.3.3.1,00970+2.1.2.9,00230+6.3.4.13,00670+2.1.2.2,00230+2.1.2.2,00670+2.1.2.9		PWY-6121,PWY-6122,PWY-6613,PWY-6277	UPA00074				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1497.7	mRNA-decapping enzyme 1A	GO:0005737,GO:0016787,GO:0010603,GO:0000184,GO:0043186,GO:0035195,GO:0005829,GO:0016020,GO:0000932,GO:0010467,GO:0000956,GO:0050072,GO:0005515,GO:0043928,GO:0000288,GO:2000637,GO:0005634,GO:0042802,GO:0045451	CG11183-PA						PF16741,PF06058				G3DSA:2.30.29.30	SSF50729			REACT_21257						
aly1497.8	CTD nuclear envelope phosphatase 1 homolog	GO:0005737,GO:0016791,GO:0006470,GO:0016021,GO:0005635,GO:0031965,GO:0004722,GO:0007474,GO:0005789,GO:0006998,GO:0030514,GO:0071595,GO:0010867	CG1696-PA				SM00577	TIGR02251	PF03031	PS50969			G3DSA:3.40.50.1000	SSF56784									
aly1497.9	AP-2 complex subunit mu	GO:0008565,GO:0008021,GO:0005048,GO:0016183,GO:0006897,GO:0016192,GO:0006886,GO:1903077,GO:0006901,GO:0008289,GO:0005739,GO:0030122,GO:0033227,GO:0005905,GO:0007269,GO:0005886,GO:0030131,GO:0030135,GO:0070062	CG7057-PC			PIRSF005992			PF00928,PF01217	PS51072	PR00314,PR00314,PR00314,PR00314,PR00314,PR00314	PS00991,PS00990	G3DSA:3.30.450.60,G3DSA:2.60.40.1170	SSF64356,SSF49447									
aly149704.1	Unknown		n/a																				
aly1500.1	Unknown	GO:0005575,GO:0003674,GO:0008150	CG9395-PC																				
aly1500.10	RAD50-interacting protein 1	GO:0060628,GO:0005783,GO:0048193,GO:0005789,GO:0003674,GO:1902504,GO:0015031,GO:0070939,GO:0022008,GO:0007049	CG8605-PA						PF04437	PS51386					73~103								
aly1500.11	Lysophospholipid acyltransferase 7	GO:0008654,GO:0016021,GO:0016020,GO:0071617,GO:0016746,GO:0030258	CG9526-PB						PF03062														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1500.12	Unknown		CG32521-PA																				
aly1500.2	NADH dehydrogenase [ubiqui] 1 beta subcomplex subunit 10	GO:0008137,GO:0005739,GO:0006120,GO:0005743,GO:0005747,GO:0070469,GO:0022008,GO:0003954,GO:0055114	CG8844-PA						PF10249														
aly1500.3	Meiosis arrest female protein 1	GO:0010923,GO:0006302,GO:0016020,GO:0005777,GO:0007143,GO:0003723,GO:0003676,GO:0000166,GO:0048477,GO:0010468	CG17018-PD						PF01936,PF11608,PF12872,PF12872,PF12872	PS50102,PS51644,PS50102,PS51644,PS51644			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928									
aly1500.4	26S proteasome non-ATPase regulatory subunit 12	GO:0004175,GO:0005838,GO:0070062,GO:0022624,GO:0043161,GO:0016020,GO:0000502,GO:0006508,GO:0008541	CG1100-PA				SM00088		PF01399				G3DSA:1.10.10.10	SSF46785	150~170								
aly1500.5	72 kDa inositol polyphosphate 5-phosphatase	GO:0005856,GO:0001726,GO:0016311,GO:0046030,GO:0004439,GO:0000139,GO:0046488,GO:0046856,GO:0046855,GO:0005886,GO:0032580,GO:0005930	CG10426-PA				SM00128		PF03372				G3DSA:3.60.10.10	SSF56219									
aly1500.6	Glutamate receptor ionotropic, delta-1	GO:0045211,GO:0070062,GO:0008328,GO:0035235,GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0034220,GO:0030054,GO:0050907,GO:0005886,GO:0035176,GO:0030425,GO:0035249,GO:0004970	CG14076-PC						PF00060				G3DSA:3.40.190.10,G3DSA:1.10.287.70	SSF53850,SSF53850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1500.7	Probable glutamate receptor	GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0045211,GO:0030054,GO:0050907,GO:0004970	CG14076-PC						PF00060				G3DSA:1.10.287.70,G3DSA:3.40.190.10	SSF53850,SSF53850										
aly1500.8	Putative inorganic phosphate cotransporter	GO:0051938,GO:0015293,GO:0044341,GO:0015319,GO:0016021,GO:0006541,GO:0005314,GO:0005316,GO:0015321,GO:0015114,GO:0005886,GO:0006814,GO:0055085,GO:0007005	CG5304-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1500.9	Unknown	GO:0005783,GO:0048193	n/a						PF04437														
aly150360.1	Exosome complex exonuclease RRP44	GO:0071027,GO:0005085,GO:0090305,GO:0043547,GO:0005730,GO:0005634,GO:0016020,GO:0005654,GO:0006364,GO:0005652,GO:0006402,GO:0010468,GO:0071034,GO:0022008,GO:0090503,GO:0016075,GO:0004519,GO:0000176,GO:0000177,GO:0000175,GO:0003723,GO:0006397	CG6413-PA				SM00955		PF00773					SSF50249									
aly15071.1	Unknown		n/a																				
aly1508.1	Inorganic pyrophosphatase	GO:0005737,GO:0035076,GO:0006338,GO:0035206,GO:0004427,GO:0006355,GO:0005634,GO:0000287,GO:0016589,GO:0045747,GO:0006796,GO:0006351,GO:0042766	CG4634-PA						PF00719			PS00387	G3DSA:3.90.80.10	SSF50324		00190+3.6.1.1	REACT_21259,REACT_71						
aly1508.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1508.3	Protein ST7 homolog	GO:0005575,GO:0003674,GO:0016021,GO:0008150	CG3634-PA						PF04184														
aly1508.4	SH2 domain-containing protein 5	GO:0005575,GO:0045211,GO:0003674,GO:0005515,GO:0014069,GO:0008150,GO:0030054	CG33993-PA				SM00462,SM00252		PF00640,PF00017	PS50001,PS01179			G3DSA:2.30.29.30,G3DSA:3.30.505.10	SSF55550,SSF50729									
aly1508.5	Craniofacial development protein 2	GO:0005737,GO:0005634	n/a										G3DSA:3.60.10.10	SSF56219									
aly1508.6	Unknown		n/a																				
aly150803.1	Unknown		n/a																				
aly15087.1	Calsenilin	GO:0005267,GO:0005783,GO:0043523,GO:0007165,GO:0003677,GO:0048266,GO:0001078,GO:0005634,GO:0003714,GO:0048812,GO:0005509,GO:0019233,GO:0005794,GO:0048190,GO:0015459,GO:0006915,GO:0008076,GO:1901379,GO:0072659,GO:0005829,GO:0006357,GO:0006351,GO:0009978,GO:0005244	CG5890-PA				SM00054,SM00054,SM00054		PF13202,PF13499	PS50222,PS50222,PS50222	PR00450,PR00450,PR00450,PR00450	PS00018,PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									
aly15087.2	Biogenesis of lysosome-related organelles complex 1 subunit 3	GO:0003674,GO:0008150,GO:0031083	CG34255-PA						PF15753						126~153								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly15090.1	Zinc finger protein 561	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG15436-PA				SM00355,SM00355			PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly150964.1	GTP-binding protein yptV4	GO:0031982,GO:0007422,GO:0055037,GO:0003924,GO:0005622,GO:0032482,GO:0045202,GO:0005886,GO:0015031,GO:0007264,GO:0016192,GO:0005525	CG3870-PA						PF00071	PS51419			G3DSA:3.40.50.300	SSF52540									
aly151.1	Xanthine dehydrogenase	GO:0008762,GO:0004855,GO:0004854,GO:0005875,GO:0006650,GO:0050660,GO:0043546,GO:0006206,GO:0005777,GO:0006525,GO:0006568,GO:0005506,GO:0016491,GO:0048072,GO:0045471,GO:0016903,GO:0009115,GO:0008340,GO:0055114,GO:0009055,GO:0016614,GO:0005829,GO:0051537,GO:0006144	CG6045-PA			PIRSF000127	SM01008,SM01092		PF02738,PF01799,PF01315,PF03450,PF00941	PS51387,PS51085		PS00197	G3DSA:3.30.365.10,G3DSA:3.30.390.50,G3DSA:3.10.20.30,G3DSA:1.10.150.120,G3DSA:3.90.1170.50,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.465.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10	SSF56176,SSF54665,SSF55447,SSF56003,SSF47741,SSF54292									
aly151.10	Cyclin-dependent kinase 10	GO:0006468,GO:0097472,GO:0071011,GO:0071013,GO:0051726,GO:0000398,GO:0005622,GO:0043410,GO:0004674,GO:0004693,GO:0005634,GO:0005524	CG1362-PA				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly151.11	Zinc finger protein weckle	GO:0003676,GO:0009950,GO:0005634,GO:0005886,GO:0008270,GO:0007311,GO:0008063,GO:0042803	CG15073-PA				SM00868,SM00355,SM00355,SM00355		PF07776,PF13912			PS00028		SSF57716,SSF57667	371~398								
aly151.12	Neuronal acetylcholine receptor subunit alpha-10	GO:0007630,GO:0007632,GO:0006810,GO:0043197,GO:0005262,GO:0006812,GO:0005230,GO:0016020,GO:0030425,GO:0005892,GO:0045211,GO:0004889,GO:0014069,GO:0007268,GO:0060079,GO:0007271,GO:0016021,GO:0030054	CG32538-PE					TIGR00860	PF02931,PF02932		PR00252,PR00252,PR00252,PR00252,PR00254,PR00254,PR00254	PS00236	G3DSA:2.70.170.10,G3DSA:1.20.120.370	SSF90112,SSF63712			REACT_13685						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly151.13	Unknown	GO:0006811,GO:0016020	n/a										G3DSA:1.20.120.370	SSF90112									
aly151.14	T-complex-associated testis-expressed protein 1		CG14325-PB										G3DSA:3.80.10.10	SSF52047	430~450								
aly151.15	Unknown		n/a																				
aly151.16	Unknown		CG15506-PA																				
aly151.17	G-protein coupled receptor 126	GO:0004930,GO:0042552,GO:0016021,GO:0007218,GO:0005886,GO:0007186	CG11318-PA				SM00303		PF01825,PF00002	PS50261,PS50221	PR00249,PR00249,PR00249,PR00249,PR00249,PR00249												
aly151.18	Unknown		n/a										G3DSA:2.40.10.10	SSF50494									
aly151.19	Unknown		n/a																				
aly151.2	Unknown		n/a																				
aly151.20	Unknown		n/a																				
aly151.21	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly151.22	Cytosolic carboxypeptidase 1	GO:0005737,GO:0015631,GO:0035610,GO:0021702,GO:0004181,GO:0050905,GO:0035609,GO:0005739,GO:0021772,GO:0002164,GO:0003407,GO:0008270,GO:0001754,GO:0017076,GO:0006508,GO:0005634,GO:0005829,GO:0007005	CG44533-PH						PF00246				G3DSA:3.40.630.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF53187										
aly151.23	Protein hook	GO:0016197,GO:0005737,GO:0006897,GO:0005874,GO:0008017,GO:0030705,GO:0045467,GO:0045202,GO:0008340,GO:0005768,GO:0006909	CG10653-PA						PF05622,PF05622					SSF116907	466~493,501~542,163~183,229~318,346~415									
aly151.24	Probable RNA helicase armi	GO:0000184,GO:0007616,GO:0030425,GO:0030424,GO:0007293,GO:0045202,GO:0000578,GO:0003678,GO:0005737,GO:0043186,GO:0070725,GO:0005739,GO:0016246,GO:0043025,GO:0005524,GO:0031023,GO:2000002,GO:0016325,GO:0032508,GO:0007317,GO:0007319,GO:0007318,GO:0048477,GO:0005829,GO:0005515,GO:0046843	CG11513-PB						PF14444,PF13087,PF13086,PF13086				G3DSA:3.40.50.300,G3DSA:2.60.40.1260	SSF52540,SSF74853										
aly151.25	Unknown		n/a												53~73								
aly151.26	Gem-associated protein 2	GO:0000387,GO:0000245,GO:0071254,GO:0032797,GO:0005829,GO:0097504,GO:0007629,GO:0034719,GO:0008344,GO:0005681	CG10419-PA			PIRSF038038			PF04938															
aly151.27	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	GO:0047115,GO:0047837,GO:0055114,GO:0016491	CG3609-PA						PF01408				G3DSA:3.30.360.10,G3DSA:3.40.50.720	SSF55347,SSF51735										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly151.28	Cystathionine gamma-lyase	GO:0005737,GO:2001234,GO:0043066,GO:0070062,GO:0051092,GO:0051289,GO:0004123,GO:0000096,GO:0080146,GO:0070814,GO:0044540,GO:0005654,GO:0003824,GO:0019344,GO:0030170,GO:0044524,GO:0018272,GO:0006750,GO:0005634,GO:0043123	CG5345-PA			PIRSF001434			PF01053				G3DSA:3.40.640.10,G3DSA:3.90.1150.10	SSF53383										
aly151.29	Cystathionine gamma-lyase	GO:0005737,GO:0051092,GO:0043066,GO:0004123,GO:0000096,GO:0080146,GO:0070814,GO:0044540,GO:0003824,GO:0019344,GO:0030170,GO:0018272,GO:0006750,GO:0044524,GO:0043123	CG5345-PA			PIRSF001434			PF01053				G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383	368~387									
aly151.3	Unknown		n/a																				
aly151.30	WD repeat and HMG-box DNA-binding protein 1	GO:0005737,GO:0000278,GO:0035185,GO:0005654,GO:0042023,GO:0005515,GO:0003677	CG13350-PA				SM00320,SM00320,SM00320,SM00320		PF12341,PF00400,PF00400	PS50294,PS50294,PS50082,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978										
aly151.31	Mitochondrial enolase superfamily member 1	GO:0044275,GO:0050023,GO:0000287,GO:0016853,GO:0005739	n/a				SM00922		PF13378,PF02746			PS00909	G3DSA:3.30.390.10,G3DSA:3.20.20.120	SSF51604,SSF54826										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly151.32	Receptor-interacting serine/threonine-protein kinase 1	GO:2001237,GO:0005123,GO:0019730,GO:0019731,GO:0006963,GO:0070231,GO:2001238,GO:0097191,GO:0006964,GO:0070926,GO:0031264,GO:2000379,GO:0007165,GO:0007166,GO:0050829,GO:0060545,GO:0035556,GO:0046777,GO:0032403,GO:0043235,GO:0005737,GO:0007257,GO:0061057,GO:0004674,GO:0071356,GO:0009617,GO:0051260,GO:0005739,GO:0033209,GO:0070513,GO:0043065,GO:0097342,GO:1901026,GO:0071550,GO:0004672,GO:0035666,GO:0097300,GO:2001240,GO:0005524,GO:0043123,GO:0036289,GO:0032760,GO:0070266,GO:0045089,GO:0097343,GO:0010939,GO:0006919,GO:0034612,GO:0045087,GO:0006915,GO:0051291,GO:0006952,GO:0043124,GO:0046330,GO:0034142,GO:0006955,GO:0044257,GO:1990000,GO:0006959,GO:0051092,GO:0002756,GO:0031625,GO:0071363,GO:0007399,GO:0012501,GO:0045651,GO:0005829,GO:0045121,GO:0034138,GO:0032481,GO:0005622,GO:0002224,GO:0043154,GO:0097527,GO:0002230,GO:0045944,GO:0042802,GO:0005515,GO:0043068,GO:1902041,GO:0097296,GO:0032757,GO:0001934,GO:0042742	CG5576-PA						PF00531	PS50017			G3DSA:1.10.533.10	SSF47986										
aly151.33	Mitochondrial import receptor subunit TOM40 homolog	GO:0015450,GO:0046930,GO:0006626,GO:0005739,GO:0055085,GO:0005742,GO:0005741,GO:0015288,GO:0006811	CG8330-PA						PF01459				G3DSA:2.40.160.10										
aly151.34	Short stature homeobox protein 2 (Fragment)	GO:0043565,GO:0003700,GO:0005634,GO:0006355,GO:0000976,GO:0003677,GO:0007275	CG34367-PC				SM00389		PF00046	PS50071	PR00031,PR00031	PS00027	G3DSA:1.10.10.60	SSF46689									
aly151.35	Unknown	GO:0003700,GO:0006355,GO:0005634,GO:0000976	CG34367-PC						PF03826	PS50803													

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly151.36	Glycosaminoglycan xylosylkinase homolog	GO:0005794,GO:0005783	CG3631-PC						PF06702,PF13772				G3DSA:3.10.490.10,G3DSA:3.10.490.10	SSF110857,SSF110857									
aly151.37	Insulin receptor	GO:0032148,GO:0048589,GO:0032147,GO:0008585,GO:0008584,GO:0007296,GO:0007169,GO:0051897,GO:0023014,GO:0016020,GO:0004716,GO:0004714,GO:0004713,GO:0042127,GO:0005159,GO:2000252,GO:0060250,GO:0003007,GO:0008361,GO:0007285,GO:0045995,GO:0007568,GO:0007446,GO:0043235,GO:0045793,GO:0043231,GO:0005901,GO:0045821,GO:0045840,GO:0060267,GO:0006468,GO:0019087,GO:0046326,GO:0016049,GO:0043548,GO:0045725,GO:0005520,GO:0007186,GO:0007584,GO:0005524,GO:0005525,GO:0007626,GO:0009887,GO:0007623,GO:2000377,GO:0043410,GO:0051446,GO:0043559,GO:0006635,GO:0005009,GO:0048639,GO:0030307,GO:0031017,GO:0009790,GO:0045429,GO:0007411,GO:0008544,GO:0046777,GO:0001700,GO:0043560,GO:0038083,GO:0045740,GO:0034059,GO:0008284,GO:0060180,GO:0008286,GO:0016322,GO:0006974,GO:0045893,GO:0005911,GO:0048132,GO:0048133,GO:0051425,GO:0006979,GO:0040014,GO:0071363,GO:0005515,GO:0000187,GO:0030325,GO:2000194,GO:0018108,GO:0042593,GO:0032869,GO:0005899,GO:0040007,GO:0010507,GO:0030335,GO:0030238,GO:0046620,GO:0046622,GO:0051290,GO:0005887,GO:0005886,GO:0042220,GO:0008340,GO:0070062,GO:0031994,GO:0031995,GO:0040018,GO:0007391,GO:0007390,GO:0001934	CG18402-PA				SM00261,SM00060,SM00060,SM00060		PF00757,PF07714,PF01030,PF01030	PS50011,PS50853,PS50853,PS50853		PS00107	G3DSA:2.60.40.10,G3DSA:3.80.20.20,G3DSA:2.10.220.10,G3DSA:3.30.200.20,G3DSA:3.80.20.20,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF57184,SSF52058,SSF52058,SSF56112,SSF49265,SSF49265,SSF49265,SSF49265									
aly151.38	UPF0489 protein C5orf22 homolog	GO:0005575,GO:0003674,GO:0046580	CG6818-PB						PF12640						218~242								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly151.39	Lamin-C	GO:0034399,GO:0030833,GO:0070732,GO:0005638,GO:0031081,GO:0006325,GO:0006342,GO:0005635,GO:0005198,GO:0035989,GO:0005652,GO:0007084,GO:0005637,GO:0060415	CG10119-PB						PF00932,PF00038				G3DSA:2.60.40.1260,G3DSA:1.20.5.170	SSF64593,SSF74853,SSF64593	53~94,615~615,317~390,259~305,103~211								
aly151.4	Unknown	GO:0005575,GO:0003674,GO:0008150	CG34370-PG				SM00042		PF00431	PS01180			G3DSA:2.60.120.290	SSF49854									
aly151.40	Superkiller viralicidic activity 2-like 2	GO:0005654,GO:0005730,GO:0071013,GO:0044822,GO:0004004,GO:0004386,GO:0000460,GO:0000398,GO:0003676,GO:0022008,GO:0005634,GO:0005524	CG4152-PA			PIRSF005198	SM00490,SM00487		PF00271,PF00270,PF13234,PF08148	PS51192,PS51194			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	812~835								
aly151.41	Voltage-dependent calcium channel subunit alpha-2/delta-4	GO:0051924,GO:0070588,GO:0005891,GO:0005246,GO:0005245,GO:0046872,GO:0050908	CG4587-PH				SM00327		PF02743,PF13768,PF08399,PF08473	PS50234			G3DSA:3.40.50.410,G3DSA:3.30.450.20	SSF53300									
aly151.42	Protein patched	GO:0006898,GO:0042078,GO:0016311,GO:0007476,GO:0035225,GO:0048103,GO:0048100,GO:0005929,GO:0001746,GO:0007411,GO:0042981,GO:0030228,GO:0005737,GO:0007346,GO:0007367,GO:0007455,GO:0016021,GO:0016020,GO:0008406,GO:0030707,GO:0006508,GO:0048471,GO:0048477,GO:0009880,GO:2000274,GO:0048099,GO:0045879,GO:0055088,GO:0005887,GO:0005886,GO:0042306,GO:0007350,GO:0008158,GO:0030139,GO:0009952,GO:0007224,GO:0007422,GO:0045169,GO:0004888,GO:0005515	CG2411-PA						PF02460,PF02460	PS50156			G3DSA:1.20.1640.10	SSF82866									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly151.43	Ubiquitin-protein ligase E3C	GO:0005737,GO:0016874,GO:0005634,GO:0042787,GO:0004842,GO:0000209	CG3356-PA				SM00119		PF00632,PF00612	PS50237,PS50096			G3DSA:3.30.2160.10	SSF56204	27~47				UPA00143				
aly151.44	SLIT and NTRK-like protein 5	GO:0030534,GO:0007625,GO:0005515,GO:0043235,GO:0021756,GO:0016021,GO:0009410,GO:0051965,GO:0048813,GO:0072358,GO:0007409,GO:0007268,GO:0043588	CG18480-PA				SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly151.45	Tyrosine-protein kinase shark	GO:0045199,GO:0030154,GO:0007306,GO:0007169,GO:0005737,GO:0007254,GO:0038083,GO:0004715,GO:0004713,GO:0016477,GO:0005524,GO:0042127,GO:0006468,GO:0045087,GO:0005938,GO:0043277,GO:0031234,GO:0007394,GO:0007391,GO:0048812,GO:0005102,GO:0046843	CG18247-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00252		PF00017,PF00017,PF12796,PF12796,PF07714	PS50001,PS50088,PS50088,PS50001,PS50297,PS50011	PR00401,PR00401,PR00401,PR00401,PR00401,PR00401	PS00107	G3DSA:3.30.200.20,G3DSA:3.30.505.10,G3DSA:3.30.505.10,G3DSA:1.25.40.20	SSF55550,SSF55550,SSF48403,SSF56112										
aly151.46	Basement membrane-specific heparan sulfate proteoglycan core protein	GO:0008022,GO:0030204,GO:0030203,GO:0048704,GO:0031012,GO:0008104,GO:0042157,GO:0001525,GO:0001523,GO:0005925,GO:0005615,GO:0005576,GO:0002062,GO:0046872,GO:0022617,GO:0060351,GO:0005796,GO:0007603,GO:0043202,GO:0005886,GO:0070062,GO:0005605,GO:0005975,GO:0007420,GO:0001958,GO:0048738,GO:0030198,GO:0006027,GO:0006024,GO:0044281	CG6739-PA				SM00192,SM00192,SM00192,SM00063		PF01392,PF00057,PF00057	PS50068,PS50068,PS50038,PS50068	PR00261,PR00261,PR00261	PS01209,PS01209,PS01209	G3DSA:1.10.2000.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10	SSF63501,SSF57424,SSF57424,SSF57424	648~668									
aly151.47	Unknown		n/a												34~54								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly151.48	Unknown	GO:0030246	CG43164-PC						PF00059	PS50041			G3DSA:3.10.100.10	SSF56436,SSF56436									
aly151.49	Unknown		n/a																				
aly151.5	Pancreatic lipase-related protein 2	GO:0009395,GO:0009791,GO:0047714,GO:0032094,GO:0005615,GO:0033993,GO:0008970,GO:0016042,GO:0005575,GO:0042589,GO:0051384,GO:0005509,GO:0019376,GO:0004806,GO:0004620,GO:0016298,GO:0043434,GO:0047372	CG6295-PA						PF00151		PR00821,PR00821,PR00821,PR00821,PR00823,PR00823,PR00823		G3DSA:3.40.50.1820	SSF53474		00561+3.1.1.3		PWY-6857					
aly151.50	Unknown		n/a																				
aly151.51	Unknown		n/a																				
aly151.6	Unknown		n/a																				
aly151.7	HD domain-containing protein 2	GO:0046872,GO:0008081	CG11050-PA				SM00471		PF13023				G3DSA:1.10.3210.10	SSF109604									
aly151.8	Protein N-terminal glutamine amidohydrolase	GO:0007611,GO:0016811,GO:0008355	CG8253-PA						PF09764				G3DSA:3.10.620.10										
aly151.9	Methionine aminopeptidase 1D, mitochondrial	GO:0004177,GO:0070084,GO:0005739,GO:0070006,GO:0006508,GO:0046872,GO:0008235	CG5188-PA	MF_01974				TIGR00500	PF00557		PR00599,PR00599,PR00599,PR00599		G3DSA:3.90.230.10	SSF55920									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly151032.1	Intersectin-2	GO:0005737,GO:0008021,GO:0008104,GO:0006897,GO:0007269,GO:0042734,GO:0005070,GO:0005813,GO:0045179,GO:0009967,GO:0045746,GO:0002052,GO:0051124,GO:0005509,GO:0005515,GO:0005886,GO:0005089,GO:0045860,GO:1903861,GO:0048488,GO:0070062	CG1099-PD				SM00326		PF00018	PS50002	PR00452,PR00452,PR00452,PR00452		G3DSA:2.30.30.40	SSF50044									
aly1511.1	Unknown	GO:0005575,GO:0003674,GO:0008150,GO:0005515	CG42313-PA						PF13927	PS50835			G3DSA:2.60.40.10	SSF48726									
aly1511.2	Cell adhesion molecule 4	GO:0007155,GO:0016021	CG34113-PO				SM00409,SM00409,SM00409,SM00408,SM00408,SM00408		PF00047,PF07679,PF08205	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726									
aly15122.1	Small conductance calcium-activated potassium channel protein	GO:0009881,GO:0071805,GO:0006813,GO:0016057,GO:0016021,GO:0016286,GO:0005516,GO:0005886,GO:0043025,GO:0015269,GO:0007165	CG10706-PS				SM01053		PF03530,PF07885,PF02888		PR01451,PR01451		G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81327,SSF81324	449~476								
aly15122.2	Unknown		n/a																				
aly1513.1	Protein vein	GO:0016203,GO:0007494,GO:0030031,GO:0008586,GO:0035556,GO:0035310,GO:0007298,GO:0008355,GO:0007479,GO:0005615,GO:0007476,GO:0007477,GO:0007474,GO:0043066,GO:0045742,GO:0008284,GO:0007482,GO:0005154,GO:0007173,GO:0005886,GO:0007267,GO:0008201,GO:0007420,GO:0007422,GO:0005622,GO:0005576	CG10491-PA				SM00408,SM00409		PF07679,PF00008	PS50835,PS50026		PS01186,PS00022	G3DSA:2.60.40.10,G3DSA:2.10.25.10	SSF57196,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1513.2	Mitotic spindle assembly checkpoint protein MAD2A	GO:0045841,GO:1901673,GO:0045930,GO:0090267,GO:0042177,GO:0005875,GO:0051301,GO:0005737,GO:0007346,GO:0072686,GO:0005634,GO:0005635,GO:0000922,GO:0005654,GO:0043066,GO:0048471,GO:0042802,GO:0060564,GO:0090231,GO:0000278,GO:1990047,GO:0005819,GO:0000775,GO:0000776,GO:0000777,GO:0000070,GO:0005643,GO:0005829,GO:0005828,GO:0007094,GO:0042803,GO:0007093	CG17498-PA						PF02301	PS50815			G3DSA:3.30.900.10	SSF56019										
aly1513.3	ATP-binding cassette sub-family B member 7, mitochondrial	GO:0043190,GO:0042626,GO:0016021,GO:0006879,GO:0015232,GO:0005215,GO:0015886,GO:0016226,GO:0005743,GO:0055085,GO:0005524	CG7955-PA				SM00382		PF00856,PF00664,PF00005	PS50893,PS50929,PS50280		PS00211	G3DSA:1.20.1560.10,G3DSA:3.90.1410.10,G3DSA:3.40.50.300	SSF82199,SSF90123,SSF52540									
aly1513.4	Lebercilin-like protein	GO:0006909	CG6652-PA						PF15619						70~114,169~203,212~232,119~160								
aly1513.5	Unknown		n/a																				
aly1513.6	Neuropeptide FF receptor 2	GO:0009582,GO:0008528,GO:0004930,GO:0042277,GO:0015629,GO:2000479,GO:0045761,GO:0016021,GO:0005886,GO:0007218,GO:0004983,GO:0032870,GO:0007268,GO:1901652,GO:0005887,GO:0008188,GO:0008340,GO:0007186,GO:0043408	CG10823-PA						PF00001	PS50262	PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly15157.1	StAR-related lipid transfer protein 3 (Fragment)	GO:0005770,GO:0015485,GO:0017127,GO:0006694	CG3522-PA						PF01852	PS50848			G3DSA:3.30.530.20	SSF55961									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly15157.2	Histone H1E	GO:0005634,GO:0000786,GO:0006334,GO:0006333,GO:0003677	CG33864-PA				SM00526		PF00538	PS51504	PR00624,PR00624,PR00624,PR00624,PR00624		G3DSA:1.10.10.10	SSF46785									
aly15159.1	Protein brunelleschi	GO:0007111,GO:0007110,GO:0006891,GO:0007112,GO:0036063,GO:0000916,GO:0005794,GO:0032313,GO:0000281,GO:0017112,GO:0030008,GO:0043147,GO:0043087,GO:0048137,GO:0005737,GO:0043547	CG2478-PA																				
aly15162.1	von Willebrand factor D and EGF domain-containing protein	GO:0006909,GO:0005044,GO:0016021,GO:0006910,GO:0046331,GO:0042742,GO:0005515,GO:0009986,GO:0042834,GO:0005576	CG6124-PC				SM00181,SM00181,SM00181																
aly15163.1	Unknown		n/a										G3DSA:3.30.40.10										
aly151803.1	Unknown		n/a										G3DSA:3.60.10.10										
aly15192.1	Calcium release-activated calcium channel protein 1	GO:0004252,GO:0015279,GO:0016020,GO:0007399,GO:0002115,GO:0016021,GO:0051928,GO:0051533,GO:0005887,GO:0005886	CG11430-PE						PF07856														
aly15192.2	MORN repeat-containing protein 3	GO:0005575,GO:0003674,GO:0005634,GO:0008150	CG30429-PA				SM00698,SM00698,SM00698,SM00698,SM00698,SM00698		PF02493,PF02493,PF02493,PF02493,PF02493,PF02493				G3DSA:2.20.110.10,G3DSA:2.20.110.10	SSF82185,SSF82185									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly15192.3	28S ribosomal protein S22, mitochondrial	GO:0003735,GO:0006412,GO:0005739,GO:0005763	CG12261-PA						PF10245						87~107								
aly15192.4	Zinc finger CCHC domain containing protein 8 homolog	GO:0005575,GO:0008150,GO:0008270,GO:0003676	CG4622-PA				SM00581		PF04046						724~744								
aly15192.5	Small integral membrane protein 14	GO:0016021,GO:0005783,GO:0005789	CG13585-PA						PF11027														
aly152.1	Unknown	GO:0055088,GO:0004674,GO:0006468,GO:0005524,GO:0042594	CG42856-PB						PF02149	PS50032			G3DSA:3.30.310.80	SSF103243									
aly152.10	Gamma-secretase subunit pen-2	GO:0007219,GO:0004175,GO:0055037,GO:0005770,GO:0070765,GO:0007220,GO:0005886,GO:0016021	CG33198-PA						PF10251														
aly152.11	Leucine-rich repeat-containing protein 34		n/a				SM00368,SM00368,SM00368,SM00368,SM00368,SM00368,SM00368						G3DSA:3.80.10.10	SSF52047									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly152.12	Ankyrin repeat and SOCS box protein 3	GO:0005737,GO:0007016,GO:0005200,GO:0046427,GO:0019730,GO:0008283,GO:0005811,GO:0005622,GO:0016567,GO:0043066,GO:0003723,GO:0005515,GO:0007169,GO:0035556,GO:0001751,GO:0051298	CG33106-PC				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF13606,PF12796,PF12796	PS50088,PS50297,PS50088,PS50088,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403									
aly152.13	Unknown		CG7953-PA				SM00700		PF06585														
aly152.14	26S proteasome complex subunit DSS1	GO:0000502,GO:0008233,GO:0000724,GO:0022008,GO:0006508	CG13779-PA						PF05160						57~75								
aly152.2	Serine/threonine-protein kinase SIK3 homolog	GO:0006468,GO:0000287,GO:0055088,GO:0004674,GO:0042594,GO:0004672,GO:0005524	CG42856-PB				SM00220		PF00069	PS50011		PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.8.10	SSF56112									
aly152.3	Serine/threonine-protein kinase SIK3 homolog	GO:0006468,GO:0000287,GO:0055088,GO:0004674,GO:0042594,GO:0005524	CG42856-PB										G3DSA:3.30.200.20	SSF56112									
aly152.4	Ubiquitin carboxyl-terminal hydrolase 2	GO:0004843,GO:0048511,GO:0006511,GO:0048471,GO:0046872,GO:0016579,GO:0036459	CG14619-PI						PF00443	PS50235		PS00973,PS00972	G3DSA:2.20.210.10	SSF54001									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly152.5	26S proteasome non-ATPase regulatory subunit 13	GO:0004175,GO:0005838,GO:0022624,GO:0043161,GO:0005515,GO:0006508,GO:0007096,GO:0008541	CG10230-PA				SM00088		PF01399					SSF46785	136~156								
aly152.6	Protein bric-a-brac 1	GO:0007478,GO:0048092,GO:0048086,GO:0003700,GO:0007455,GO:0005634,GO:0007548,GO:0048071,GO:0048070,GO:0006355,GO:0006351,GO:0003677,GO:0003680,GO:0046660	CG8924-PB				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695,SSF46689	369~389								
aly152.7	Unknown	GO:0003677	n/a										G3DSA:1.10.10.60	SSF46689									
aly152.8	Ets DNA-binding protein pokkuri	GO:0048666,GO:0051168,GO:0008406,GO:0046578,GO:0042058,GO:0045467,GO:0007298,GO:0030178,GO:0003705,GO:0035155,GO:0005737,GO:0043565,GO:0001191,GO:0042461,GO:0000122,GO:0005634,GO:0001709,GO:0000165,GO:0005654,GO:0007517,GO:0048749,GO:0009880,GO:0035157,GO:0060233,GO:0007254,G	CG15085-PA						PF02198	PS51433			G3DSA:1.10.150.50	SSF47769									
aly152.9	Unknown	GO:0005515	n/a				SM00192			PS50835,PS50068			G3DSA:4.10.400.10,G3DSA:2.60.40.10	SSF57424,SSF48726									
aly15220.1	Connectin	GO:0016200,GO:0007156,GO:0009986,GO:0044295,GO:0031594,GO:0005886,GO:0007155,GO:0007413,GO:0031225	CG7503-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855				G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly15220.10	Unknown		n/a																				
aly15220.11	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly15220.12	Nuclear valosin-containing protein-like	GO:0005737,GO:0005730,GO:0005634,GO:0016020,GO:0005739,GO:0016887,GO:0005886,GO:0022008,GO:0044822,GO:0005524	CG8571-PA				SM00382,SM00382		PF16725,PF00004,PF00004			PS00674,PS00674	G3DSA:1.10.8.60,G3DSA:1.10.8.60,G3DSA:1.10.8.60,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540										
aly15220.2	Connectin	GO:0016200,GO:0007156,GO:0009986,GO:0044295,GO:0031594,GO:0005886,GO:0007155,GO:0007413,GO:0031225	CG7503-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF13855				G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly15220.3	Unknown		n/a										G3DSA:2.60.40.10	SSF48726									
aly15220.4	Unknown		CG9170-PB																				
aly15220.5	Centrosomal protein of 164 kDa	GO:0006996,GO:0042384,GO:0005615,GO:0006281,GO:0000086,GO:0005813,GO:0005829,GO:0005814,GO:0005654,GO:0005515,GO:0007067,GO:0000278,GO:0051301,GO:0097539	CG9170-PB				SM00456		PF00397	PS50020		PS01159	G3DSA:2.20.70.10	SSF51045	844~882,766~823								
aly15220.6	26S proteasome non-ATPase regulatory subunit 8	GO:0004175,GO:0005838,GO:0070062,GO:0022624,GO:0008283,GO:0043161,GO:0005634,GO:0009987,GO:1903955,GO:0007052,GO:0006511,GO:0006508,GO:0000502,GO:0000022,GO:0022008,GO:0008541,GO:0031647	CG4157-PA						PF10075				G3DSA:1.20.190.10,G3DSA:1.10.10.10										
aly15220.7	Nuclear RNA export factor 1	GO:0005737,GO:0030534,GO:0016973,GO:0051168,GO:0047485,GO:0007616,GO:0005635,GO:0031965,GO:0000166,GO:0005654,GO:0003723,GO:0005515,GO:0006378,GO:0006406	CG1664-PA						PF13855,PF03943	PS51450,PS51450,PS50177			G3DSA:3.80.10.10,G3DSA:3.10.450.50,G3DSA:1.10.8.10	SSF52058,SSF46934,SSF54427									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly15220.8	Insulin-like receptor	GO:0042127,GO:0005887,GO:0048589,GO:0007626,GO:0030307,GO:0008286,GO:0008585,GO:0046622,GO:0009790,GO:0007296,GO:0008340,GO:0007411,GO:0005899,GO:0046777,GO:0001700,GO:0016049,GO:0040007,GO:0016021,GO:0051290,GO:0043560,GO:0004713,GO:0005520,GO:0046872,GO:0010507,GO:0005524,GO:0008284,GO:0060180,GO:0006468,GO:0007623,GO:0046620,GO:0007584,GO:2000252,GO:0060250,GO:0016322,GO:2000377,GO:0006974,GO:0008361,GO:0007285,GO:0005911,GO:0005886,GO:0042220,GO:0048133,GO:0006979,GO:0034059,GO:0048132,GO:0045793,GO:0007568,GO:0007446,GO:0043559,GO:0040018,GO:0040014,GO:0007391,GO:0007390,GO:0005515,GO:0005009,GO:0043548	CG18402-PA				SM00261		PF00757,PF01030,PF01030	PS50853,PS50853			G3DSA:3.80.20.20,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.10.220.10,G3DSA:2.60.40.10,G3DSA:3.80.20.20	SSF49265,SSF49265,SSF57184,SSF49265,SSF52058,SSF52058										
aly15220.9	Unknown		CG11409-PB												172~192								
aly1523.1	Unknown		n/a										G3DSA:3.30.40.10	SSF57903	134~161								
aly1523.10	Lipase member H	GO:0006629,GO:0052689,GO:0016042,GO:0005575,GO:0003824,GO:0008150,GO:0005886,GO:0003674,GO:0004620,GO:0008201,GO:0005615	CG18258-PA						PF00151		PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly1523.11	Pancreatic lipase-related protein 2	GO:0009395,GO:0047714,GO:0004806,GO:0006629,GO:0005615,GO:0005575,GO:0003824,GO:0008150,GO:0005509,GO:0019376,GO:0003674,GO:0004620,GO:0047372	CG18258-PA						PF00151		PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1523.12	Pancreatic lipase-related protein 2	GO:0009395,GO:0047714,GO:0004806,GO:0006629,GO:0005615,GO:0005575,GO:0003824,GO:0008150,GO:0005509,GO:0019376,GO:0003674,GO:0004620,GO:0047372	CG18258-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly1523.13	Lipase member I	GO:0006629,GO:0016020,GO:0052689,GO:0016042,GO:0005575,GO:0003824,GO:0005576,GO:0008150,GO:0005886,GO:0003674,GO:0004620,GO:0008201,GO:0005615	CG18258-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly1523.14	Unknown		n/a																				
aly1523.2	Unknown	GO:0016831,GO:0019752,GO:0030170	CG1486-PA																				
aly1523.3	Unknown		n/a																				
aly1523.4	Lactosylceramide 4-alpha-galactosyltransferase	GO:0005795,GO:0006629,GO:0006486,GO:0035248,GO:0016021,GO:0009247,GO:0000139,GO:0045747,GO:0043066,GO:0008378,GO:0006688,GO:0006664,GO:0008376,GO:0050512	CG17223-PA						PF04488,PF04572					SSF53448					UPA00378				
aly1523.5	Zinc finger and SCAN domain-containing protein 2	GO:0003700,GO:0005634,GO:0030154,GO:0007283,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0007275,GO:0006351	CG17328-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776,PF13912,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57716									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1523.6	40S ribosomal protein S24	GO:0022627,GO:0000166,GO:0003735,GO:0005622,GO:0006412,GO:0005840	CG3751-PA	MF_00545					PF01282			PS00529	G3DSA:3.30.70.330	SSF54189									
aly1523.7	Monocarboxylate transporter 14	GO:0015718,GO:0015293,GO:0008028,GO:0016021,GO:0034220,GO:0005886,GO:0055085	CG3456-PA						PF07690,PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1523.8	Monocarboxylate transporter 14	GO:0015718,GO:0015293,GO:0008028,GO:0016021,GO:0034220,GO:0005886,GO:0055085	CG3409-PA						PF07690,PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	470~490								
aly1523.9	Hexosaminidase D	GO:0005737,GO:0004563,GO:0005975,GO:0005634,GO:0004553	CG7985-PA						PF00728				G3DSA:3.20.20.80	SSF51445		00604+3.2.1.52,00520+3.2.1.52,00511+3.2.1.52,00603+3.2.1.52,00513+3.2.1.52,00531+3.2.1.52		PWY-6902					
aly15231.1	Unknown		n/a																				
aly15248.1	Unknown	GO:0005214,GO:0040003,GO:0005578	CG14534-PA				SM00690		PF03103														
aly15270.1	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6467-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly152804.1	Unknown		n/a						PF14529				G3DSA:3.60.10.10	SSF56219	46~66								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly15289.1	Probable multidrug resistance-associated protein lethal(2)03659	GO:0043190,GO:0042626,GO:0005215,GO:0016021,GO:0006810,GO:0042060,GO:0007275,GO:0008559,GO:0055085,GO:0005524	CG7627-PA				SM00382		PF00005,PF00664	PS50929,PS50893		PS00211	G3DSA:1.20.1560.10,G3DSA:3.40.50.300	SSF52540,SSF90123									
aly1529.1	Unknown		n/a																				
aly1529.2	Unknown		n/a																				
aly1529.3	Unknown		n/a																				
aly15300.1	Unknown		n/a																				
aly15300.2	Unknown		n/a																				
aly1531.1	Titin	GO:0035206,GO:0007498,GO:0030017,GO:0005875,GO:0051301,GO:0007062,GO:0007517,GO:0007519,GO:0031674,GO:0003779,GO:0030018,GO:0016203,GO:0008307,GO:0045214,GO:0000794,GO:0007520,GO:0007522,GO:0005863,GO:0007525,GO:0040011,GO:0004687,GO:0005515,GO:0007076	CG1915-PP				SM00060,SM00060,SM00060,SM00060,SM00060,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00326,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409		PF14604,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF00041,PF00041,PF00041,PF00041,PF00041	PS50835,PS50002,PS50835,PS50835,PS50835,PS50853,PS50835,PS50835,PS50835,PS50853,PS50853,PS50835,PS50835,PS50853,PS50853,PS50835,PS50835,PS50835,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.30.30.40,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF49265,SSF50044,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726	566~586							
aly1531.10	Unknown		n/a												43~70								
aly1531.11	Unknown		n/a												26~64								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1531.12	Cold shock domain-containing protein E1	GO:0005737,GO:0042714,GO:0070966,GO:0003676,GO:0005794,GO:0044822,GO:0017148,GO:0005743,GO:0006355,GO:0046331,GO:0005886,GO:0003730,GO:0005515,GO:0003677,GO:0070937,GO:0009047	CG7015-PB				SM00357,SM00357,SM00357,SM00357,SM00357		PF12901,PF00313,PF00313,PF00313,PF00313,PF00313			PS00352,PS00352	G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:2.40.50.140	SSF50249,SSF50249,SSF50249,SSF50249,SSF50249										
aly1531.13	Peptidoglycan recognition protein	GO:0032500,GO:0005887,GO:0005515,GO:0008329,GO:0008745,GO:0045087,GO:0006955,GO:0006965,GO:0008063,GO:0006952,GO:0016045,GO:0050830,GO:0005576,GO:0008270,GO:0008592,GO:0009253,GO:0032494,GO:0016019,GO:0042834	CG11709-PA				SM00701,SM00644		PF01510				G3DSA:3.40.80.10	SSF55846									
aly1531.14	Peptidoglycan-recognition protein SC2	GO:0008745,GO:0045087,GO:0009253,GO:0006952,GO:0045824,GO:0008270,GO:0005887,GO:0006955,GO:0042834,GO:0005576	CG14745-PA				SM00701		PF01510				G3DSA:3.40.80.10	SSF55846									
aly1531.15	UNC93-like protein	GO:0003674,GO:0016021,GO:0008150,GO:0005886	CG4928-PA						PF05978				G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1531.16	DnaJ homolog subfamily C member 11	GO:0005743,GO:0070062,GO:0005739	CG8531-PA				SM00271		PF00226,PF11875	PS50076	PR00625,PR00625,PR00625,PR00625	PS00636	G3DSA:1.10.287.110	SSF46565									
aly1531.17	WD repeat-containing protein 47	GO:0005737,GO:0005575,GO:0008150,GO:0003674,GO:0005874,GO:0007275	CG2812-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00668		PF00400,PF00400	PS50897,PS50082,PS50082,PS50082,PS50082,PS50294,PS50082			G3DSA:2.130.10.10	SSF50978									
aly1531.18	Cytochrome P450 6B7	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0070330,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1531.19	Cytochrome P450 6B3	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0070330,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA										G3DSA:1.10.630.10				REACT_13433						
aly1531.2	Unknown	GO:0005576,GO:0008150,GO:0008083,GO:0008201	CG1221-PA						PF01091,PF01091				G3DSA:2.30.90.10										
aly1531.20	Cytochrome P450 6a2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0046680,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA						PF00067				G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly1531.21	Unknown		CG13288-PC						PF15860														
aly1531.22	Unknown		n/a										G3DSA:3.30.40.10	SSF57997,SSF57903	119~167								
aly1531.23	Unknown		n/a																				
aly1531.24	Unknown		n/a																				
aly1531.3	Unknown		n/a																				
aly1531.4	Syntaxin-6	GO:0007032,GO:0005794,GO:0043195,GO:0016192,GO:0048193,GO:0016081,GO:0016021,GO:0006906,GO:0090161,GO:0005769,GO:0042147,GO:0032588,GO:0005515,GO:0007269,GO:0005886,GO:0005484,GO:0006886,GO:0032880,GO:0031201,GO:0048471	CG7736-PC				SM00397		PF09177,PF05739	PS50192			G3DSA:1.20.5.110,G3DSA:1.20.58.90	SSF58038,SSF47661	47~67,196~223		REACT_11184						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1531.5	Exosome component 10	GO:0071044,GO:0000184,GO:0071028,GO:0000176,GO:0071027,GO:0071048,GO:0009048,GO:0003676,GO:0005737,GO:0006139,GO:0008408,GO:0005730,GO:0005634,GO:0016020,GO:0000166,GO:0005654,GO:0005652,GO:0010468,GO:0071035,GO:0071034,GO:0044822,GO:0000460,GO:0035327,GO:0090503,GO:0000178,GO:0004532,GO:0000956,GO:0006378	CG7292-PB				SM00341,SM00474		PF01612,PF00570,PF08066	PS50967			G3DSA:3.30.420.10	SSF47819,SSF53098									
aly1531.6	Unknown		n/a																				
aly1531.7	Discoidin domain-containing receptor 2	GO:0038063,GO:0048146,GO:0031214,GO:0018108,GO:0001503,GO:0007165,GO:0030500,GO:0007169,GO:0005925,GO:0046777,GO:0070062,GO:0016021,GO:0038062,GO:0004714,GO:0004713,GO:0004672,GO:0010763,GO:0003416,GO:0045669,GO:0005524,GO:0090091,GO:0006468,GO:0016324,GO:0035988,GO:0005887,G	CG33531-PF				SM00231,SM00219		PF07714,PF00754	PS50011,PS50022	PR00109,PR00109,PR00109,PR00109	PS01286,PS00109	G3DSA:1.10.510.10,G3DSA:2.60.120.260,G3DSA:3.30.200.20	SSF49785,SSF56112									
aly1531.8	Ubiquitin-conjugating enzyme E2-22 kDa	GO:0005737,GO:0031625,GO:0070628,GO:0051726,GO:0004842,GO:0005634,GO:0061630,GO:0016881,GO:0043161,GO:0016874,GO:0000209,GO:0005524	CG8284-PA				SM00212,SM00165		PF00627,PF00179	PS50030,PS50127		PS00183	G3DSA:3.10.110.10,G3DSA:1.10.8.10	SSF46934,SSF54495					UPA00143				
aly1531.9	Bestrophin-3	GO:0043271,GO:1902476,GO:0016021,GO:0005777,GO:0034707,GO:0006820,GO:0005886,GO:0015698,GO:0005253,GO:0005254	CG10173-PA						PF01062														
aly15317.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1532.1	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0060179,GO:0009744,GO:0046872,GO:0070328,GO:0006629,GO:0017105,GO:0019216,GO:0031410,GO:0006723,GO:0005811,GO:0006631,GO:0042593,GO:0042811,GO:0048047,GO:0004768,GO:0010506,GO:0016021,GO:0055114,GO:0005783	CG5887-PA						PF00487		PR00075,PR00075,PR00075,PR00075,PR00075,PR00075													
aly1532.2	Unknown		n/a																				
aly1532.3	Unknown		CG15887-PA																				
aly1532.4	Aminopeptidase M1-C	GO:0004177,GO:0031090,GO:0008270,GO:0006508,GO:0008237,GO:0005783	CG8774-PA						PF01433					SSF63737									
aly1532.5	Glutamyl aminopeptidase	GO:0004177,GO:0033227,GO:0042277,GO:0008283,GO:0016021,GO:0006725,GO:0003081,GO:0031983,GO:0008270,GO:0012506,GO:0070006,GO:0006508,GO:0016477,GO:0008237	CG8773-PB						PF11838,PF01433		PR00756,PR00756,PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF63737,SSF55486									
aly1532.6	Odorant receptor 13a	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG15302-PA						PF02949														
aly1532.7	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0060179,GO:0009744,GO:0046872,GO:0070328,GO:0005783,GO:0017105,GO:0019216,GO:0031410,GO:0006723,GO:0005811,GO:0006631,GO:0042593,GO:0042811,GO:0048047,GO:0004768,GO:0010506,GO:0016021,GO:0055114	CG5887-PA						PF00487		PR00075,PR00075,PR00075,PR00075,PR00075,PR00075	PS00476						PWY-5987,PWY-5996						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1532.8	Neuromedin-U receptor 2	GO:0005229,GO:0007631,GO:0036401,GO:0007204,GO:0006940,GO:0006821,GO:0008188,GO:0001607,GO:0007417,GO:0004930,GO:0016021,GO:0042924,GO:0043006,GO:0048265,GO:0007186,GO:0005525,GO:0007625,GO:0019722,GO:1902476,GO:0007218,GO:0006816,GO:0002023,GO:0005887,GO:0007267,GO:0048016,GO:0007200,GO:0005829,GO:0050482,GO:0005622	CG9918-PD						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1532.9	Neuromedin-U receptor 2	GO:0005229,GO:0036401,GO:0007204,GO:0006821,GO:0008188,GO:0001607,GO:0007417,GO:0004930,GO:0016021,GO:0042924,GO:0043006,GO:0048265,GO:0007186,GO:0005525,GO:0007625,GO:1902476,GO:0007218,GO:0006816,GO:0002023,GO:0005887,GO:0005886,GO:0048016,GO:0007200,GO:0005829,GO:0050482,GO:0005622	CG8784-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly153429.1	Unknown		n/a																				
aly15357.1	Unknown		n/a																				
aly15357.2	Unknown	GO:0032027,GO:0005516,GO:0005515,GO:0005938	CG18285-PA						PF00612	PS50096			G3DSA:1.20.5.190										
aly153829.1	Unknown		n/a																				
aly153842.1	Unknown		n/a						PF13961														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly15386.1	Leucine-rich repeat neuronal protein 2	GO:0016021,GO:0006967,GO:0004888,GO:0007165,GO:0005515,GO:0007155,GO:0004872	CG5528-PA				SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF13306				G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058										
aly15386.2	Toll-like receptor 11	GO:0009617,GO:0002755,GO:0050729,GO:0006954,GO:0016021,GO:0050707,GO:0006967,GO:0034170,GO:0004888,GO:0007165,GO:0005515,GO:0045087	CG5528-PA						PF01582	PS50104			G3DSA:3.40.50.10140	SSF52200	3~3,29~29								
aly15386.3	Toll-like receptor 1	GO:0016020,GO:0005887,GO:0042116,GO:0005886,GO:0006967,GO:0034130,GO:0035354,GO:0007165,GO:0071727,GO:0042535,GO:0016021,GO:0050707,GO:0045087,GO:0006954,GO:0006955,GO:0002755,GO:0045410,GO:0030670,GO:0042495,GO:0004888,GO:0005515,GO:0046982,GO:0004872	CG5528-PA						PF01582	PS50104			G3DSA:3.40.50.10140	SSF52200									
aly1539.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00216,PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473	326~346,46~66		REACT_15518						
aly1539.10	Unknown		n/a																				
aly1539.11	Unknown		n/a																				
aly1539.12	Unknown		n/a																				
aly1539.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1539.14	G/T mismatch-specific thymine DNA glycosylase	GO:0005080,GO:0006298,GO:0030983,GO:0009790,GO:0032091,GO:0043566,GO:0000122,GO:0005634,GO:0040029,GO:0005654,GO:0003690,GO:0042803,GO:0006284,GO:0019104,GO:0006289,GO:0001104,GO:0008263,GO:0005886,GO:0035562,GO:0080111,GO:0032183,GO:0006974,GO:0006351,GO:0016568	CG1981-PA				SM00986,SM00987		PF03167				G3DSA:3.40.470.10	SSF52141										
aly1539.15	Zinc finger protein 667	GO:0005737,GO:0005819,GO:0003700,GO:0005634,GO:0003712,GO:0006357,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0005876,GO:0006351	CG8474-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667,SSF57667										
aly1539.16	Hexokinase type 2	GO:0005975,GO:0060361,GO:0005829,GO:0004396,GO:0004340,GO:0019158,GO:0046835,GO:0019318,GO:0051156,GO:0001678,GO:0008865,GO:0006096,GO:0005524,GO:0005536	CG3001-PA						PF03727,PF00349	PS51748	PR00475,PR00475,PR00475,PR00475,PR00475,PR00475,PR00475	PS00378	G3DSA:3.40.367.20,G3DSA:3.30.420.40	SSF53067,SSF53067		00010+2.7.1.1,00051+2.7.1.1,00520+2.7.1.1,00524+2.7.1.1,00521+2.7.1.1,00052+2.7.1.1,00500+2.7.1.1	REACT_474,REACT_15518	PWY-2722,PWY-621,PWY-5661						
aly1539.17	Epidermal growth factor receptor kinase substrate 8-like protein 2	GO:0005737,GO:0043234,GO:0043547,GO:1900029,GO:0035023,GO:0031982,GO:0003779,GO:0005886,GO:0007266,GO:0032587,GO:0070062	CG8907-PB											SSF47769									
aly1539.18	Epidermal growth factor receptor kinase substrate 8	GO:0048149,GO:0070358,GO:0005903,GO:0045202,GO:0030054,GO:0030832,GO:0070062,GO:0016601,GO:0031532,GO:0008344,GO:0003779,GO:0032420,GO:0051017,GO:0051016,GO:0030426,GO:0008360,GO:0014069,GO:0005938,GO:0051764,GO:0032587,GO:0031982,GO:0010458,GO:0036336,GO:0035591,GO:0048365,GO:0017146	CG8907-PB				SM00326		PF08416	PS50002			G3DSA:2.30.30.40	SSF50044,SSF50729	247~267									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1539.19	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	GO:0030036,GO:0030175,GO:0005902,GO:0071944,GO:0010642,GO:0005737,GO:0045177,GO:0007476,GO:0017081,GO:0070293,GO:0042048,GO:0032782,GO:0045859,GO:0001726,GO:0034635,GO:0012505,GO:0014067,GO:0031528,GO:0016055,GO:0051898,GO:0005515,GO:2000146	CG10939-PA				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156										
aly1539.2	Facilitated trehalose transporter Tret1-2 homolog	GO:0005355,GO:0035428,GO:0015992,GO:0005353,GO:0015771,GO:0005215,GO:0016021,GO:0016020,GO:0046323,GO:0005887,GO:0005886,GO:0005351,GO:0055085	CG8234-PA						PF00083	PS50850		PS00217,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	216~243								
aly1539.20	Unknown		n/a																				
aly1539.21	Unknown		CG14445-PC																				
aly1539.3	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850		PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1539.4	Lysine-specific demethylase lid	GO:0070822,GO:0032922,GO:0006351,GO:0045893,GO:0043970,GO:0006325,GO:0034721,GO:0005634,GO:0043992,GO:0007526,GO:0034720,GO:0016706,GO:0016577,GO:0032453,GO:0034647,GO:0008270,GO:0005515,GO:0003677,GO:0055114,GO:0045475	CG9088-PA				SM00249,SM00249,SM00558		PF02373,PF02928,PF08429,PF00628	PS51184,PS50016			G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57903,SSF51197,SSF51197,SSF57903									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1539.5	Lysine-specific demethylase 5D	GO:0070822,GO:0043970,GO:0006325,GO:0005634,GO:0043992,GO:0034720,GO:0016706,GO:0032453,GO:0034647,GO:0008270,GO:0005515,GO:0003677,GO:0055114,GO:0045475	CG9088-PA				SM01014,SM00501,SM00545		PF02375,PF01388	PS51011,PS51183			G3DSA:1.10.150.60	SSF46774									
aly1539.6	Calsyntenin-1	GO:0016339,GO:0016020,GO:0045211,GO:0005576,GO:0005509,GO:0005887,GO:0007268,GO:0044331,GO:0007156	CG11059-PC				SM00112,SM00112		PF00028	PS50268,PS50268	PR00205,PR00205,PR00205		G3DSA:2.60.120.200,G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49899,SSF49313									
aly1539.7	Unknown		n/a																				
aly1539.8	Fez family zinc finger protein 2	GO:0019827,GO:0007399,GO:0050767,GO:0005634,GO:0030154,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG31670-PC				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667										
aly1539.9	Transcriptional activator protein Pur-alpha	GO:0031935,GO:1990124,GO:0030154,GO:0030425,GO:0000784,GO:0003677,GO:0005737,GO:0043565,GO:0000900,GO:0005634,GO:0006357,GO:0003691,GO:0043025,GO:0003697,GO:0006351,GO:0008284,GO:0032422,GO:0044822,GO:0008134,GO:0045892,GO:0007399,GO:0006268,GO:0006270,GO:0003705,GO:0005662,GO:0003723,GO:0003729	CG1507-PB				SM00712,SM00712,SM00712		PF04845														
aly15406.1	RNA exonuclease 4	GO:0004527,GO:0005634,GO:0003676	CG6833-PA						PF00929				G3DSA:3.30.420.10	SSF53098									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1546.1	CCAAT/enhancer-binding protein	GO:0043565,GO:0046427,GO:0003700,GO:0005634,GO:0006355,GO:0045944,GO:0009977,GO:0003677,GO:0007298,GO:0046982,GO:0001708,GO:0006351	CG4354-PA				SM00338		PF07716	PS50217			G3DSA:1.20.5.170	SSF57959	275~309								
aly1547.1	Two pore potassium channel protein sup-9	GO:0005267,GO:0071805,GO:0006813,GO:0016021,GO:0006937,GO:0055120,GO:0036195,GO:0005887,GO:0046982	CG9637-PC						PF07885,PF07885		PR01095,PR01095,PR01095,PR01333,PR01333		G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324,SSF81324									
aly1547.2	U3 small nucleolar ribonucleoprotein protein MPP10	GO:0032040,GO:0005732,GO:0005730,GO:0005634,GO:0010923,GO:0044822,GO:0030529,GO:0000375,GO:0006364,GO:0005694,GO:0008380,GO:0006396,GO:0034457	CG13097-PA						PF04006						501~521,288~308								
aly1547.3	Nuclear factor 1 C-type	GO:0003700,GO:0005634,GO:0006355,GO:0006260,GO:0006351,GO:0003677	CG2380-PB				SM00523		PF10524,PF03165,PF00859	PS51080					45~74								
aly1547.4	One cut domain family member 2	GO:0015629,GO:0030154,GO:0001077,GO:0001889,GO:0003677,GO:0009653,GO:0031018,GO:0043565,GO:0005634,GO:0005654,GO:0006366,GO:0002064,GO:0030335,GO:0042384,GO:0030512,GO:0045165,GO:0003700,GO:0001952,GO:0006355,GO:0045944,GO:0006351,GO:0048935,GO:0031016,GO:0000978	CG1922-PA				SM00389		PF00046,PF02376	PS51042,PS50071			G3DSA:1.10.260.40,G3DSA:1.10.10.60	SSF47413,SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1547.5	Potassium voltage-gated channel protein Shal	GO:0043204,GO:0071805,GO:0006813,GO:0016021,GO:0005886,GO:0051260,GO:0008076,GO:0030425,GO:0005249,GO:0007268,GO:0005250,GO:0005251,GO:0055085	CG9262-PB				SM00225		PF11601,PF00520,PF02214		PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR01491,PR01491,PR01497,PR01497,PR01497,PR01497,PR01497,PR01497		G3DSA:1.20.120.350,G3DSA:1.10.287.70,G3DSA:3.30.710.10	SSF54695,SSF81324										
aly15478.1	Unknown		n/a																				
aly155.1	Unknown		n/a						PF13843														
aly155.10	L-lactate dehydrogenase	GO:0005737,GO:0044262,GO:0016616,GO:0019752,GO:0007525,GO:0007520,GO:0004459,GO:0005975,GO:0006096,GO:0055114	CG10160-PA	MF_00488		PIRSF000102		TIGR01771	PF00056,PF02866		PR00086,PR00086,PR00086,PR00086,PR00086	PS00064	G3DSA:3.90.110.10,G3DSA:3.40.50.720	SSF56327,SSF51735		00270+1.1.1.27,00010+1.1.1.27,00620+1.1.1.27,00640+1.1.1.27		PWY-6901,PWY-5481	UPA00554				
aly155.11	ATP synthase subunit epsilon, mitochondrial	GO:0015986,GO:0015992,GO:0046933,GO:0000275,GO:0046331,GO:0046961,GO:0008340,GO:0008553,GO:0006979	CG9032-PA						PF04627				G3DSA:1.10.1620.20	SSF48690									
aly155.12	Solute carrier family 35 member F6	GO:0008284,GO:0005794,GO:0005351,GO:0070062,GO:0009306,GO:0016021,GO:0006810,GO:0005739,GO:0008643,GO:0005765,GO:0000139,GO:1901029	CG10007-PA			PIRSF036436			PF06027					SSF103481									
aly155.13	Unknown		n/a							PS51257													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly155.14	Neuronal pentraxin-2	GO:0008306,GO:0008030,GO:0030246,GO:0005576,GO:0007268,GO:0046872	CG3100-PA				SM00159		PF00354		PR00895,PR00895,PR00895,PR00895		G3DSA:2.60.120.200	SSF49899									
aly155.15	Unknown		n/a																				
aly155.16	E3 ubiquitin-protein ligase MYCBP2	GO:0021785,GO:0050808,GO:0008582,GO:0030424,GO:0030509,GO:0045886,GO:0008270,GO:0032880,GO:0006355,GO:0016023,GO:0004842,GO:0005634,GO:0016020,GO:0051493,GO:0021952,GO:0015630,GO:2000331,GO:0006914,GO:0007628,GO:0005886,GO:0030514,GO:0016874,GO:0040011,GO:0016567,GO:0042177,GO:0006351,GO:0005515	CG32592-PA																				
aly155.17	Unknown		n/a																				
aly155.18	Unknown		n/a										G3DSA:3.80.10.10,G3DSA:3.80.10.10										
aly155.19	Unknown	GO:0005575,GO:0003674,GO:0008150	CG5541-PA						PF13229	PS50042			G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52058									
aly155.2	Solute carrier family 35 member B1 homolog	GO:0006487,GO:0016021,GO:0070983,GO:0005789,GO:0005459,GO:0007411,GO:0008643,GO:0055085,GO:0034976	CG5802-PA						PF08449					SSF103481,SSF103481									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly155.3	Coiled-coil domain-containing protein AGAP005037	GO:0005575,GO:0008150,GO:0003674	CG32809-PG						PF03915						907~927,1341~1368,1154~1174,1092~1112,157~177								
aly155.4	Tyrosine-protein phosphatase non-receptor type 11	GO:0000187,GO:0033628,GO:0019221,GO:0060334,GO:0007498,GO:0006470,GO:0007596,GO:0035335,GO:0030220,GO:0007418,GO:0042593,GO:0050900,GO:0060325,GO:0038127,GO:0035264,GO:0035265,GO:0060338,GO:0007411,GO:0036302,GO:0008543,GO:0008069,GO:0048609,GO:0007362,GO:0042445,GO:0005070,GO:0045500,GO:0005634,GO:0006641,GO:0005739,GO:0033277,GO:0048873,GO:0043066,GO:0048806,GO:0033629,GO:0051463,GO:0048008,GO:0031295,GO:0045931,GO:0005737,GO:0008286,GO:0000278,GO:0007507,GO:0007229,GO:0045087,GO:0005158,GO:0032528,GO:0048839,GO:0008595,GO:0060333,GO:0007173,GO:0060337,GO:0060125,GO:0046887,GO:0048011,GO:0045314,GO:0048013,GO:0035855,GO:0048015,GO:0040014,GO:0043234,GO:0007424,GO:0007427,GO:0038095,GO:0000077,GO:0007420,GO:0004728,GO:0061582,GO:0004726,GO:0004725,GO:0007444,GO:0007465,GO:0007428,GO:0004721,GO:0046825,GO:2001275,GO:0005515,GO:0009755,GO:0008293,GO:0070374,GO:0005829,GO:0046676	CG3954-PB				SM00252,SM00404,SM00194		PF00102,PF00017	PS50056,PS50055,PS50001	PR00401,PR00401,PR00401,PR00401,PR00401,PR00700,PR00700,PR00700,PR00700,PR00700,PR00700	PS00383	G3DSA:3.30.505.10,G3DSA:3.90.190.10,G3DSA:3.90.190.10	SSF52799,SSF52799,SSF55550										
aly155.5	Sodium-dependent nutrient amino acid transporter 1	GO:0002009,GO:0005328,GO:0003333,GO:0016021,GO:0006814,GO:0015804,GO:0005283,GO:1903825,GO:0005887,GO:0006836,GO:0042940,GO:0042943,GO:0015175,GO:0005326	CG3897-PD						PF00209	PS50267				SSF161070									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly155.6	E3 ubiquitin-protein ligase MYCBP2	GO:0021785,GO:0050808,GO:0008582,GO:0030424,GO:0030509,GO:0045886,GO:0008270,GO:0032880,GO:0006355,GO:0016023,GO:0004842,GO:0005634,GO:0016020,GO:0051493,GO:0021952,GO:0015630,GO:2000331,GO:0006914,GO:0007628,GO:0005886,GO:0030514,GO:0016874,GO:0040011,GO:0016567,GO:0042177,GO:0006351,GO:0005515	CG32592-PA				SM00184		PF13540,PF13540,PF08005,PF08005,PF13639	PS50012,PS50089,PS50012	PR00633,PR00633,PR00633	PS00626,PS00626	G3DSA:3.30.40.10,G3DSA:2.60.120.260,G3DSA:2.130.10.30,G3DSA:2.130.10.30	SSF49785,SSF50985,SSF50985,SSF57850										
aly155.7	Unknown		n/a																				
aly155.8	Triple functional domain protein	GO:0005089,GO:0016319,GO:0050770,GO:0007480,GO:0031532,GO:0007422,GO:0005737,GO:0030426,GO:0030036,GO:0030424,GO:0035025,GO:0045887,GO:0046331,GO:0005524,GO:0048675,GO:0007411,GO:0007412,GO:0004674,GO:0031234,GO:0071772,GO:0007417	CG18214-PA				SM00516		PF13716				G3DSA:3.40.525.10	SSF52087	165~185									
aly155.9	Triple functional domain protein	GO:0005089,GO:0016319,GO:0050770,GO:0007480,GO:0031532,GO:0007422,GO:0005737,GO:0030426,GO:0030036,GO:0030424,GO:0035025,GO:0045887,GO:0046331,GO:0005524,GO:0048675,GO:0007411,GO:0007412,GO:0004674,GO:0031234,GO:0071772,GO:0007417	CG18214-PA				SM00409,SM00325,SM00325,SM00233,SM00233,SM00150,SM00150,SM00150,SM00150		PF00435,PF00621,PF00621,PF07679,PF00069	PS50010,PS50835,PS50003,PS50003,PS50011,PS50002,PS50010		PS00107	G3DSA:1.20.58.60,G3DSA:1.10.510.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.900.10,G3DSA:1.20.900.10,G3DSA:2.60.40.10,G3DSA:2.30.29.30,G3DSA:2.30.29.30,G3DSA:3.30.200.20,G3DSA:3.30.200.20,G3DSA:2.30.30.40	SSF48726,SSF46966,SSF56112,SSF46966,SSF46966,SSF50729,SSF48065,SSF50729,SSF50044,SSF46966,SSF48065									
aly15558.1	Putative polypeptide N-acetylgalactosaminyltransferase 10	GO:0005794,GO:0006493,GO:0006486,GO:0032504,GO:0016021,GO:0004653,GO:0030246,GO:0000139,GO:0046872	CG30463-PA						PF00652	PS50231			G3DSA:2.80.10.50	SSF50370										
aly15586.1	Protein real-time	GO:0016021,GO:0006810,GO:0005739,GO:0008526	CG9528-PB				SM01100,SM00516		PF03765,PF04707,PF00650	PS50904,PS50191			G3DSA:3.40.525.10,G3DSA:3.40.525.10	SSF52087,SSF101576,SSF46938	540~541									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly15586.2	Ubiquitin-like modifier-activating enzyme 1	GO:0016319,GO:0046578,GO:0030425,GO:0004839,GO:0019915,GO:0030057,GO:0010008,GO:0005737,GO:0070062,GO:0005765,GO:0040008,GO:0005739,GO:0043067,GO:0005524,GO:0008283,GO:0044822,GO:0019941,GO:0016322,GO:0006974,GO:0004842,GO:0000792,GO:0005829,GO:0030867,GO:0016567,GO:0005634	CG1782-PA				SM00985	TIGR01408	PF16190,PF10585,PF09358,PF16191,PF00899,PF00899		PR01849,PR01849,PR01849,PR01849,PR01849	PS00865,PS00536	G3DSA:3.40.50.720,G3DSA:3.40.50.720,G3DSA:1.10.3240.10,G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF69572,SSF69572					UPA00143				
aly15586.3	Centriolar coiled-coil protein of 110 kDa	GO:0006996,GO:0043234,GO:0051298,GO:0000086,GO:0005813,GO:0005829,GO:0005814,GO:0030030,GO:0007099,GO:0005515,GO:0032465,GO:0000278	CG14617-PB						PF16025	PS50096													
aly15586.4	Protein-S-isoprenylcysteine O-methyltransferase	GO:0006481,GO:0016021,GO:0004671,GO:0005783,GO:0005789	CG11268-PA						PF04140	PS51564						00900+2.1.1.100							
aly15586.5	Unknown		n/a																				
aly1561.1	Neuropeptide Y receptor type 2	GO:0003151,GO:0004930,GO:0001601,GO:0036400,GO:0040018,GO:0016021,GO:0005886,GO:0007218,GO:0031513,GO:0004983,GO:0003214,GO:0005887,GO:0008188,GO:0007193,GO:0070374,GO:0007186,GO:2000253	CG7395-PA						PF00001	PS50262	PR01012,PR01012,PR01012,PR01012,PR01012,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly15649.1	Protein yellow	GO:0060179,GO:0004167,GO:0006583,GO:0048066,GO:0048067,GO:0005576,GO:0042438,GO:0042435,GO:0007275	CG18550-PA						PF03022				G3DSA:2.120.10.30										
aly15649.2	Protein yellow	GO:0005737,GO:0060179,GO:0016853,GO:0048082,GO:0048065,GO:0048066,GO:0048067,GO:0005576,GO:0042438,GO:0007275,GO:0070451,GO:0006583	CG3757-PA						PF03022														
aly1565.1	Unknown		n/a																				
aly1565.2	Unknown		n/a																				
aly1565.3	Unknown		n/a																				
aly15656.1	E3 ubiquitin-protein ligase FANCL	GO:0005737,GO:0006974,GO:0031625,GO:0006281,GO:0042127,GO:0016874,GO:0005635,GO:0005575,GO:0006513,GO:0002230,GO:0008270,GO:0061630,GO:0004842,GO:0043240,GO:0007276	CG12812-PA						PF11793,PF09765				G3DSA:3.30.40.10	SSF57850					UPA00143				
aly15656.2	Unknown	GO:0003677	CG4404-PA				SM00595		PF02944,PF10545	PS51031,PS51029													
aly15656.3	Unknown	GO:0005575,GO:0003674,GO:0008150	CG10973-PB										G3DSA:1.25.10.10	SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly15656.4	Urokinase-type plasminogen activator	GO:0004252,GO:0071222,GO:2000345,GO:0014911,GO:0014910,GO:0007596,GO:0061041,GO:0014909,GO:0043403,GO:0007165,GO:0005925,GO:0055093,GO:0001525,GO:0005615,GO:0070997,GO:0031639,GO:0033628,GO:0071456,GO:0006508,GO:0010469,GO:0014823,GO:0035729,GO:0008284,GO:2000379,GO:2000097,GO:0006935,GO:0009986,GO:0071333,GO:0071498,GO:0060279,GO:0007283,GO:0072734,GO:0005886,GO:0022008,GO:0070062,GO:0042730,GO:0007566,GO:0005576	CG11529-PA						PF00089	PS50240		PS00135	G3DSA:2.40.10.10	SSF50494										
aly15656.5	Collagenase	GO:0006508,GO:0005576,GO:0030574,GO:0004252	CG10472-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494										
aly15663.1	Alkylglycerol monooxygenase	GO:0006633,GO:0005783,GO:0006643,GO:0016021,GO:0050479,GO:0005789,GO:0046485,GO:0005506,GO:0055114,GO:0016491	n/a						PF04116														
aly1568.1	Unknown		n/a																				
aly156922.1	Unknown	GO:0043186,GO:0003723,GO:0005515	CG7082-PA																				
aly157.1	Unknown		n/a						PF04500														
aly157.10	Unknown		n/a																				
aly157.11	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly157.12	Unknown		n/a						PF04500														
aly157.13	Unknown		n/a																				
aly157.14	Unknown		n/a						PF04500														
aly157.15	Unknown		n/a																				
aly157.16	Unknown		n/a						PF04500														
aly157.17	Unknown		n/a						PF04500														
aly157.18	Unknown		CG42776-PA						PF04500														
aly157.19	Unknown		n/a						PF04500														
aly157.2	Unknown		CG42773-PA						PF04500														
aly157.20	Unknown		n/a						PF04500														
aly157.21	Unknown		n/a																				
aly157.22	Unknown		CG44877-PA						PF04500														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly157.23	Unknown		n/a																				
aly157.24	Unknown		n/a						PF04500														
aly157.25	Unknown		n/a						PF04500														
aly157.26	Unknown		n/a						PF04500,PF04500														
aly157.27	Unknown		n/a						PF04500														
aly157.28	Unknown		n/a						PF04500				G3DSA:2.20.25.90										
aly157.29	Unknown		CG13845-PA						PF04500,PF04500														
aly157.3	Unknown		CG44877-PA						PF04500														
aly157.30	Unknown		CG44882-PA						PF04500														
aly157.31	Unknown		n/a						PF04500,PF04500														
aly157.32	Unknown		n/a						PF04500														
aly157.4	Unknown		n/a						PF04500,PF04500														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly157.5	Unknown		n/a						PF04500														
aly157.6	Unknown		n/a						PF04500														
aly157.7	Unknown		n/a						PF04500														
aly157.8	Unknown		n/a						PF04500														
aly157.9	Unknown		n/a						PF04500														
aly157194.1	Unknown		n/a																				
aly15743.1	Malate dehydrogenase	GO:0005811,GO:0044262,GO:0016615,GO:0016616,GO:0006919,GO:0035209,GO:0035070,GO:0006099,GO:0005739,GO:0006108,GO:0003824,GO:0043067,GO:0030060,GO:0005759,GO:0005975,GO:0043068,GO:0055114	CG7998-PA										G3DSA:3.90.110.10,G3DSA:3.40.50.720										
aly1576.1	Limbic system associated membrane protein	GO:0050767,GO:0043005,GO:0016337,GO:0005515,GO:0007399,GO:0009986,GO:0035641,GO:0005911,GO:0005886,GO:0043025,GO:0031225	CG42596-PC				SM00409,SM00409,SM00408,SM00408		PF07679,PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly1576.2	Unknown		n/a																				
aly1576.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1577.1	Fatty acid synthase	GO:0006633,GO:0047451,GO:0016295,GO:0005835,GO:0004320,GO:0016296,GO:0016788,GO:0004317,GO:0004312,GO:0004313,GO:0047117,GO:0004316,GO:0008270,GO:0004314,GO:0004315,GO:0004319,GO:0055114,GO:0016491	CG17374-PC										G3DSA:3.40.50.720	SSF51735									
aly1577.10	WSCD family member AAEL009094	GO:0005575,GO:0016021,GO:0008150,GO:0008146	CG9164-PC						PF00685				G3DSA:3.40.50.300	SSF52540									
aly1577.11	Ribonuclease P protein subunit p29	GO:0090502,GO:0030677,GO:0090501,GO:0008033,GO:0033204,GO:0000172,GO:0004526,GO:0005655,GO:0006364,GO:0006379,GO:0003723	CG8038-PA	MF_00754		PIRSF027081	SM00538		PF01868				G3DSA:2.30.30.210	SSF101744	44~64								
aly1577.12	CCR4-NOT transcription complex subunit 10	GO:0005737,GO:0005634,GO:0006355,GO:0030014,GO:0031047,GO:0005515,GO:0017148,GO:0006417,GO:0006402,GO:0006351	CG18616-PA						PF07719				G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452									
aly1577.13	Unknown		n/a																				
aly1577.14	Gustatory receptor for sugar taste 43a	GO:0060259,GO:0033041,GO:0032098,GO:0016021,GO:0050916,GO:0008527,GO:0050912,GO:0071332,GO:0005886,GO:0008343,GO:0050909,GO:0001582	CG1712-PC						PF08395														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1577.15	Unknown		n/a																				
aly1577.2	Fatty acid synthase	GO:0006633,GO:0047451,GO:0008144,GO:0008270,GO:0001649,GO:0016491,GO:0070062,GO:0016295,GO:0005835,GO:0004320,GO:0071353,GO:0005739,GO:0030879,GO:0042802,GO:0042803,GO:0005794,GO:0044822,GO:0004315,GO:0016788,GO:0047117,GO:0042587,GO:0005886,GO:0055114,GO:0008610,GO:0006084,GO:0042470,GO:0005829,GO:0004312,GO:0004313,GO:0016296,GO:0004314,GO:0070402,GO:0004319	CG17374-PC										G3DSA:3.90.180.10	SSF50129									
aly1577.3	Fatty acid synthase	GO:0006633,GO:0047451,GO:0004314,GO:0004313,GO:0005835,GO:0004320,GO:0016295,GO:0016296,GO:0016788,GO:0004317,GO:0004312,GO:0003824,GO:0047117,GO:0004316,GO:0008270,GO:0008152,GO:0004315,GO:0004319,GO:0055114,GO:0016491	CG17374-PC				SM00827,SM00825		PF02801,PF16197,PF00698,PF00109				G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.366.10	SSF53901,SSF53901,SSF52151	415~435								
aly1577.4	General odorant-binding protein 84a	GO:0005549,GO:0007606,GO:0005576,GO:0008145,GO:0005550	CG1176-PC				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly1577.5	Zinc metalloproteinase nas-15	GO:0006508,GO:0005576,GO:0004222,GO:0008270,GO:0017090	CG6763-PA				SM00235		PF01400		PR00480,PR00480,PR00480,PR00480,PR00480		G3DSA:3.40.390.10	SSF55486									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1577.6	Max-binding protein MNT	GO:0043565,GO:0006909,GO:0030308,GO:0000122,GO:0003700,GO:0005634,GO:0051726,GO:0006355,GO:0048812,GO:0006351,GO:0005515,GO:0003677,GO:0046983,GO:0046982	CG13316-PI				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459	301~335								
aly1577.7	Phosphorylase b kinase gamma catalytic chain, liver/testis isoform	GO:0048598,GO:0006468,GO:0005964,GO:0005978,GO:0004689,GO:0004674,GO:0005516,GO:0006007,GO:0005524	CG1830-PD				SM00220		PF00069	PS50011	PR01049,PR01049,PR01049,PR01049,PR01049,PR01049	PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112			REACT_474						
aly1577.8	Myotubularin-related protein 3	GO:0005737,GO:0006644,GO:0004438,GO:0008138,GO:0016311,GO:0006470,GO:0004725,GO:0016020,GO:0052629,GO:0004722,GO:0019898,GO:0005654,GO:0046856,GO:0006661,GO:0035335,GO:0046872,GO:0005829,GO:0044281	CG3632-PE				SM00404		PF06602	PS50056,PS51339		PS00383	G3DSA:3.90.190.10,G3DSA:2.30.29.30	SSF50729,SSF52799									
aly1577.9	Lateral signaling target protein 2 homolog	GO:0046872	CG6051-PB				SM00064		PF01363	PS50178			G3DSA:3.30.40.10	SSF57903									
aly158309.1	Probable low-specificity L-threonine aldolase 2	GO:0006567,GO:0006545,GO:0005829,GO:0006520,GO:0003824,GO:0030170,GO:0008732,GO:0004793	CG10184-PA						PF01212				G3DSA:3.40.640.10	SSF53383									
aly15847.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1585.1	DNA polymerase alpha subunit B	GO:0005737,GO:0005654,GO:0000278,GO:0000722,GO:0000060,GO:0006271,GO:0006270,GO:0000082,GO:0032201,GO:0003887,GO:0006260,GO:0006261,GO:0003677,GO:0046982,GO:0005658,GO:0000723	CG5923-PC			PIRSF018300			PF04042,PF08418								REACT_152,REACT_383,REACT_22172							
aly1585.10	N-terminal kinase-like protein	GO:0006468,GO:0005524,GO:0004672	CG1973-PB						PF00069	PS50011			G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.25.10.10	SSF48371,SSF56112	765~785									
aly1585.11	39S ribosomal protein L11, mitochondrial	GO:0003735,GO:0006417,GO:0006412,GO:0005762,GO:0031047	CG3351-PA	MF_00736			SM00649	TIGR01632	PF03946,PF00298				G3DSA:3.30.1550.10,G3DSA:1.10.10.250	SSF54747,SSF46906	157~180									
aly1585.12	N-acylneuraminate-9-phosphatase	GO:0016787,GO:0046380,GO:0005975,GO:0016311,GO:0006045,GO:0008152,GO:0050124	CG15771-PA					TIGR01549,TIGR02253,TIGR01509	PF13419				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF56784										
aly1585.13	Nephrin	GO:0072015,GO:0007254,GO:0030838,GO:0070062,GO:0007588,GO:0032836,GO:0044062,GO:0007519,GO:0017022,GO:0005622,GO:0007520,GO:0005887,GO:0005886,GO:0007155,GO:0042995,GO:0036057	CG34113-PO				SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408		PF07679,PF08205,PF13927,PF13927	PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1585.14	Transforming acidic coiled-coil-containing protein 1	GO:0000242,GO:0008104,GO:0035046,GO:0007279,GO:0000226,GO:0032886,GO:0007067,GO:0005815,GO:0007143,GO:0051301,GO:0007344,GO:0045111,GO:0007026,GO:0005813,GO:0005634,GO:0000922,GO:0005875,GO:0007049,GO:0005737,GO:0015630,GO:0008283,GO:0008017,GO:0007052,GO:0022027,GO:0000235,GO:0019904,GO:0021987,GO:0022008,GO:0005876,GO:0005515,GO:0007097	CG9765-PK						PF05010						174~208,255~275,280~321,82~148								
aly1585.15	Neurochondrin homolog	GO:0005575,GO:0043025,GO:0003012,GO:0003674,GO:0030425	CG2330-PA						PF05536				G3DSA:1.25.10.10										
aly1585.16	Unknown		n/a																				
aly1585.2	Mitochondrial amidoxime-reducing component 1	GO:0005739,GO:0008940,GO:0043546,GO:0042126,GO:0005743,GO:0016021,GO:0030151,GO:0003824,GO:0005741,GO:0030170,GO:0055114	CG1665-PA						PF03473,PF03476	PS51340				SSF50800,SSF141673									
aly1585.3	Signal recognition particle 14 kDa protein	GO:0005786,GO:0030942,GO:0008312,GO:0006614,GO:0003729	CG5417-PB						PF02290				G3DSA:3.30.720.10	SSF54762			REACT_15380						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1585.4	Zinc finger FYVE domain-containing protein 26 homolog	GO:0046872	CG5270-PB																				
aly1585.5	Zinc finger FYVE domain-containing protein 26 homolog	GO:0046872	CG5270-PB				SM00064		PF01363	PS50178			G3DSA:3.30.40.10	SSF57903									
aly1585.6	Probable cardiolipin synthase (CMP-forming)	GO:0016780,GO:0008654,GO:0016021,GO:0016020,GO:0017169,GO:0008808,GO:0005743,GO:0006754,GO:0007006	CG4774-PB						PF01066														
aly1585.7	Transforming acidic coiled-coil-containing protein 3	GO:0000242,GO:0008104,GO:0035046,GO:0007279,GO:0000226,GO:0032886,GO:0007067,GO:0001666,GO:0007143,GO:0005876,GO:0007344,GO:0030953,GO:0007026,GO:0005813,GO:0000922,GO:0022008,GO:0005875,GO:0005737,GO:0015630,GO:0008283,GO:0008017,GO:0007052,GO:0022027,GO:0000235,GO:0019904,GO:0021987,GO:0042994,GO:0051726,GO:0005515,GO:0030097,GO:0007097	CG9765-PK						PF05010						301~321,230~279,90~148								
aly1585.8	Complex I intermediate-associated protein 30, mitochondrial	GO:0032981,GO:0017004,GO:0006120,GO:0051082,GO:0005747,GO:0042594,GO:0009408,GO:0001666,GO:0055093,GO:0007005,GO:0006119	CG7598-PA						PF08547					SSF49785	71~91								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1585.9	Probable glucosamine 6-phosphate N-acetyltransferase	GO:0006048,GO:0004343,GO:0008080	CG1969-PF																				
aly15859.1	Unknown		n/a						PF13843														
aly158676.1	Protein HID1	GO:0005737,GO:0005794,GO:0005797,GO:0070062,GO:0006886,GO:0000138,GO:0031001,GO:0005881,GO:0090498	CG8841-PC						PF09742														
aly15880.1	Facilitated trehalose transporter Tret1	GO:0015574,GO:0015771,GO:0016021,GO:0015749,GO:0005886,GO:0015145,GO:0055085	CG31100-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly15880.2	Sugar transporter ERD6-like 10	GO:0005355,GO:0022891,GO:0016021,GO:0055085,GO:0008643	CG4797-PB						PF00083				G3DSA:1.20.1250.20	SSF103473									
aly15880.3	Unknown		n/a																				
aly158825.1	Unknown	GO:0005515	n/a										G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly159.1	Adenylate cyclase type 2	GO:0046872,GO:0040015,GO:0016021,GO:0004016,GO:0002165,GO:0042594,GO:0035556,GO:0005622,GO:0006171,GO:0005524	CG7978-PB				SM00044,SM00044		PF00211,PF00211,PF16214	PS50125,PS50125		PS00452,PS00452	G3DSA:3.30.70.1230,G3DSA:3.30.70.1230	SSF55073,SSF55073									
aly159.10	Sorting nexin-14	GO:0038032,GO:0080025,GO:0035091,GO:0016021,GO:0005770,GO:0000046,GO:0030425,GO:0005764,GO:0005765,GO:0015031,GO:0031902	n/a						PF02194,PF00787				G3DSA:3.30.1520.10	SSF64268,SSF48097									
aly159.11	Glycine cleavage system H protein, mitochondrial	GO:0005739,GO:0005960,GO:0006546,GO:0019464,GO:0035220	CG7758-PA	MF_00272				TIGR00527	PF01597	PS50968		PS00189	G3DSA:2.40.50.100	SSF51230									
aly159.12	Lysosomal alpha-glucosidase	GO:0017177,GO:0005975,GO:0005765,GO:0005980,GO:0030246,GO:0005764,GO:0003824,GO:0005576,GO:0032450,GO:0004558,GO:0005875	CG14476-PB				SM00018		PF13802,PF01055,PF16863,PF00088	PS51448		PS00707	G3DSA:4.10.110.10	SSF74650,SSF57492,SSF51445,SSF144511,SSF51011									
aly159.13	Mitochondrial cardiolipin hydrolase	GO:0046872,GO:0043186,GO:0046843,GO:0016021,GO:0005739,GO:0016042,GO:0005741,GO:0030717,GO:0004519,GO:0051321,GO:0034587,GO:0048477,GO:0031047	CG12314-PA						PF13091				G3DSA:3.30.870.10,G3DSA:3.30.870.10	SSF56024,SSF56024									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly159.14	Myc protein	GO:0048639,GO:0045927,GO:0030307,GO:0009792,GO:0003677,GO:0042981,GO:0035212,GO:0005634,GO:0044719,GO:0050769,GO:0045746,GO:0048477,GO:0009880,GO:0008283,GO:0046620,GO:0009987,GO:0035363,GO:0042023,GO:0008361,GO:0001558,GO:0045893,GO:0022008,GO:0043234,GO:0051726,GO:0003700,GO:0040018,GO:0006355,GO:0006351,GO:0005515,GO:0046983,GO:0010506	CG10798-PB				SM00353		PF00010	PS50888	PR00044,PR00044,PR00044,PR00044		G3DSA:4.10.280.10	SSF47459	320~340								
aly159.15	tRNA dimethylallyltransferase, mitochondrial	GO:0052381,GO:0004161,GO:0005739,GO:0009058,GO:0006400,GO:0046872,GO:0005524	CG31381-PA	MF_00185					PF01745,PF01715				G3DSA:1.10.287.890,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	454~477	00908+2.5.1.75,00908+2.5.1.27		PWY-2681,PWY-2781					
aly159.16	Dimethyladenosine transferase 1, mitochondrial	GO:0006996,GO:0000179,GO:0006417,GO:0006355,GO:0000154,GO:0044822,GO:0016433,GO:0003712,GO:0005739,GO:0005759,GO:0006351,GO:0003677,GO:0006390,GO:0042645,GO:0007005	CG42631-PA				SM00650	TIGR00755	PF09813,PF00398	PS51689			G3DSA:3.40.50.150,G3DSA:1.10.8.100	SSF53335									
aly159.17	F-box only protein 32	GO:0071549,GO:0005730,GO:0014894,GO:0016567,GO:0005515,GO:0030018	CG11658-PA										G3DSA:1.20.1280.50	SSF81383	122~142								
aly159.18	COMM domain-containing protein 3	GO:0005737,GO:0005634,GO:0006814,GO:0005575,GO:0006355,GO:0008150,GO:0006351,GO:0003674	CG12106-PA						PF07258	PS51269					57~79								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly159.19	Probable E3 ubiquitin-protein ligase sinah	GO:0007423,GO:0004842,GO:0005634,GO:0010498,GO:0045676,GO:0016567,GO:0006511,GO:0008270,GO:0016874	CG13030-PC						PF03145	PS51081			G3DSA:3.90.890.10	SSF49599					UPA00143				
aly159.2	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	GO:0000381,GO:0008026,GO:0007476,GO:0004004,GO:0000398,GO:0003676,GO:0005681,GO:0002121,GO:0008380,GO:0005524,GO:0006397	CG32604-PA				SM00487,SM00490		PF00271,PF07717	PS51192,PS51194			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	326~346,951~971,147~167								
aly159.20	Unknown	GO:0005575,GO:0003674,GO:0008150	CG32597-PC																				
aly159.3	Ancient ubiquitous protein 1	GO:0016021,GO:0016746,GO:0005789	n/a																				
aly159.4	Mucolipin-3	GO:0005737,GO:0007626,GO:0016021,GO:0005261,GO:0005262,GO:0006874,GO:0006914,GO:0005886,GO:0000046,GO:0006816,GO:0042491,GO:0005764,GO:0005765,GO:0046331,GO:0034703,GO:0032008,GO:0006811,GO:0006812,GO:0031902,GO:0044130	CG8743-PA						PF08016														
aly159.5	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0046427,GO:0015771,GO:0005215,GO:0016021,GO:0005886,GO:0055085	CG10960-PB					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00217,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly159.6	TBC1 domain family member 12	GO:0032313,GO:0005096,GO:0005097	CG7112-PB				SM00164		PF00566	PS50086			G3DSA:1.10.8.270,G3DSA:1.10.8.270	SSF47923,SSF47923,SSF47923	206~226								
aly159.7	Retinol dehydrogenase 11	GO:0016062,GO:0004745,GO:0016021,GO:0052650,GO:0005789,GO:0004090,GO:0001917,GO:0008152,GO:0042572,GO:0005622,GO:0042574	CG11200-PB						PF00106		PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly159.8	Unknown		n/a																				
aly159.9	Unknown		n/a																				
aly15906.1	Unknown		n/a																				
aly15906.2	Unknown		n/a										G3DSA:2.60.40.1360	SSF74650									
aly159083.1	Unknown		n/a																				
aly1591.1	Lebocin-1/2	GO:0045087,GO:0005576,GO:0042742	n/a																				
aly1591.10	Sterile alpha and TIR motif-containing protein 1	GO:0005737,GO:0005515,GO:0045087,GO:0048678,GO:0030424,GO:0007165,GO:0043005,GO:1901214,GO:0043025	CG43119-PI				SM00255,SM00454,SM00454		PF13676,PF07647,PF07647	PS50105,PS50104			G3DSA:3.40.50.10140,G3DSA:1.10.150.50,G3DSA:1.10.150.50,G3DSA:1.25.10.10	SSF47769,SSF48371,SSF47769,SSF52200									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1591.11	Unknown		n/a																				
aly1591.12	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0006909,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0008340,GO:0035336,GO:0008611	CG30427-PC						PF03015,PF07993				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly1591.13	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246,GO:0005537	CG13686-PB				SM00034,SM00034		PF00059,PF00059	PS50041,PS50041		PS00615,PS00615	G3DSA:3.10.100.10,G3DSA:3.10.100.10	SSF56436,SSF56436									
aly1591.14	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246	n/a				SM00034,SM00034		PF00059	PS50041		PS00615,PS00615	G3DSA:3.10.100.10,G3DSA:3.10.100.10	SSF56436,SSF56436									
aly1591.15	Unknown		n/a										G3DSA:3.10.100.10	SSF56436									
aly1591.16	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246	n/a				SM00034,SM00034		PF00059,PF00059	PS50041,PS50041		PS00615	G3DSA:3.10.100.10,G3DSA:3.10.100.10	SSF56436,SSF56436									
aly1591.17	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246	n/a										G3DSA:3.10.100.10	SSF56436									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1591.18	Asialoglycoprotein receptor 2	GO:0031647,GO:0016021,GO:0006898,GO:0030246,GO:0055088,GO:0004873,GO:0007166,GO:0009100,GO:0030282,GO:0005537	CG11211-PA				SM00034		PF00059	PS50041			G3DSA:3.10.100.10	SSF56436									
aly1591.19	Unknown		n/a																				
aly1591.2	Lebocin-4	GO:0045087,GO:0005576,GO:0042742	n/a																				
aly1591.20	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246	n/a				SM00034,SM00034		PF00059,PF00059	PS50041,PS50041			G3DSA:3.10.100.10,G3DSA:3.10.100.10	SSF56436,SSF56436									
aly1591.21	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246	n/a				SM00034,SM00034		PF00059,PF00059	PS50041,PS50041		PS00615,PS00615	G3DSA:3.10.100.10,G3DSA:3.10.100.10	SSF56436,SSF56436									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1591.22	Ecdysone receptor	GO:0016319,GO:0007552,GO:0035206,GO:0008258,GO:0007616,GO:0030425,GO:0045944,GO:0042220,GO:0007291,GO:0008270,GO:0043401,GO:0003677,GO:0008231,GO:0008230,GO:0007298,GO:0008232,GO:0004879,GO:0070491,GO:0005737,GO:0043565,GO:0007517,GO:0008544,GO:0005634,GO:0035188,GO:0007476,GO:0043065,GO:0006357,GO:0035297,GO:0044130,GO:0035053,GO:0048477,GO:0048666,GO:0035076,GO:0035075,GO:0035073,GO:0035072,GO:0007155,GO:0045938,GO:0006914,GO:0001225,GO:0016322,GO:0007488,GO:0007281,GO:0008362,GO:0035180,GO:0045892,GO:0045893,GO:0007409,GO:0007286,GO:0005496,GO:0008340,GO:0035193,GO:0040034,GO:0007443,GO:0007468,GO:0018990,GO:0007422,GO:0003700,GO:0010506,GO:0007561,GO:0005700,GO:0007390,GO:0048738,GO:0006355,GO:0048813,GO:0001077,GO:0000976,GO:0006351,GO:0005515,GO:0046982,GO:0004884,GO:0010002	CG1765-PB				SM00399,SM00430		PF00105,PF00104	PS51030	PR01283,PR01283,PR01283,PR01283,PR01283,PR01283,PR01283,PR01283,PR00047,PR00047,PR00047,PR00047,PR00398,PR00398,PR00398,PR00398,PR00398	PS00031	G3DSA:3.30.50.10,G3DSA:1.10.565.10,G3DSA:1.10.565.10	SSF57716,SSF48508			REACT_71						
aly1591.23	Unknown		n/a																				
aly1591.24	Unknown		n/a																				
aly1591.3	Lebocin-4	GO:0045087,GO:0005576,GO:0042742	n/a																				
aly1591.4	NCK-interacting protein with SH3 domain	GO:0010976,GO:0017022,GO:0008180	CG2258-PB				SM00326		PF09431,PF14604	PS50002	PR00452,PR00452,PR00452		G3DSA:2.30.30.40,G3DSA:2.30.30.40	SSF50044									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1591.5	Cytochrome b reductase 1	GO:0000293,GO:0007626,GO:0008805,GO:0016021,GO:0007476,GO:0007613,GO:0031526,GO:0010039,GO:0030133,GO:0046872	CG8776-PA				SM00665		PF03188	PS50939													
aly1591.6	Probable 28S rRNA (cytosine-C(5))-methyltransferase	GO:0008757,GO:0044822,GO:0005730,GO:0003723,GO:0006364	CG8545-PA					TIGR00446	PF17125,PF01189	PS51686	PR02008,PR02008,PR02008,PR02008,PR02008,PR02012,PR02012,PR02012	PS01153	G3DSA:3.40.50.150	SSF53335	54~89								
aly1591.7	Coenzyme Q-binding protein COQ10 homolog B, mitochondrial	GO:0005743	CG9410-PB						PF03364				G3DSA:3.30.530.20	SSF55961									
aly1591.8	Peptidyl-prolyl cis-trans isomerase H	GO:0005737,GO:0046540,GO:0000413,GO:0006461,GO:0006457,GO:0030532,GO:0071011,GO:0071001,GO:0045070,GO:0000398,GO:0016607,GO:0003755,GO:0043021,GO:0016018,GO:0005681	CG17266-PA			PIRSF001467			PF00160	PS50072	PR00153,PR00153,PR00153,PR00153,PR00153	PS00170	G3DSA:2.40.100.10	SSF50891									
aly1591.9	DnaJ homolog subfamily C member 24	GO:0005737,GO:0005856,GO:0017183,GO:0032781,GO:0008198,GO:0008270,GO:0055114,GO:0001671	CG2911-PA				SM00271		PF00226,PF05207	PS50076,PS51074	PR00625,PR00625,PR00625		G3DSA:1.10.287.110	SSF144217,SSF46565					UPA00559				
aly15987.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1599.1	Exportin-7	GO:0005737,GO:0005049,GO:0005643,GO:0005634,GO:0008536,GO:0006611,GO:0006886	CG33180-PF																				
aly16.1	Focal adhesion kinase 1	GO:0007179,GO:0007596,GO:0051893,GO:0051897,GO:0040023,GO:0051493,GO:0045667,GO:0004715,GO:0004713,GO:0042127,GO:0019901,GO:0008360,GO:0007173,GO:0007172,GO:0030168,GO:0010632,GO:0048870,GO:0060396,GO:0030198,GO:0005829,GO:0006921,GO:0006468,GO:2000811,GO:0000226,GO:0005925,GO:0005856,GO:0003779,GO:0016477,GO:0005524,GO:0012501,GO:0061177,GO:0005938,GO:0048010,GO:0048013,GO:0038096,GO:0001570,GO:0043552,GO:0007229,GO:2000060,GO:0051964,GO:1900024,GO:0061176,GO:0038007,GO:0030154,GO:0009790,GO:0030010,GO:0007411,GO:0043087,GO:0046777,GO:0005737,GO:0038083,GO:0005634,GO:0021955,GO:0008284,GO:0042169,GO:0016324,GO:0014068,GO:0031234,GO:0001890,GO:0008432,GO:0050771,GO:0001764,GO:0005102,GO:0045860,GO:0018108,GO:0045886,GO:0004871,GO:0001525,GO:0022408,GO:0001725,GO:0005815,GO:0033628,GO:0043066,GO:0004672,GO:0043542,GO:0030335,GO:0030027,GO:0046621,GO:0045087,GO:0006915,GO:0005886,GO:0007155,GO:0007264,GO:0003007,GO:0007016,GO:0007010,GO:0010594,GO:0001932,GO:0001934	CG10023-PD				SM00295,SM00219		PF03623,PF07714,PF00373	PS50057,PS50011	PR00109,PR00109,PR00109,PR00109,PR00109	PS00109	G3DSA:1.20.80.10,G3DSA:1.20.120.330,G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF54236,SSF56112,SSF47031,SSF68993,SSF50729									
aly16.10	Putative transcription factor SOX-15	GO:0008285,GO:0000122,GO:0003700,GO:0005634,GO:0035220,GO:0006355,GO:0043066,GO:0045892,GO:0006351,GO:0003677,GO:0022416	CG8404-PA				SM00398		PF00505	PS50118,PS51516			G3DSA:1.10.30.10	SSF47095									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly16.11	BSD domain-containing protein 1		n/a				SM00751		PF03909	PS50858				SSF140383									
aly16.12	Unknown		n/a																				
aly16.13	Vesicular inhibitory amino acid transporter	GO:0015495,GO:0003333,GO:0007632,GO:0015171,GO:0030659,GO:0006836,GO:0016021	CG8394-PA						PF01490														
aly16.14	Unknown		n/a																				
aly16.15	Tetratricopeptide repeat protein 4	GO:0005634	CG3189-PA				SM00028,SM00028,SM00028		PF13414	PS50293			G3DSA:1.25.40.10	SSF48452									
aly16.16	N6-adenosine-methyltransferase subunit METTL3	GO:0016607,GO:0036396,GO:0030708,GO:0019827,GO:0080009,GO:0005634,GO:0008593,GO:1990744,GO:0016422,GO:0000398,GO:0030707,GO:0008173,GO:0031053,GO:0003723,GO:0001510,GO:0042981,GO:0006382,GO:0061157,GO:0060968	CG5933-PA						PF05063	PS51563,PS51143				SSF53335	8~28								
aly16.17	Protein NDUFAF4 homolog	GO:0005575,GO:0008150,GO:0003674,GO:0032981	CG11722-PA						PF06784														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly16.18	Dual specificity protein phosphatase CDC14A	GO:0005737,GO:0005819,GO:0008138,GO:0008283,GO:0006470,GO:0004725,GO:0004721,GO:0005654,GO:0051301,GO:0005813,GO:0005634,GO:0007049	CG7134-PA				SM00195		PF00782,PF14671	PS50056		PS00383	G3DSA:3.90.190.10,G3DSA:3.90.190.10	SSF52799,SSF52799									
aly16.19	40S ribosomal protein S12	GO:0003735,GO:0005622,GO:0022627,GO:0006412,GO:0005840	CG11271-PA						PF01248		PR00972,PR00972,PR00972,PR00972	PS01189	G3DSA:3.30.1330.30	SSF55315									
aly16.2	Transcription elongation factor B polypeptide 1	GO:0008023,GO:0030891,GO:0005705,GO:0007474,GO:0070449,GO:0048813,GO:0006511,GO:0042787,GO:0005700,GO:0032403,GO:0031462,GO:0032968,GO:0022008,GO:0006351	CG9291-PA				SM00512		PF03931				G3DSA:3.30.710.10	SSF54695			REACT_6185		UPA00143				
aly16.20	Zinc finger MYND domain-containing protein 10	GO:0034451,GO:0046872,GO:0007605,GO:0036159,GO:0036158,GO:0035082,GO:0005929,GO:0019230,GO:0043025,GO:0044458	CG11253-PA						PF01753	PS50865		PS01360		SSF144232	163~183								
aly16.21	60S ribosomal protein L7	GO:0035073,GO:0005840,GO:0022625,GO:0019843,GO:0003735,GO:0007052,GO:0003723,GO:0000022,GO:0003729,GO:0006412,GO:0051298	CG4897-PA					TIGR01310	PF00327,PF08079			PS00634	G3DSA:3.30.1390.20,G3DSA:3.30.1390.20	SSF55129									
aly16.22	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly16.23	Transcription factor AP-2-epsilon	GO:0043565,GO:0007485,GO:0000122,GO:0003700,GO:0005634,GO:0007480,GO:0016348,GO:0006355,GO:0045944,GO:0006351,GO:0048728,GO:0003677	CG7807-PD						PF03299		PR01748,PR01748,PR01748												
aly16.24	Proteasome subunit beta type-5	GO:0005737,GO:0051603,GO:0004175,GO:0005839,GO:0008283,GO:0043161,GO:0051297,GO:0010499,GO:0004298,GO:0007052,GO:0006508,GO:0000022,GO:0005634,GO:0022008	CG12323-PA						PF00227	PS51476	PR00141,PR00141,PR00141,PR00141	PS00854	G3DSA:3.60.20.10	SSF56235			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_110						
aly16.25	Probable enoyl CoA hydratase	GO:0004165,GO:0006631,GO:0006909,GO:0004300,GO:0008152,GO:0071456	CG5844-PA						PF00378				G3DSA:3.90.226.10	SSF52096									
aly16.26	Derlin-1	GO:0000836,GO:0005770,GO:0031648,GO:0030968,GO:0030433,GO:0030970,GO:0005789,GO:0030176,GO:0006515,GO:0008233,GO:0005769	CG10908-PA						PF04511					SSF144091									
aly16.27	NADH dehydrogenase [ubiqui] 1 beta subcomplex subunit 9	GO:0070062,GO:0008137,GO:0005739,GO:0006120,GO:0098779,GO:0005743,GO:0005747,GO:0003954	CG9306-PA						PF05347														
aly16.28	Clavesin-1	GO:0005802,GO:0080025,GO:0005215,GO:0006810,GO:0005622,GO:0046331,GO:1903146,GO:0007040,GO:0030136,GO:0005768,GO:0031901,GO:0016918	CG10657-PA				SM01100,SM00516		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087,SSF46938	295~315								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly16.29	Sister chromatid cohesion protein PDS5 homolog B-B	GO:0008285,GO:0007064,GO:0005634,GO:0030717,GO:0008278,GO:0005488,GO:0003677,GO:0007059,GO:0005700,GO:0051301,GO:0007062	CG17509-PA										G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371	1048~1068								
aly16.3	Zinc finger protein PLAG1	GO:0005634,GO:0060252,GO:0060736,GO:0042023,GO:0010629,GO:0001077,GO:0006260,GO:0008270,GO:0035264,GO:0003677,GO:0022612,GO:0007067,GO:0046872,GO:0000978,GO:0000981,GO:0060968	CG3941-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF13894,PF12874,PF13909	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667									
aly16.30	Facilitated trehalose transporter Tret1	GO:0015574,GO:0015771,GO:0016021,GO:0016020,GO:0015749,GO:0005886,GO:0015145,GO:0055085	CG33281-PA				SM00020		PF00089,PF00083	PS50240,PS50850	PR00722,PR00722,PR00722	PS00216,PS00134	G3DSA:1.20.1250.20,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494,SSF103473									
aly16.31	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0046427,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG10960-PB						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly16.32	Mannose-1-phosphate guanyltransferase alpha-A	GO:0009298,GO:0009058,GO:0004475,GO:0005525	CG8207-PA						PF00132,PF00483				G3DSA:3.90.550.10,G3DSA:2.160.10.10	SSF53448			REACT_17015						
aly16.33	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly16.34	Homologous-pairing protein 2 homolog	GO:0006310,GO:0035259,GO:0051321,GO:0030331,GO:0050692,GO:0005634,GO:0050681,GO:0030374,GO:0046966,GO:0045944,GO:0003677,GO:0046983,GO:0042803	n/a						PF07106						117~137,66~93								
aly16.4	Ubiquitin carboxyl-terminal hydrolase 20	GO:0061136,GO:0043161,GO:0006897,GO:0007399,GO:0005813,GO:0071108,GO:0008277,GO:0004197,GO:0008270,GO:0006511,GO:0048471,GO:0016579,GO:0004843,GO:0070536	CG8494-PA				SM00695		PF06337	PS51283			G3DSA:3.30.2230.10	SSF143791									
aly16.5	Ubiquitin carboxyl-terminal hydrolase 20	GO:0071108,GO:0006897,GO:0007399,GO:0005813,GO:0004197,GO:0004843,GO:0008277,GO:0006511,GO:0008270,GO:0048471,GO:0016579,GO:0036459,GO:0070536	CG8494-PA				SM00695		PF02148,PF00443	PS50271,PS51283,PS50235		PS00973,PS00972	G3DSA:3.30.40.10,G3DSA:3.30.2230.10	SSF54001,SSF57850,SSF143791									
aly16.6	UPF0693 protein C10orf32 homolog		CG18065-PA						PF16088						48~75								
aly16.7	A disintegrin and metalloproteinase with thrombospondin motifs 16	GO:0003073,GO:0004222,GO:0008283,GO:0005575,GO:0008270,GO:0001658,GO:0006508,GO:1902017,GO:0005578	CG11169-PA						PF13582	PS50215			G3DSA:3.40.390.10	SSF55486									
aly16.8	Transmembrane protein 14C	GO:0005743,GO:0030218,GO:0016021,GO:0016020,GO:0005739,GO:0006783,GO:0008150,GO:0070453,GO:0006839,GO:0003674	CG5532-PA						PF03647														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly16.9	Glutamate--cysteine ligase regulatory subunit	GO:2001237,GO:0048149,GO:0035229,GO:0035226,GO:0017109,GO:0019899,GO:0007611,GO:0043524,GO:0008355,GO:0050880,GO:0071722,GO:0007616,GO:0030234,GO:0006974,GO:0051409,GO:0006979,GO:0008637,GO:0004357,GO:0005829,GO:0042493,GO:0006534,GO:0006536,GO:0051900,GO:0006750,GO:0046982	CG4919-PA										G3DSA:3.20.20.100	SSF51430,SSF51430									
aly1603.1	Unknown		n/a																				
aly1603.10	Cytochrome c oxidase assembly factor 6 homolog	GO:0004129,GO:0044822,GO:0005739	CG42376-PA						PF02297				G3DSA:1.10.10.140	SSF47694									
aly1603.11	Methylenetetrahydrofolate reductase	GO:0050660,GO:0050667,GO:0072341,GO:0006730,GO:0070829,GO:0006555,GO:0035999,GO:0004489,GO:0031060,GO:0032403,GO:0009086,GO:0005829,GO:0055114	CG7560-PA						PF02219				G3DSA:3.20.20.220	SSF51730		00670+1.5.1.20,00720+1.5.1.20		PWY-2201,PWY-3841	UPA00193				
aly1603.12	Serine/threonine-protein kinase SIK2	GO:0005737,GO:0006468,GO:0005634,GO:0000287,GO:0008286,GO:0046626,GO:0004674,GO:0042594,GO:0035556,GO:0046777,GO:0005524	CG4290-PA				SM00220		PF00069	PS50030,PS50011		PS00108,PS00107	G3DSA:1.10.8.10,G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly1603.13	N-alpha-acetyltransferase 30	GO:0005737,GO:0008080,GO:0031417,GO:0005575,GO:0017196,GO:0008150,GO:0004596	CG11412-PA						PF00583	PS51186			G3DSA:3.40.630.30	SSF55729									
aly1603.14	NEDD8-activating enzyme E1 regulatory subunit	GO:0043234,GO:0045116,GO:0019781,GO:0008641,GO:0004839,GO:0005515	CG7828-PB			PIRSF039099			PF00899				G3DSA:3.40.50.720,G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF69572					UPA00885				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.15	Transmembrane protein 185B	GO:0016021	CG14194-PA						PF10269														
aly1603.16	Coiled-coil domain-containing protein 142		CG13842-PB						PF14923						582~602								
aly1603.17	Ribonuclease 3	GO:0030422,GO:0031053,GO:0010628,GO:0031054,GO:0007294,GO:0050829,GO:0010586,GO:0005730,GO:0004525,GO:0005634,GO:0030727,GO:0042254,GO:0005654,GO:0010467,GO:0046872,GO:0042803,GO:0044822,GO:2000628,GO:0070878,GO:0050830,GO:0022008,GO:0001530,GO:0070877,GO:0090502,GO:0090501,GO:0016075,GO:0003725,GO:0003723	CG8730-PA	MF_00104			SM00358,SM00535,SM00535		PF00636,PF00035,PF14622	PS50137,PS50142,PS50142		PS00517	G3DSA:1.10.1520.10,G3DSA:1.10.1520.10,G3DSA:3.30.160.20,G3DSA:1.10.1520.10	SSF54768,SSF69065,SSF69065,SSF69065									
aly1603.18	Unknown	GO:0016075,GO:0004525,GO:0005634,GO:0030727,GO:0031053,GO:0003725,GO:0003723,GO:0007294,GO:0022008	CG8730-PA																				
aly1603.19	Mitochondrial tRNA-specific 2-thiouridylase 1	GO:0005737,GO:0030488,GO:0000049,GO:0008033,GO:0016783,GO:0004808,GO:0005739,GO:0002143,GO:0005524	CG3021-PA	MF_00144				TIGR00420	PF03054				G3DSA:2.30.30.280,G3DSA:3.40.50.620,G3DSA:2.40.30.10	SSF52402									
aly1603.2	Unknown	GO:0016021	CG10165-PA				SM00665		PF03188	PS50939													
aly1603.20	Transcription initiation factor TFIID subunit 8	GO:0006367,GO:0009987,GO:0045944,GO:0005515,GO:0005669,GO:0046982	CG7128-PA				SM00576		PF07524,PF10406						154~174								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.21	Proteasome subunit beta type-2	GO:0005737,GO:0051603,GO:0004175,GO:0005839,GO:0032504,GO:0043161,GO:0009987,GO:0010499,GO:0004298,GO:0006974,GO:0016020,GO:0005654,GO:0070062	CG17331-PB						PF00227	PS51476		PS00854	G3DSA:3.60.20.10	SSF56235			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_110						
aly1603.22	Synaptobrevin homolog YKT6	GO:0005887,GO:0006904,GO:0006906,GO:0006903,GO:0005484,GO:0030133,GO:0031201,GO:0005783,GO:0005737,GO:0006888,GO:0070062,GO:0016021,GO:0006887,GO:0005739,GO:0019706,GO:0005794,GO:0042147,GO:0030659,GO:0008152,GO:0006890,GO:0016192,GO:0005829,GO:0000139,GO:0015031,GO:0005768,GO:0000149	CG1515-PA						PF13774,PF00957	PS50859,PS50892			G3DSA:3.30.450.50,G3DSA:1.20.5.110	SSF58038,SSF64356									
aly1603.23	Bromo adjacent homology domain-containing 1 protein	GO:0031507,GO:0006338,GO:0006342,GO:0007476,GO:0005654,GO:0000785,GO:0005677,GO:0045892,GO:0000976,GO:0003682,GO:0006351	CG32529-PA				SM00439		PF01426	PS51038					663~683								
aly1603.24	Unknown		n/a																				
aly1603.25	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	GO:0016319,GO:0042048,GO:0005654,GO:0005743,GO:0003858,GO:0008152,GO:0005759,GO:0002121,GO:0016491	CG13377-PA						PF00106				G3DSA:3.40.50.720	SSF51735									
aly1603.26	Deoxyribonuclease-2-alpha	GO:0070062,GO:0030218,GO:0006309,GO:0006308,GO:0005764,GO:0045476,GO:0003677,GO:0006259,GO:0004531	CG7780-PA						PF03265														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.27	Probable methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	GO:0006573,GO:0004491,GO:0018478,GO:0006206,GO:0005739,GO:0008152,GO:0055114,GO:0016491	CG17896-PB					TIGR01722	PF00171			PS00070	G3DSA:3.40.605.10,G3DSA:3.40.309.10	SSF53720		00280+1.2.1.27,00640+1.2.1.18+1.2.1.27,00562+1.2.1.18,00410+1.2.1.18		PWY-5642,PWY-6373					
aly1603.28	Transposable element P transposase	GO:0004803,GO:0006313,GO:0015074,GO:0016740,GO:0003693,GO:0046872	n/a						PF12017						71~91								
aly1603.29	Protein TIS11	GO:0005634,GO:0061158,GO:0010629,GO:0003730,GO:0003677,GO:0016246,GO:0046872,GO:0035925,GO:0005829,GO:1900153	CG4070-PA				SM00356,SM00356		PF00642,PF00642	PS50103,PS50103			G3DSA:4.10.1000.10,G3DSA:4.10.1000.10	SSF90229,SSF90229									
aly1603.3	Unknown	GO:0016021	CG10165-PA				SM00665		PF03188	PS50939													
aly1603.30	Unknown	GO:0005575,GO:0008150,GO:0003674	CG32815-PC																				
aly1603.31	Nuclear factor related to kappa-B-binding protein	GO:0003700,GO:0005634,GO:0031011,GO:0003677	CG11970-PA						PF14465														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.32	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	GO:0007498,GO:0006470,GO:0030155,GO:0007300,GO:0007301,GO:0014706,GO:0046329,GO:0072357,GO:0051301,GO:0002168,GO:0005737,GO:0005634,GO:0007476,GO:0000164,GO:0016311,GO:0007049,GO:0046872,GO:0050115,GO:0016203,GO:0017018,GO:0007312,GO:0007155,GO:0007059,GO:0031991,GO:0005977,GO:0004722,GO:0004721	CG2096-PA				SM00156		PF16891,PF00149		PR00114,PR00114,PR00114,PR00114,PR00114,PR00114	PS00125	G3DSA:3.60.21.10	SSF56300									
aly1603.33	Unknown		n/a																				
aly1603.34	Unknown	GO:0030241,GO:0031672,GO:0035220,GO:0022416	CG6803-PB						PF15929														
aly1603.35	Homeobox protein Nkx-2.2	GO:0048714,GO:0048565,GO:0031018,GO:0021782,GO:0021530,GO:0003713,GO:0030154,GO:0048468,GO:0001159,GO:0003327,GO:0007419,GO:0010629,GO:0010628,GO:0021554,GO:0003677,GO:0009749,GO:0007417,GO:0043565,GO:0003329,GO:0000122,GO:0003323,GO:0005634,GO:0005654,GO:0003326,GO:0014019,GO:0045665,GO:0045666,GO:0000981,GO:0021522,GO:0048665,GO:0007389,GO:0021529,GO:0008134,GO:0048708,GO:0045597,GO:0045595,GO:0060580,GO:0014003,GO:0007400,GO:0051091,GO:0009953,GO:0007420,GO:0007399,GO:0007398,GO:0003700,GO:0007	CG6172-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly1603.36	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.37	Vam6/Vps39-like protein	GO:0030897,GO:0016192,GO:0005765,GO:0005083,GO:0031902,GO:0035542,GO:0048812,GO:0003674,GO:0008593,GO:0006886	CG7146-PA						PF00780,PF00637,PF10367,PF10366	PS50236,PS50219				SSF50978										
aly1603.38	Glycogen synthase kinase-3 beta	GO:0032436,GO:0009649,GO:2000738,GO:0030426,GO:0010800,GO:0007219,GO:0007367,GO:0006983,GO:0016020,GO:0090163,GO:0035372,GO:0044297,GO:0051059,GO:0019901,GO:0042752,GO:0010977,GO:0010975,GO:0044027,GO:0007520,GO:0097481,GO:0043025,GO:0005829,GO:0016055,GO:0045842,GO:0006611,GO:0071109,GO:0035556,GO:0046827,GO:0043227,GO:0030178,GO:0032091,GO:0032092,GO:0043547,GO:0008407,GO:0005654,GO:0030877,GO:1901030,GO:0048471,GO:0016477,GO:0048477,GO:0005524,GO:0009887,GO:0007623,GO:0007622,GO:0016301,GO:0045879,GO:0008013,GO:0035309,GO:0007051,GO:0035019,GO:0042306,GO:0007350,GO:0001085,GO:0009968,GO:0007423,GO:0070059,GO:0051534,GO:0002039,GO:0045169,GO:0006355,GO:0050321,GO:0051124,GO:0000320,GO:0016310,GO:0021766,GO:0003382,GO:0032886,GO:0046777,GO:0005737,GO:0006349,GO:0005634,GO:0030707,GO:0008283,GO:0014902,GO:0031333,GO:0031334,GO:0007409,GO:0035324,GO:0031625,GO:0005977,GO:0001954,GO:0045944,GO:0005515,GO:0045610,GO:0018105,GO:0033138,GO:0097192,GO:0045886,GO:0034236,GO:0043508,GO:0046959,GO:0045444,GO:0060070,GO:0007143,GO:0008355,GO:0072686,GO:0045732,GO:0005813,GO:0007476,GO:0030529,GO:0004674,GO:0043066,GO:0004672,GO:0006468,GO:0014043,GO:0045475,GO:0005886,GO:0035293,GO:0044337,GO:0007507,GO:0072347,GO:0007010,GO:0010614,GO:0043198,GO:0036016,GO:0045773,GO:0001837,GO:0030162	CG2621-PQ				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112										
aly1603.39	Leucine-rich repeat-containing protein 58	GO:0005515	CG32687-PA				SM00365,SM00365,SM00365,SM00365,SM00365,SM00369,SM00369,SM00369,SM00369,SM00369,SM00364,SM00364,SM00364,SM00364,SM00364		PF13855,PF13855,PF00560	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.4	Unknown	GO:0016021	n/a				SM00665		PF03188														
aly1603.40	28S ribosomal protein S2, mitochondrial	GO:0098779,GO:0015935,GO:0005739,GO:0006412,GO:0003735,GO:0002230,GO:0005763,GO:0032543	CG2937-PA	MF_00291_B					PF00318,PF00318		PR00395,PR00395,PR00395,PR00395		G3DSA:3.40.50.10490	SSF52313									
aly1603.41	DnaJ homolog subfamily C member 17	GO:0000122,GO:0071011,GO:0000398,GO:0000166,GO:0003723,GO:1901998	CG17187-PA				SM00271		PF00226,PF00076	PS50076,PS50102	PR00625,PR00625,PR00625		G3DSA:3.30.70.330,G3DSA:1.10.287.110	SSF54928,SSF46565	78~105,117~137								
aly1603.42	CWF19-like protein 2 homolog	GO:0005575,GO:0003824,GO:0008150	CG9213-PA						PF04677,PF04676														
aly1603.43	Serine/threonine-protein kinase PAK mbt	GO:0016319,GO:0000187,GO:0018105,GO:0030036,GO:0042981,GO:0023014,GO:0005737,GO:0007346,GO:0031098,GO:0004674,GO:0004672,GO:0016477,GO:0005524,GO:0048749,GO:0006468,GO:0046331,GO:0005913,GO:0005912,GO:0005886,GO:0045315,GO:0007266,GO:0001751,GO:0007030,GO:0045792,GO:0007010,GO:2000047,GO:0048365,GO:0005515,GO:0004702	CG18582-PA				SM00285		PF00069,PF00786	PS50108,PS50011		PS00107	G3DSA:3.30.200.20,G3DSA:3.90.810.10,G3DSA:1.10.510.10	SSF56112									
aly1603.44	26S protease regulatory subunit 6B	GO:0005737,GO:0016787,GO:0004175,GO:0005838,GO:0043161,GO:0005634,GO:0017111,GO:0006974,GO:0030163,GO:0000502,GO:0006508,GO:0001673,GO:0005524,GO:0008540	CG16916-PA				SM00382	TIGR01242	PF00004		PR00300,PR00300,PR00300	PS00674	G3DSA:3.40.50.300,G3DSA:1.10.8.60	SSF52540	34~68		REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_110						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.45	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6592-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1603.46	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6592-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1603.47	Semaphorin-2A	GO:0030534,GO:0007632,GO:0070983,GO:0042756,GO:0007399,GO:0007431,GO:0016020,GO:0016201,GO:0007629,GO:0005576,GO:0004872,GO:0005515,GO:0030154,GO:0007411,GO:0071678	CG4700-PB				SM00630		PF01403	PS51004			G3DSA:2.60.40.10,G3DSA:2.130.10.10,G3DSA:3.30.1680.10	SSF101912,SSF48726,SSF103575									
aly1603.48	Spermatogenesis-associated protein 17	GO:0005737,GO:0032027,GO:0005515	CG13544-PA				SM00015,SM00015		PF00612,PF00612	PS50096,PS50096													
aly1603.49	Uncharacterized oxidoreductase TM_0325	GO:0008152,GO:0016491	CG31549-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080	PS00061	G3DSA:3.40.50.720	SSF51735									
aly1603.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.50	Pupal cuticle protein Edg-78E	GO:0005214,GO:0040003,GO:0008011,GO:0008010,GO:0031012	CG12045-PA						PF00379	PS51257,PS51155													
aly1603.51	Chymotrypsin BII	GO:0004252,GO:0005615,GO:0030574,GO:0006508	CG6467-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1603.52	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6467-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1603.53	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6467-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1603.54	UDP-glucuronosyltransferase 2B4	GO:0009813,GO:0052695,GO:0052696,GO:0016021,GO:0006711,GO:0005789,GO:0006805,GO:0032870,GO:0008152,GO:0015020,GO:0002121,GO:0043231	CG17323-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly1603.55	UDP-glucuronosyltransferase 2B1	GO:0052696,GO:0071361,GO:0070980,GO:0016021,GO:0071385,GO:0009813,GO:0071394,GO:0005789,GO:0071378,GO:0008152,GO:0016758,GO:0015020,GO:0017144,GO:0032496,GO:0002121,GO:0043231	CG17323-PA						PF00201,PF00201,PF00201,PF00201,PF00201			PS00375,PS00375,PS00375,PS00375,PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000,G3DSA:3.40.50.2000,G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756,SSF53756,SSF53756,SSF53756,SSF53756									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.56	UDP-glucuronosyltransferase 2B1	GO:0052696,GO:0071361,GO:0070980,GO:0016021,GO:0071385,GO:0009813,GO:0071394,GO:0005789,GO:0071378,GO:0008152,GO:0015020,GO:0017144,GO:0032496,GO:0002121,GO:0043231	CG17323-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly1603.57	Unknown		n/a																				
aly1603.58	Mitochondrial import inner membrane translocase subunit Tim9	GO:0015450,GO:0006626,GO:0005743,GO:0005744,GO:0015031,GO:0046872	CG1660-PB						PF02953				G3DSA:1.10.287.810	SSF144122									
aly1603.59	Histone acetyltransferase Tip60	GO:0006351,GO:0007399,GO:0000123,GO:0043967,GO:0043486,GO:0005634,GO:0005705,GO:0004402,GO:0006974,GO:0006355,GO:0048167,GO:0043524,GO:0035267,GO:0016573,GO:0010468,GO:2000331	CG6121-PA				SM00298		PF11717,PF01853	PS51726			G3DSA:3.40.630.30,G3DSA:2.30.30.270,G3DSA:2.30.30.270	SSF55729,SSF54160									
aly1603.6	Unknown		n/a																				
aly1603.60	Jun dimerization protein 2	GO:0043565,GO:0007399,GO:0003700,GO:0005634,GO:0031063,GO:0055088,GO:0006355,GO:0006357,GO:0006351,GO:0005515,GO:0006955,GO:0046983	CG11405-PB				SM00338		PF00170	PS50217	PR00042,PR00042,PR00042,PR00042	PS00036	G3DSA:1.20.5.170	SSF57959	209~236								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.61	Unknown		n/a																				
aly1603.62	Histone-lysine N-methyltransferase setd3	GO:0006351,GO:0018027,GO:0018026,GO:0018023,GO:0005634,GO:0003713,GO:0046331,GO:0046975,GO:0010452,GO:0045893	CG32732-PA						PF09273,PF00856	PS51565,PS50280			G3DSA:3.90.1410.10,G3DSA:3.90.1420.10	SSF82199,SSF81822		00310+2.1.1.43							
aly1603.63	Unknown	GO:0005214,GO:0016021,GO:0000902	CG15020-PA				SM00241		PF00100	PS51034													
aly1603.64	Tight junction-associated protein 1	GO:0005737,GO:0005794,GO:0007030,GO:0005802,GO:0005654,GO:0005886,GO:0005768,GO:0005923	CG42324-PK												114~141,54~74								
aly1603.65	Unknown		CG4213-PA												206~233,769~792,996~1016,240~260,136~170,60~8								
aly1603.66	Organic solute transporter alpha-like protein	GO:0005215,GO:0016021,GO:0006810,GO:0005886	CG6836-PA						PF03619														
aly1603.67	Unknown		n/a												140~160								
aly1603.68	Xaa-Pro dipeptidase	GO:0004177,GO:0070062,GO:0004181,GO:0006520,GO:0016805,GO:0030145,GO:0030574,GO:0008239,GO:0006508	CG5663-PA				SM01011		PF00557,PF05195			PS00491	G3DSA:3.90.230.10,G3DSA:3.40.350.10	SSF53092,SSF55920									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.69	Ankyrin repeat and SOCS box protein 3	GO:0007016,GO:0005200,GO:0045170,GO:0008092,GO:0045169,GO:0016567,GO:0007165,GO:0005886,GO:0035556,GO:0005622	CG1651-PB				SM00969,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796,PF07525,PF13637	PS50088,PS50297,PS50088,PS50088,PS50225,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403					UPA00143				
aly1603.7	Alkylated DNA repair protein alkB homolog 1	GO:0006307,GO:0080111,GO:0006281,GO:0016706,GO:0070989,GO:0005634,GO:0005739,GO:0042245,GO:0003906,GO:0008198,GO:0070579,GO:0055114	CG33250-PA						PF13532	PS51471			G3DSA:2.60.120.590,G3DSA:2.60.120.590	SSF51197,SSF51197									
aly1603.70	Unknown		n/a																				
aly1603.71	Unknown		n/a												303~330								
aly1603.72	Beta-1,4-N-acetylgalactosaminyltransferase bre-4	GO:0005794,GO:0005975,GO:0006486,GO:0006044,GO:0016021,GO:0009247,GO:0033842,GO:0016757,GO:0008376,GO:0046872	CG14517-PA						PF02709,PF13733		PR02050,PR02050,PR02050,PR02050		G3DSA:3.90.550.10	SSF53448					UPA00378				
aly1603.73	Motile sperm domain-containing protein 1	GO:0016021	n/a						PF00635	PS50202			G3DSA:2.60.40.360	SSF49354									
aly1603.74	Nitrogen permease regulator 3-like protein	GO:0005737,GO:0045792,GO:0048477,GO:0005634,GO:0003674,GO:0034198,GO:0032007,GO:0008150,GO:0044754,GO:0035859,GO:0038202	CG8783-PB						PF03666						169~189								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.75	ATP-binding cassette sub-family B member 10, mitochondrial	GO:0042626,GO:0015421,GO:0006783,GO:0005215,GO:0016021,GO:0005739,GO:0005743,GO:0005886,GO:0006839,GO:0008559,GO:0032592,GO:0055085,GO:0005524,GO:0042803	CG3156-PA						PF00887,PF00664,PF00005,PF13897	PS50929,PS51228			G3DSA:3.40.50.300,G3DSA:1.20.80.10,G3DSA:1.20.1560.10	SSF47027,SSF90123,SSF52540,SSF101576	137~166								
aly1603.76	Collagenase	GO:0006508,GO:0005576,GO:0030574,GO:0004252	CG6592-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1603.77	ABC transporter B family member 13	GO:0042626,GO:0010329,GO:0010315,GO:0015421,GO:0006783,GO:0005215,GO:0016021,GO:0010541,GO:0005743,GO:0010540,GO:0005886,GO:0006839,GO:0008559,GO:0055085,GO:0005524	CG3156-PA						PF00005				G3DSA:3.40.50.300	SSF52540									
aly1603.78	Probable 4-coumarate--CoA ligase 1	GO:0016207,GO:0046627,GO:0009062,GO:0019433,GO:0004467,GO:0071616,GO:0009698,GO:0005524	CG9009-PA						PF00501,PF13193			PS00455	G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.30.300.30	SSF56801									
aly1603.79	Serine/threonine-protein phosphatase 4 regulatory subunit 2	GO:0000278,GO:0019888,GO:0035304,GO:0030289,GO:0022008,GO:0000775	CG2890-PA						PF09184														
aly1603.8	N-alpha-acetyltransferase 38-B, NatC auxiliary subunit	GO:0005737,GO:0005634,GO:0043066,GO:0031417,GO:0030532	CG31950-PA				SM00651		PF01423				G3DSA:2.30.30.100	SSF50182									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1603.80	Glutaredoxin-related protein 5, mitochondrial	GO:0005737,GO:0051537,GO:0005739,GO:0016226,GO:0030097,GO:0045454,GO:0046872,GO:0015035,GO:0009055	CG14407-PA					TIGR00365	PF00462	PS51354			G3DSA:3.40.30.10	SSF52833									
aly1603.81	Alpha-actinin, sarcomeric	GO:0007016,GO:0031532,GO:0051017,GO:0051015,GO:0003779,GO:0045214,GO:0007629,GO:0051764,GO:0005925,GO:0030018,GO:0005509	CG4376-PC				SM00054,SM00054,SM00150,SM00150,SM00150,SM00033,SM00033		PF00435,PF00435,PF00435,PF00435,PF00307,PF00307,PF08726	PS50021,PS50222,PS50021,PS50222		PS00020,PS00019,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.418.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.10.418.10,G3DSA:1.10.238.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60	SSF46966,SSF46966,SSF47576,SSF47473,SSF46966,SSF46966	273~300,438~458								
aly1603.82	Rap1 GTPase-activating protein 1	GO:1903697,GO:0007615,GO:0030424,GO:0032861,GO:0007165,GO:0043087,GO:0008355,GO:0005737,GO:0043547,GO:0005634,GO:0016020,GO:0043025,GO:0042803,GO:0005096,GO:0008016,GO:0003924,GO:0017016,GO:0008152,GO:0046582,GO:0005829,GO:0000139,GO:0005515	CG44424-PI				SM00225		PF02145,PF00651,PF00412	PS50085			G3DSA:3.30.710.10,G3DSA:3.30.710.10,G3DSA:2.10.110.10	SSF111347,SSF54695,SSF54695										
aly1603.83	Unknown		n/a						PF14214				G3DSA:3.40.50.300	SSF52540,SSF52540,SSF56219,SSF52540,SSF52540,SSF52540	203~223,1299~1319								
aly1603.84	Unknown	GO:0001104,GO:0016592,GO:0006357	CG14431-PB																				
aly1603.9	Thyroid adenoma-associated protein homolog	GO:0005575,GO:0003674,GO:0008150,GO:0005488	CG3368-PA						PF10350				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly16031.1	Tankyrase-1	GO:0018107,GO:0000242,GO:0005200,GO:0006471,GO:0090364,GO:0035220,GO:0070213,GO:0000781,GO:0018105,GO:0000784,GO:0003950,GO:0007067,GO:0070198,GO:0051028,GO:0051301,GO:0000922,GO:0032212,GO:0032210,GO:0000209,GO:0051225,GO:0090263,GO:0005794,GO:0031965,GO:0007052,GO:0022416,GO:0043392,GO:0000775,GO:0070212,GO:0007016,GO:0005643,GO:0005829,GO:0016055,GO:0000139,GO:0045944,GO:0005515,GO:0015031,GO:0008270	CG4719-PB				SM00454,SM00248,SM00248,SM00248,SM00248		PF00536,PF13857,PF13857,PF00644	PS50088,PS50105,PS50088,PS51059,PS50297,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:3.90.228.10,G3DSA:1.10.150.50	SSF47769,SSF56399,SSF48403									
aly16031.2	Beta-sarcoglycan	GO:0005737,GO:0005856,GO:0007517,GO:0055013,GO:0016021,GO:0048747,GO:0016012,GO:0008307,GO:0097084,GO:0042383	CG5657-PA						PF04790														
aly16031.3	Proteasome subunit alpha type-2	GO:0005737,GO:0004175,GO:0005839,GO:0000502,GO:0008283,GO:0043161,GO:0005634,GO:0009987,GO:0010499,GO:0004298,GO:0007052,GO:0006511,GO:0019773,GO:0006508,GO:0000022,GO:0090307	CG5266-PA				SM00948		PF00227,PF10584	PS51475		PS00388	G3DSA:3.60.20.10	SSF56235			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_110							
aly160983.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0022857,GO:0005886,GO:0055085	CG1213-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1610.1	Nuclear receptor subfamily 2 group E member 1	GO:0016319,GO:0001748,GO:0055057,GO:0008270,GO:0043401,GO:0003677,GO:0001746,GO:0007275,GO:0004879,GO:0007362,GO:0043565,GO:0009948,GO:0005634,GO:0007369,GO:0048749,GO:0035271,GO:0045165,GO:0051726,GO:0003700,GO:0003705,GO:0003707,GO:0006355,GO:0045944,GO:0006351,GO:0008293,GO:0001708	CG1378-PA				SM00399		PF00105	PS51030	PR00047,PR00047,PR00047,PR00047	PS00031	G3DSA:1.10.565.10,G3DSA:3.30.50.10	SSF57716			REACT_71						
aly1610.10	Unknown		n/a											SSF56219									
aly1610.11	EF-hand calcium-binding domain-containing protein 1	GO:0005509	CG2256-PC							PS50222,PS50222			G3DSA:1.10.238.10	SSF47473									
aly1610.12	SCY1-like protein 2	GO:0090090,GO:0005794,GO:0006468,GO:2000286,GO:2000370,GO:0008333,GO:0002092,GO:0005488,GO:0004672,GO:0048471,GO:0010008,GO:0005102,GO:0005524,GO:0030136	CG34356-PF										G3DSA:1.25.10.10	SSF48371,SSF48371	532~534								
aly1610.13	SCY1-like protein 2	GO:0090090,GO:0005794,GO:0006468,GO:2000286,GO:2000370,GO:0008333,GO:0002092,GO:0004672,GO:0048471,GO:0030136,GO:0005102,GO:0005524,GO:0010008	CG34356-PF				SM00220		PF00069	PS50011			G3DSA:1.10.510.10	SSF56112,SSF56112									
aly1610.14	Unknown		n/a																				
aly1610.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1610.3	Solute carrier family 46 member 3	GO:0016021,GO:0055085,GO:0004016	CG42514-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly1610.4	Putative serine protease K12H4.7	GO:0006508,GO:0045087,GO:0004185,GO:0008236	CG9953-PA						PF05577				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474									
aly1610.5	Probable citrate synthase 2, mitochondrial	GO:0046912,GO:0044262,GO:0004108,GO:0005739,GO:0006099,GO:0005759,GO:0005975,GO:0005875	CG3861-PA					TIGR01793	PF00285		PR00143,PR00143,PR00143,PR00143,PR00143,PR00143	PS00480	G3DSA:1.10.580.10	SSF48256	36~56				UPA00223				
aly1610.6	RUS1 family protein C16orf58	GO:0016021,GO:0016020	CG10338-PA						PF04884														
aly1610.7	Peptidoglycan-recognition protein LF	GO:0019731,GO:0008745,GO:0045087,GO:0009617,GO:0006952,GO:0031240,GO:0098542,GO:0008270,GO:0005887,GO:0009253,GO:0046329,GO:0008340,GO:0061057,GO:0042834	CG4437-PA				SM00644,SM00701		PF01510				G3DSA:3.40.80.10	SSF55846									
aly1610.8	Sodium channel protein Nach	GO:0035002,GO:0016021,GO:0005272,GO:0035725,GO:0006814	CG34059-PA						PF00858		PR01078,PR01078,PR01078,PR01078		G3DSA:2.60.470.10,G3DSA:2.60.470.10,G3DSA:2.60.470.10,G3DSA:1.10.287.770										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1610.9	Sodium/potassium/calcium exchanger 5	GO:0042470,GO:0015293,GO:0050896,GO:0006811,GO:0005802,GO:0032588,GO:0055085,GO:0034220,GO:0035725,GO:0008273,GO:0016021,GO:0048022	CG17167-PD					TIGR00367	PF01699,PF01699								REACT_15518						
aly161121.1	Unknown	GO:0005737,GO:0019010	CG10527-PA				SM00696,SM00696		PF11901,PF11901														
aly1614.1	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG4920-PA				SM00020		PF12032,PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1614.2	Serine protease easter	GO:0004252,GO:0009950,GO:0045087,GO:0008063,GO:0031638,GO:0006952,GO:0050830,GO:0005576,GO:0007311,GO:0045752,GO:0006508,GO:0008233,GO:0008236	CG5896-PB				SM00020		PF12032,PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1614.3	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0035006,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG1102-PC				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1614.4	Nephrin	GO:0043234,GO:0007517,GO:0051393,GO:0030507,GO:0016021,GO:0016020,GO:0003094,GO:0019904,GO:0005886,GO:0007155,GO:0036057,GO:0045121	CG34114-PB				SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408		PF08205,PF08205,PF07679	PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726									
aly16161.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1620.1	Unknown		n/a						PF14469														
aly1620.10	Sodium/potassium/calcium exchanger Nckx30C	GO:0048749,GO:0015293,GO:0016021,GO:0006816,GO:0006814,GO:0035725,GO:0048812,GO:0008273,GO:0055085	CG18660-PD						PF01699								REACT_15518						
aly1620.11	Unknown		n/a												167~187								
aly1620.2	Putative phosphatidate phosphatase	GO:0007424,GO:0045177,GO:0016020,GO:0016791,GO:0009880,GO:0016311,GO:0035234,GO:0016021,GO:0019991,GO:0035233,GO:0007280,GO:0045824,GO:0005886,GO:0050829,GO:0042803,GO:0008195,GO:0008354,GO:0005918	CG8804-PB				SM00014		PF01569				G3DSA:1.20.144.10	SSF48317									
aly1620.3	Putative phosphatidate phosphatase	GO:0007424,GO:0045177,GO:0019991,GO:0016791,GO:0009880,GO:0016311,GO:0035234,GO:0016021,GO:0016020,GO:0035233,GO:0007602,GO:0007280,GO:0045824,GO:0050829,GO:0005918,GO:0008195,GO:0008354,GO:0042803	CG11426-PA				SM00014		PF01569				G3DSA:1.20.144.10	SSF48317									
aly1620.4	Threonine--tRNA ligase, cytoplasmic	GO:0006435,GO:0005737,GO:0015629,GO:0004829,GO:0043039,GO:0016876,GO:0022008,GO:0005524,GO:0070062	CG5353-PA	MF_00184			SM00863	TIGR00418	PF07973,PF03129,PF02824,PF00587	PS50862	PR01047,PR01047,PR01047,PR01047,PR01047		G3DSA:3.30.980.10,G3DSA:3.30.980.10,G3DSA:3.30.54.20,G3DSA:3.40.50.800,G3DSA:3.30.930.10,G3DSA:3.10.20.30	SSF55186,SSF52954,SSF81271,SSF55681		00970+6.1.1.3	REACT_71						
aly1620.5	Unknown		n/a												12~32								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1620.6	Unknown	GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0050907,GO:0004970	CG14076-PC										G3DSA:3.40.190.10	SSF53850									
aly1620.7	Glutamate receptor 1	GO:0007631,GO:0005783,GO:0055037,GO:0019899,GO:0050907,GO:0046959,GO:0035249,GO:0030054,GO:0004971,GO:0016021,GO:0016020,GO:0015276,GO:0009612,GO:0001966,GO:0004970,GO:0043005,GO:0043025,GO:0007614,GO:0008328,GO:0035235,GO:0005234,GO:0045211,GO:0050913,GO:0032589,GO:0014069,GO:0030425,GO:0006972,GO:0005886,GO:0043058,GO:0008306,GO:0045202	CG14076-PC						PF00060				G3DSA:1.10.287.70,G3DSA:3.40.190.10	SSF53850,SSF53850									
aly1620.8	Hemocyte protein-glutamine gamma-glutamyltransferase	GO:0018149,GO:0042381,GO:0003810,GO:0045087,GO:0016020,GO:0046872	CG7356-PA			PIRSF000459	SM00460		PF00868,PF00927,PF00927,PF01841			PS00547	G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.90.260.10,G3DSA:2.60.40.10	SSF49309,SSF81296,SSF49309,SSF54001									
aly1620.9	Nicalin	GO:0031648,GO:0009966,GO:0016021,GO:0016020,GO:0005789,GO:0043254	CG4972-PA						PF04389				G3DSA:3.40.630.10	SSF53187									
aly1621.1	Unknown		n/a												361~388								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1621.2	Tetraspanin-33	GO:0006909,GO:0051604,GO:0016021,GO:0097197,GO:0019899,GO:0090002,GO:0045747,GO:0003674,GO:0005886,GO:0007298,GO:0009986	CG10742-PA			PIRSF002419			PF00335		PR00259,PR00259,PR00259	PS00421		SSF48652									
aly1621.3	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly1621.4	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131		G3DSA:3.20.20.80	SSF51445									
aly1621.5	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly1621.6	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232			PS00653	G3DSA:3.20.20.80	SSF51445									
aly1621.7	Cytosolic beta-glucosidase	GO:0005975,GO:0005829,GO:0016139,GO:0008422,GO:0004565,GO:0006687,GO:0004553,GO:0017042,GO:0046477,GO:0006665,GO:0044281	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131		G3DSA:3.20.20.80	SSF51445									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly162152.1	Unknown		n/a																				
aly1624.1	Pleckstrin homology-like domain family B member 1	GO:0010717,GO:0007018,GO:1904261,GO:0045180,GO:0010470,GO:0005871,GO:0070507,GO:0003777	CG5004-PA						PF00498				G3DSA:2.30.29.30,G3DSA:2.60.200.20	SSF50729,SSF49879	1398~1421,860~894,955~975,793~827,906~940,420~460,1376~1396,980~1021								
aly1624.2	m7GpppX diphosphatase	GO:0005737,GO:0016787,GO:0000290,GO:0036245,GO:0045292,GO:0005739,GO:0005654,GO:0000340,GO:0046331,GO:0050072,GO:0043069,GO:0005634	CG2091-PA						PF11969,PF05652,PF09814				G3DSA:3.30.428.10	SSF54197,SSF102860									
aly1624.3	Neurotrimin	GO:0019897,GO:0050767,GO:0043005,GO:0016337,GO:0005911,GO:0007399,GO:0009986,GO:0042063,GO:0007409,GO:0005886,GO:0043025,GO:0031225	CG10382-PA				SM00409,SM00409,SM00409		PF07679,PF07679,PF07679	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly1624.4	Unknown		n/a																				
aly1624.5	Unknown		n/a																				
aly1625.1	Unknown		n/a																				
aly1625.2	Protein FAM136A	GO:0005739	CG5323-PA						PF05811				G3DSA:1.10.287.810										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1625.3	Unknown		n/a																				
aly1625.4	Unknown		n/a																				
aly1625.5	Chorion class A protein Ld2/Ld41	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														
aly1625.6	Chorion class CB protein M5H4	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														
aly1625.7	Chorion class A protein Ld2/Ld41	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														
aly1625.8	Chorion class A protein Ld2/Ld41	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723,PF01723														
aly1625.9	Unknown		n/a																				
aly16252.1	Unknown		n/a																				
aly162786.1	Unknown		n/a																				
aly16287.1	Calcineurin-binding protein cabin-1	GO:0005737,GO:0005515,GO:0006336,GO:0060548,GO:0016235,GO:0005654,GO:0004864,GO:0007166,GO:0043086,GO:0016568	n/a										G3DSA:1.25.40.10										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1631.1	60S ribosome subunit biogenesis protein NIP7 homolog	GO:0044822,GO:0005634,GO:0042255,GO:0003723,GO:0005730	CG7006-PA										G3DSA:2.30.130.10,G3DSA:2.30.130.10	SSF88697,SSF88802									
aly1631.10	EF-hand calcium-binding domain-containing protein 2	GO:0005509	CG11041-PB							PS50222,PS50222			G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly1631.11	Heterogeneous nuclear ribonucleoprotein U-like protein 1	GO:0019899,GO:0006351,GO:0071011,GO:0009615,GO:0005634,GO:0044822,GO:0000398,GO:0030529,GO:0005654,GO:0006355,GO:0010467,GO:0003723,GO:0008380,GO:0006396,GO:0003729	CG30122-PC				SM00449,SM00513		PF00622,PF13671,PF02037	PS50800,PS50188			G3DSA:1.10.720.30,G3DSA:3.40.50.300	SSF68906,SSF52540,SSF49899	234~264,523~596								
aly1631.12	Unknown		n/a																				
aly1631.13	Desumoylating isopeptidase 2	GO:0005737,GO:0060027,GO:0008233	CG7222-PA						PF05903														
aly1631.14	Coatomer subunit delta	GO:0007436,GO:0006890,GO:0006909,GO:0009306,GO:0006886,GO:0035158,GO:0010883,GO:0030131,GO:0030126	CG14813-PA						PF01217				G3DSA:3.30.450.60	SSF64356	144~171								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1631.15	Unknown		n/a																				
aly1631.16	Unknown		n/a						PF16012														
aly1631.2	Unknown		n/a																				
aly1631.3	Calpain-B	GO:0005737,GO:0016540,GO:0016020,GO:0005622,GO:0005509,GO:0006508,GO:0007298,GO:0004198	CG8107-PA				SM00230,SM00720,SM00054,SM00054		PF01067,PF13833,PF00648	PS50222,PS50222,PS50222,PS50203,PS50222	PR00704,PR00704,PR00704,PR00704,PR00704,PR00704,PR00704,PR00704	PS00139	G3DSA:3.90.70.10,G3DSA:3.90.70.10,G3DSA:2.60.120.380,G3DSA:1.10.238.10	SSF54001,SSF47473,SSF49758										
aly1631.4	Unknown		n/a																				
aly1631.5	Unknown		n/a												138~174,519~539,551~571,481~501,779~799								
aly1631.6	Replicase polyprotein 1a	GO:0039520,GO:0008270,GO:0019079,GO:0044220,GO:0039648,GO:0033644,GO:0004197,GO:0003968,GO:0003723,GO:0019082,GO:0039579,GO:0039502,GO:0039595,GO:0008242,GO:0016021,GO:0039548	n/a											SSF54928	967~970								
aly1631.7	LWamide neuropeptides	GO:0007218,GO:0005576	n/a																				
aly1631.8	Unknown		n/a																				
aly1631.9	Unknown		n/a												28~48,547~567								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly16335.1	Allantoicase	GO:0000256,GO:0004037,GO:0006144	n/a			PIRSF016516		TIGR02961	PF03561,PF03561				G3DSA:2.60.120.260,G3DSA:2.60.120.260	SSF49785,SSF49785		00230+3.5.3.4		PWY-5697	UPA00395				
aly1636.1	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG6649-PA						PF00201,PF00201,PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756,SSF53756									
aly1636.2	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG6475-PD						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly1636.3	Vitellin-degrading protease	GO:0004252,GO:0004175,GO:0006508	CG31954-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1636.4	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG4302-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1638.1	Histone-lysine N-methyltransferase eggless	GO:0018024,GO:0035220,GO:0002165,GO:0046974,GO:0008270,GO:0003677,GO:0051567,GO:0007275,GO:0005737,GO:0005634,GO:0040029,GO:0034968,GO:0016571,GO:0045814,GO:0048477,GO:0010385,GO:0045892,GO:0044026,GO:0048132,GO:0051038,GO:0060968,GO:0005694,GO:0005700,GO:0010369,GO:0006351,GO:0005515	CG30426-PA				SM00508,SM00391,SM00317,SM00468		PF05033,PF00856,PF01429	PS50867,PS50982,PS50868,PS50280			G3DSA:3.30.890.10,G3DSA:2.170.270.10	SSF82199,SSF54171		00310+2.1.1.43							
aly1638.2	HMG domain-containing protein 4	GO:0008333,GO:0006338,GO:0016055,GO:0016589,GO:0005575,GO:0006355,GO:0003674,GO:0003677,GO:0008150,GO:0003682,GO:0030178	CG4617-PA				SM00398		PF00505	PS50118			G3DSA:1.10.30.10	SSF47095									
aly1638.3	Coiled-coil domain-containing protein 51	GO:0005654,GO:0016021,GO:0005739	n/a												249~269,95~122								
aly1638.4	Unknown		n/a												45~81								
aly1639.1	Solute carrier family 28 member 3	GO:0005887,GO:0016020,GO:0005415,GO:0006810,GO:0001882	CG8083-PA						PF01773,PF07662,PF07662								REACT_1698,REACT_15518						
aly1639.2	Unknown	GO:0046872	n/a				SM00355,SM00355,SM00355					PS00028,PS00028,PS00028											
aly1639.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly16397.1	Unknown		n/a																				
aly164.1	Protein shuttle craft	GO:0000977,GO:0007399,GO:0000122,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0006366,GO:0001078,GO:0003697,GO:0003723	CG3647-PB				SM00438,SM00438,SM00438		PF01422,PF01422,PF01422	PS50016,PS50089		PS01359	G3DSA:3.30.40.10	SSF57850									
aly164.10	Dual specificity mitogen-activated protein kinase kinase 3	GO:0000187,GO:0048082,GO:0042035,GO:0007309,GO:0060048,GO:0002385,GO:0005737,GO:0007346,GO:0031435,GO:0042981,GO:0016020,GO:0000165,GO:0031098,GO:0004674,GO:0004713,GO:0004672,GO:0005524,GO:0006468,GO:0019901,GO:0007314,GO:0045893,GO:0006954,GO:0007179,GO:0045793,GO:0040018,GO:0001934,GO:0004702,GO:0045860,GO:0004708	CG12244-PA			PIRSF000654	SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly164.11	Uncharacterized protein KIAA0195	GO:0005654,GO:0016021,GO:0000166,GO:0005575,GO:0003674,GO:0008150	CG3054-PA										G3DSA:3.40.1110.10,G3DSA:3.40.1110.10,G3DSA:3.40.1110.10	SSF81665,SSF81665,SSF81665,SSF81660									
aly164.12	Cytokine receptor	GO:0007616,GO:0006470,GO:0019955,GO:0007293,GO:0050829,GO:0035335,GO:0007298,GO:0001745,GO:0006955,GO:0002009,GO:0016021,GO:0007259,GO:0008284,GO:0060429,GO:0007442,GO:0016324,GO:0016327,GO:0045475,GO:0005886,GO:0007350,GO:0007425,GO:0007424,GO:0004725,GO:0005622,GO:0004888,GO:0045824,GO:0005515,GO:0046982	CG14226-PA				SM00060,SM00060,SM00060		PF00041	PS50853,PS50853,PS50853,PS50853,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF49265,SSF49265									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly164.13	WAS protein family homolog 2	GO:0055038,GO:0055037,GO:0051020,GO:0034314,GO:0005737,GO:0031410,GO:0005634,GO:0005770,GO:0005776,GO:0005814,GO:0003779,GO:0048471,GO:0048477,GO:0031901,GO:0031941,GO:0005515,GO:0035210,GO:0051017,GO:0042147,GO:0015031,GO:0035277,GO:0051764,GO:0016197,GO:0001578,GO:0005667,GO:0043014,GO:0071203,GO:0005768,GO:0005769	CG13176-PA						PF11945	PS51082													
aly164.14	WD repeat-containing protein 13	GO:0048188,GO:0006338,GO:0044545,GO:0004402,GO:0005875,GO:0005671,GO:0016573,GO:0051568,GO:0007095,GO:0022008,GO:0044666,GO:0005634,GO:0044665	CG17437-PA				SM00320,SM00320,SM00320		PF00400	PS50082,PS50294,PS50082,PS50294		PS00678	G3DSA:2.130.10.10	SSF50978									
aly164.15	Serine/threonine-protein kinase LMTK1	GO:0005783,GO:0055037,GO:0030425,GO:0007165,GO:0007169,GO:0046777,GO:0007417,GO:0038083,GO:0016021,GO:0016020,GO:0004674,GO:0004714,GO:0005030,GO:0004713,GO:0048471,GO:0005524,GO:0006468,GO:0006915,GO:0044295,GO:0032482,GO:0051402,GO:0005886,GO:0030517,GO:0007420	CG4926-PA						PF07714	PS50011		PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112	210~230,1482~1502								
aly164.16	Zinc phosphodiesterase ELAC protein 2	GO:0072684,GO:0046872,GO:0030307,GO:0005634,GO:0036093,GO:0044822,GO:0042781,GO:0005739,GO:0005654,GO:0006409,GO:0016891,GO:0046331,GO:0042779,GO:0006388,GO:0022008,GO:0045727,GO:0048477,GO:0042780,GO:0001558	CG3298-PB						PF12706,PF13691				G3DSA:3.60.15.10,G3DSA:3.60.15.10,G3DSA:3.60.15.10	SSF56281,SSF56281,SSF56281									
aly164.17	26S proteasome non-ATPase regulatory subunit 4	GO:0005737,GO:0031624,GO:0004175,GO:0005838,GO:0043161,GO:0005634,GO:0031593,GO:0000070,GO:0006974,GO:0006511,GO:0008270,GO:0000502,GO:0006508,GO:0007059,GO:0008540	CG7619-PA				SM00327,SM00726,SM00726		PF13519,PF02809,PF02809	PS50330,PS50330,PS50234			G3DSA:3.40.50.410	SSF53300	226~246,334~354								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly164.18	Putative ATP synthase subunit f, mitochondrial	GO:0045263,GO:0005811,GO:0015992,GO:0000276,GO:0005739,GO:0031966,GO:0046331,GO:0008553,GO:0006754	CG4692-PB						PF10206														
aly164.19	Mesencephalic astrocyte-derived neurotrophic factor homolog	GO:0005783,GO:0070050,GO:0042417,GO:0005576,GO:0005509,GO:0031175,GO:0007275	CG7013-PA						PF10208				G3DSA:1.10.225.10	SSF68906									
aly164.2	Serine/arginine rich splicing factor 2	GO:0016607,GO:0005737,GO:0035062,GO:0000381,GO:0005515,GO:0036002,GO:0070062,GO:0005634,GO:0044822,GO:0000398,GO:0000166,GO:0006376,GO:0003676,GO:0000785,GO:0006397,GO:0008380,GO:0005681,GO:0003729	CG5442-PB				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly164.20	Dynein assembly factor 5, axonemal	GO:0005737,GO:0036159,GO:0045505,GO:0036158,GO:0005575,GO:0003674,GO:0005488,GO:0003341,GO:0008150	CG31320-PA										G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371	295~315								
aly164.21	Poly(A)-specific ribonuclease PARN	GO:0005737,GO:0090503,GO:0046872,GO:0000288,GO:0000289,GO:0005730,GO:0004518,GO:0005829,GO:0004535,GO:0044822,GO:0009451,GO:0007292,GO:0090305,GO:0010467,GO:0000184,GO:0003730,GO:0000166,GO:0005634,GO:0019901	n/a						PF04857,PF08675				G3DSA:3.30.70.330,G3DSA:3.30.420.10,G3DSA:3.30.420.10,G3DSA:3.30.1370.50	SSF54928,SSF53098,SSF53098,SSF82708									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly164.22	Protein cortex	GO:0006909,GO:0007279,GO:0090302,GO:0007147,GO:0007067,GO:0007144,GO:0005737,GO:0005819,GO:0007343,GO:0005813,GO:0007349,GO:0007143,GO:0010997,GO:0048477,GO:0000278,GO:0034455,GO:0051297,GO:0009987,GO:0031145,GO:0030162,GO:0030163,GO:0022008,GO:0045143,GO:0000776,GO:0051488,GO:0030718,GO:0030490,GO:0051487,GO:0006355,GO:0005515,GO:0007096,GO:0005680,GO:0008054	CG4274-PA				SM00320,SM00320,SM00320			PS50294,PS50082		PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF69322										
aly164.23	Unknown		n/a																				
aly164.24	Unknown		n/a																				
aly164.25	Unknown		n/a																				
aly164.26	Unknown		n/a																				
aly164.27	Unknown		n/a																				
aly164.28	Unknown		n/a																				
aly164.29	Leucine-rich repeat protein soc-2 homolog	GO:0070374,GO:0017016,GO:0000164,GO:0046579	CG5407-PA				SM00364,SM00364,SM00364,SM00364,SM00369,SM00369,SM00369,SM00369						G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058	357~377								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly164.3	U3 small nucleolar RNA-interacting protein 2	GO:0032040,GO:0031428,GO:0030532,GO:0005634,GO:0005730,GO:0044822,GO:0006364,GO:0005515,GO:0022008,GO:0030515,GO:0034511,GO:0003729	CG33505-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400	PS50082,PS50294,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320		G3DSA:2.130.10.10	SSF50978	72~92								
aly164.30	Cancer-related nucleoside-triphosphatase homolog	GO:0070062,GO:0044822,GO:0016020,GO:0007476,GO:0017111,GO:0000166,GO:0098519,GO:0005524	CG10581-PA	MF_00796					PF03266				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540		00230+3.6.1.15,00730+3.6.1.15		PWY-7185,PWY-7184,PWY-7198,PWY-6545,PWY-7210					
aly164.31	Probable enoyl CoA hydratase, mitochondrial	GO:0006635,GO:0005811,GO:0005739,GO:0004300,GO:0005759,GO:0005875	CG6543-PB						PF00378			PS00166	G3DSA:3.90.226.10	SSF52096									
aly164.32	Unknown	GO:0003676	n/a						PF05485	PS50950				SSF57716									
aly164.33	Unknown		n/a												145~165								
aly164.34	Glutaminyl-peptide cyclotransferase	GO:0016603,GO:0070062,GO:0017186,GO:0005739,GO:0005576,GO:0006464,GO:0006508,GO:0008233,GO:0008270	CG5976-PB						PF04389				G3DSA:3.40.630.10	SSF53187									
aly164.35	Raffinose invertase	GO:0005737,GO:0005975,GO:0004575	n/a				SM00640	TIGR01322	PF08244,PF00251				G3DSA:2.115.10.20,G3DSA:2.60.120.560	SSF75005,SSF49899		00500+3.2.1.26,00052+3.2.1.26		PWY-621	UPA00238				
aly164.36	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly164.37	Sorting nexin-8	GO:0019898,GO:0006897,GO:0090389,GO:0035091,GO:0006886,GO:0071456,GO:0016050,GO:0005547,GO:0045335,GO:0042802,GO:0034498,GO:0005886,GO:0007067,GO:0000045,GO:0005768,GO:0031901,GO:0043231	CG6757-PA				SM00312		PF00787	PS50195			G3DSA:3.30.1520.10	SSF64268										
aly164.38	N-acylneuraminate cytidylyltransferase	GO:0016020,GO:0006054,GO:0008781,GO:0006055,GO:0005802,GO:0007268,GO:0009408,GO:0005634,GO:0009103	CG32220-PA						PF02348				G3DSA:3.90.550.10	SSF53448		00540+2.7.7.38		PWY-5111,PWY-1269	UPA00358,UPA00030				
aly164.39	ATP-dependent DNA helicase Q1	GO:0016020,GO:0003677,GO:0003678,GO:0006303,GO:0006302,GO:0000724,GO:0005634,GO:0006281,GO:0005654,GO:0006260,GO:0043140,GO:0005524,GO:0000403,GO:0004003,GO:0032508,GO:0004386,GO:0006974,GO:0007131,GO:0036310,GO:0006310,GO:0008094,GO:0045003,GO:0000731,GO:0000732,GO:0000733,GO:1901291	CG6920-PA				SM00490,SM00487	TIGR00614	PF00271,PF16124,PF00270	PS51194,PS51192			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.10.10	SSF52540	4~24								
aly164.4	INO80 complex subunit C	GO:0006310,GO:0006338,GO:0005730,GO:0006281,GO:0031011,GO:0006355,GO:0006351,GO:0071339	CG12659-PC				SM00993		PF08265														
aly164.40	UPF0193 protein EVG1 homolog	GO:0005575,GO:0003674,GO:0008150	CG5280-PA						PF05250														
aly164.41	Unknown		n/a												9~53,151~176								
aly164.42	Unknown		CG30373-PA						PF15013						112~138								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly164.43	Histone H3.3	GO:0006334,GO:0003677,GO:0006333,GO:0000786,GO:0046982,GO:0005634,GO:0007140	CG8989-PA				SM00428		PF00125		PR00622,PR00622,PR00622,PR00622,PR00622,P	PS00322,PS00959	G3DSA:1.10.20.10	SSF47113									
aly164.44	RING finger protein unkempt	GO:0048749,GO:0005737,GO:0030182,GO:0050767,GO:0007476,GO:0008407,GO:0002164,GO:0008270,GO:0003677	CG4620-PD				SM00356,SM00356,SM00356,SM00356,SM00184		PF00642,PF13920	PS50103,PS50103,PS50103,PS50103,PS50089,PS50103			G3DSA:3.30.40.10,G3DSA:4.10.1000.10,G3DSA:4.10.1000.10	SSF90229,SSF57850	546~566,478~526								
aly164.45	Unknown		CG2519-PA																				
aly164.46	Unknown		CG2519-PA																				
aly164.47	Cyclin-dependent kinase 2-associated protein 1	GO:0007049	CG18292-PB						PF09806,PF09806														
aly164.48	Diphthine methyltransferase	GO:0044267,GO:0061685,GO:0017183,GO:0005829,GO:0005575,GO:0003674,GO:0008150,GO:0043687	CG3184-PA				SM00320,SM00320,SM00320,SM00320,SM00320			PS50082,PS50294		PS00678	G3DSA:2.130.10.10	SSF50978									
aly164.49	Uncharacterized protein CG5098	GO:0005575,GO:0003674,GO:0008150	CG5098-PC																				
aly164.5	Ribosome biogenesis regulatory protein homolog	GO:0005783,GO:0005730,GO:0005634,GO:0042254,GO:0002244,GO:0007080,GO:0000794,GO:0044822	CG32409-PA						PF04939						172~192								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly164.50	B9 domain-containing protein 1	GO:0005737,GO:0035869,GO:0036038,GO:0042384,GO:0060271,GO:0036064,GO:0005813,GO:0007224,GO:0008158	CG14870-PA						PF07162	PS51381													
aly164.51	Trehalase	GO:0015927,GO:0004555,GO:0016323,GO:0005991,GO:0046658	CG9364-PF						PF01204		PR00744,PR00744,PR00744,PR00744,PR00744,PR00744,PR00744	PS00927,PS00928		SSF48208		00500+3.2.1.28							
aly164.52	Trehalase	GO:0015927,GO:0004555,GO:0016323,GO:0005991,GO:0046658	CG9364-PF						PF01204	PS51257	PR00744,PR00744,PR00744,PR00744,PR00744,PR00744,PR00744	PS00928		SSF48208		00500+3.2.1.28							
aly164.53	Transcription factor Adf-1	GO:0040011,GO:0006366,GO:0050773,GO:0007616,GO:0005634,GO:0005705,GO:0007613,GO:0007611,GO:0001077,GO:0048813,GO:0006357,GO:0045944,GO:0045893,GO:0005667,GO:0003677,GO:0008345,GO:0003712,GO:0007416,GO:0008355	CG15845-PE				SM00595		PF02944,PF10545	PS51031,PS51029													
aly164.54	Acylamino-acid-releasing enzyme	GO:0005737,GO:0004252,GO:0070062,GO:0008242,GO:0031965,GO:0006508,GO:0050435,GO:0044822	n/a						PF00326,PF00326				G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474,SSF82171,SSF82171									
aly164.55	Forkhead box protein J1.2	GO:0043565,GO:0051090,GO:0060271,GO:0007389,GO:0003700,GO:0005634,GO:0001222,GO:0003705,GO:0009888,GO:0009790,GO:0042384,GO:0008301,GO:0006351,GO:0005667,GO:0000287,GO:0003690,GO:0008134	CG11799-PN				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00658,PS00657	G3DSA:1.10.10.10	SSF46785									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly164.56	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0045455,GO:0055114,GO:0016491	CG9503-PA						PF05199,PF00732			PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905,SSF54373										
aly164.57	Geranylgeranyl transferase type-2 subunit beta	GO:0018344,GO:0005968,GO:0007601,GO:0017137,GO:0006464,GO:0004662,GO:0004663,GO:0008270	CG18627-PA						PF00432,PF00432,PF00432,PF00432,PF00432				G3DSA:1.50.10.20	SSF48239									
aly164.58	Galactokinase	GO:0005737,GO:0005975,GO:0070062,GO:0006012,GO:0005829,GO:0016020,GO:0046835,GO:0004335,GO:0044281,GO:0019402,GO:0019388,GO:0005534,GO:0005524	CG5288-PD			PIRSF000530		TIGR00131	PF10509,PF00288,PF08544		PR00959,PR00959,PR00959,PR00959,PR00473,PR00473,PR00473,PR00473	PS00106	G3DSA:3.30.230.10,G3DSA:3.30.70.890	SSF55060,SSF54211		00520+2.7.1.6,00052+2.7.1.6		PWY-6317,PWY-6527,PWY-3821	UPA00214				
aly164.59	Guanylate cyclase 32E	GO:0006468,GO:0016772,GO:0004383,GO:0005886,GO:0016849,GO:0005525,GO:0006182,GO:0005622,GO:0007165,GO:0005887,GO:0004672,GO:0035556,GO:0009190,GO:0005524,GO:0004872	CG33114-PB				SM00044		PF00211,PF01094,PF07714	PS50125,PS50011		PS00452	G3DSA:3.30.70.1230,G3DSA:1.10.510.10,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.30.200.20	SSF53822,SSF56112,SSF55073									
aly164.6	DNA fragmentation factor subunit beta	GO:0005737,GO:0006921,GO:0005730,GO:0004536,GO:0005634,GO:0006915,GO:0000790,GO:0006309,GO:0005622,GO:0005654,GO:0012501,GO:0030263,GO:0019899,GO:0005829	CG9414-PA				SM00266		PF02017,PF09230	PS51135			G3DSA:3.10.20.10	SSF54277,SSF54060									
aly164.60	Oxidoreductase-like domain-containing protein 1	GO:0005739	CG5500-PA						PF09791														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly164.61	Rho GDP-dissociation inhibitor 1	GO:0005737,GO:0030336,GO:0001772,GO:0032880,GO:0070062,GO:0071407,GO:0071260,GO:0016020,GO:0005096,GO:0071526,GO:0017048,GO:0019901,GO:0008360,GO:0005615,GO:0005094,GO:0005504,GO:0007266,GO:0005634,GO:0051879,GO:0005829,GO:0071461	CG7823-PB						PF02115		PR00492,PR00492,PR00492,PR00492,PR00492		G3DSA:2.70.50.30	SSF81296			REACT_11044						
aly164.62	Unknown	GO:0004061,GO:0019441	n/a						PF04199				G3DSA:3.50.30.50	SSF102198		00630+3.5.1.9,00380+3.5.1.9		PWY-5651,PWY-6309	UPA00333				
aly164.63	Unknown	GO:0005575,GO:0030837,GO:0016055,GO:0007476,GO:0017048,GO:0035317,GO:0003779,GO:0035320,GO:0003674,GO:0005488,GO:2000039,GO:0001736	CG43772-PC						PF06367					SSF48371,SSF48371	355~413								
aly164.64	Probable chitinase 3	GO:0005737,GO:0005975,GO:0000272,GO:0005576,GO:0008061,GO:0004568,GO:0006030,GO:0006032,GO:0008201	CG1869-PA				SM00636,SM00636,SM00494		PF01607,PF00704,PF00704	PS50940		PS01095,PS01095	G3DSA:2.170.140.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.10.50.10,G3DSA:3.10.50.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF57625,SSF51445,SSF51445,SSF54556,SSF51445,SSF51445,SSF54556		00520+3.2.1.14		PWY-6902					
aly164.65	Unknown		n/a											SSF54001									
aly164.66	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly164.67	Androglobin	GO:0005737,GO:0020037,GO:0005515,GO:0006508,GO:0005506,GO:0004198,GO:0015671	n/a				SM00015		PF00612	PS50096													
aly164.68	Unknown		n/a																				
aly164.69	Guanine nucleotide-binding protein subunit gamma-e	GO:0005737,GO:0016028,GO:0005834,GO:0007601,GO:0003924,GO:0007602,GO:0071244,GO:0004871,GO:0005886,GO:0046982,GO:0007186	CG3694-PA				SM00224		PF00631	PS50058	PR00321,PR00321,PR00321		G3DSA:4.10.260.10	SSF48670			REACT_14797,REACT_15380,REACT_604,REACT_13685,REACT_15295,REACT_1505						
aly164.7	Thymidylate kinase	GO:0045445,GO:0044281,GO:0004798,GO:0009041,GO:0007049,GO:0005737,GO:0006227,GO:0046939,GO:0015949,GO:0046686,GO:0005758,GO:0005524,GO:0008283,GO:0005759,GO:0043627,GO:0006233,GO:0046940,GO:0055086,GO:0006235,GO:0071363,GO:0005829,GO:0050145	CG5757-PA	MF_00165				TIGR00041	PF02223			PS01331	G3DSA:3.40.50.300	SSF52540		00240+2.7.4.9		PWY-7210,PWY-7198,PWY-7184,PWY-7187,PWY-7197,PWY-6545					
aly164.70	Unknown		n/a										G3DSA:2.40.128.20	SSF50814									
aly164.71	Unknown		n/a																				
aly164.72	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly164.73	Unknown	GO:0006030,GO:0005576,GO:0008061	CG13806-PA				SM00494		PF01607	PS50940,PS50940			G3DSA:2.170.140.10	SSF57625									
aly164.74	Unknown		n/a																				
aly164.75	Unknown		n/a																				
aly164.76	Unknown		CG2519-PA																				
aly164.77	Unknown	GO:0003677	CG4404-PA				SM00595		PF10545	PS51029,PS51031					234~244								
aly164.78	Unknown		n/a																				
aly164.79	Unknown		n/a						PF03732														
aly164.8	Protein penguin	GO:0005730,GO:0007475,GO:0005575,GO:0003723,GO:0006417,GO:0003729	CG1685-PA				SM00025,SM00025,SM00025		PF08144	PS50302,PS50302,PS50302,PS50303,PS50302			G3DSA:1.25.10.10	SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly164.9	DNA excision repair protein ERCC-6	GO:0035060,GO:0008022,GO:0035063,GO:0042752,GO:0035264,GO:0047485,GO:0000303,GO:0016589,GO:0031491,GO:0009411,GO:0006979,GO:0016887,GO:0003677,GO:0003678,GO:0016590,GO:0006283,GO:0006290,GO:0007256,GO:0007257,GO:0007517,GO:0042766,GO:0008623,GO:0005730,GO:0006325,GO:0005634,GO:0043044,GO:0009636,GO:0000166,GO:0005654,GO:0006362,GO:0006366,GO:0061098,GO:0010332,GO:0005524,GO:0035076,GO:0006284,GO:0005667,GO:0010224,GO:0006281,GO:0008134,GO:0032784,GO:0032786,GO:0004386,GO:0031213,GO:0032403,GO:0000790,GO:0045892,GO:0045893,GO:0006289,GO:0010165,GO:0030296,GO:0008630,GO:0016584,GO:0008094,GO:0070615,GO:0006338,GO:0008023,GO:0006334,GO:0006333,GO:0005700,GO:0006355,GO:0048813,GO:0006357,GO:0045944,GO:0006351,GO:0005515,GO:0003682,GO:0045494	CG8625-PA				SM00490,SM00487		PF00176,PF00271	PS51192,PS51194			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	960~980,715~735								
aly16416.1	Exportin-7	GO:0005737,GO:0005049,GO:0005643,GO:0006886,GO:0008536,GO:0006913,GO:0006611,GO:0051028,GO:0005634	CG33180-PF				SM00913		PF03810	PS50166			G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371									
aly16416.2	Unknown		n/a																				
aly16416.3	Unknown	GO:0033181,GO:0033180,GO:0015991,GO:0046961,GO:0046933	CG8029-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly16416.4	V-type proton ATPase subunit S1	GO:0045780,GO:0045851,GO:0070062,GO:2001206,GO:0015991,GO:0016021,GO:0046933,GO:0005774,GO:0033181,GO:0033180,GO:0070374,GO:0045921,GO:0046961,GO:0051656,GO:0045669,GO:0005524	CG8029-PB																				
aly16416.5	Unknown		n/a																				
aly16416.6	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005576,GO:0005886,GO:0006508	CG5390-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly16416.7	Unknown		n/a																				
aly16437.1	Collagenase	GO:0004252,GO:0022008,GO:0005576,GO:0030574,GO:0006508	CG8869-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly16439.1	Coiled-coil domain-containing protein 124	GO:0005737,GO:0030496,GO:0051301,GO:0007049,GO:0005815	n/a																				
aly16448.1	Cytoplasmic FMR1-interacting protein	GO:0005737,GO:0045177,GO:0006909,GO:0000902,GO:0033627,GO:0030031,GO:0050807,GO:0030866,GO:0017048,GO:0008360,GO:0045202,GO:0007411,GO:0001745,GO:0022416,GO:0031209	CG4931-PA						PF05994														
aly1645.1	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947												

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1645.10	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG1919-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly1645.11	Cuticle protein 8	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly1645.12	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG1919-PA						PF00379,PF00379	PS51155,PS51155	PR00947,PR00947,PR00947												
aly1645.13	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG1919-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly1645.14	Cuticle protein 18.6, isoform A	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly1645.15	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG1919-PA						PF00379	PS51155,PS51257	PR00947,PR00947,PR00947												
aly1645.16	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly1645.17	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG9295-PC						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly1645.18	Cuticle protein 19	GO:0040003,GO:0005214,GO:0008010,GO:0008012,GO:0031012,GO:0042302	CG9290-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly1645.19	Unknown	GO:0008150,GO:0005634,GO:0031965,GO:0003677	CG12023-PA																				
aly1645.2	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly1645.20	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1645.3	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly1645.4	Adult-specific cuticular protein ACP-20	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly1645.5	Cuticle protein 7	GO:0040003,GO:0005214,GO:0008011,GO:0008010,GO:0031012,GO:0022008,GO:0042302	CG31876-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly1645.6	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly1645.7	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly1645.8	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG1919-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly1645.9	Cuticle protein 19	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG1919-PA																				
aly16464.1	Zinc finger BED domain-containing protein 1	GO:0004803,GO:0000228,GO:0046872,GO:0008152,GO:0003677	n/a											SSF140996									
aly16464.2	Unknown	GO:0046983	n/a						PF05699					SSF53098									
aly16464.3	Unknown		n/a																				
aly16474.1	Cytochrome P450 307a1	GO:0001700,GO:0042335,GO:0007494,GO:0005783,GO:0020037,GO:0048566,GO:0016705,GO:0007591,GO:0004497,GO:0007391,GO:0005789,GO:0005575,GO:0008258,GO:0006697,GO:0005506,GO:0007417,GO:0048477,GO:0055114,GO:0016491	CG41624-PB						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264,SSF48264			REACT_13433							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1651.1	WD repeat-containing protein 82	GO:0051013,GO:0035097,GO:0048188,GO:0005515,GO:0051568,GO:0008352,GO:0080182	CG17293-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400	PS50082,PS50294,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10	SSF50978									
aly1651.10	GDP-fucose protein O-fucosyltransferase 1	GO:0016337,GO:0005783,GO:0009790,GO:0030173,GO:0046922,GO:0036065,GO:0005737,GO:0007219,GO:0031410,GO:0045746,GO:0045747,GO:0005112,GO:0005794,GO:0016266,GO:0046331,GO:0030163,GO:0008593,GO:0006493,GO:0006897,GO:0007399,GO:0008417,GO:0006355,GO:0036066,GO:0006004	CG12366-PA						PF10250							00514+2.4.1.221			UPA00378				
aly1651.11	WD repeat-containing protein 55 homolog	GO:0005575,GO:0016505,GO:0050829,GO:0005515	CG14722-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50082,PS50294,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978									
aly1651.12	Protein timeless	GO:0071482,GO:0007617,GO:0008062,GO:0046957,GO:0060086,GO:0005737,GO:0050764,GO:0000122,GO:0005634,GO:0048512,GO:0042749,GO:0048471,GO:0050766,GO:0007623,GO:0007622,GO:0007620,GO:0008134,GO:0006606,GO:0045187,GO:0045475,GO:0009649,GO:0009648,GO:0042306,GO:0030431,GO:0043234,GO:0005515,GO:0046982,GO:2000678	CG3234-PB						PF04821														
aly1651.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1651.14	Actin-related protein 2/3 complex subunit 5	GO:0005737,GO:0042995,GO:0030833,GO:0006909,GO:0015629,GO:0030027,GO:0070062,GO:0003779,GO:0005200,GO:0005885,GO:0034314,GO:0016477,GO:0005925,GO:0000902	CG9881-PA			PIRSF039096			PF04699				G3DSA:1.25.40.190	SSF69103									
aly1651.15	Programmed cell death protein 10	GO:0060439,GO:0005886,GO:0001525,GO:0006915,GO:0000139	CG5073-PA						PF06840						82~109								
aly1651.16	Protein escargot	GO:0035147,GO:0055059,GO:0035220,GO:0003677,GO:0001078,GO:0007417,GO:0042332,GO:0000122,GO:0005634,GO:0001709,GO:0046872,GO:0035215,GO:0035156,GO:0007424,GO:0042048,GO:0048076,GO:0007489,GO:0032876,GO:0045893,GO:0030718,GO:0007427,GO:0007422,GO:0003700,GO:0006357,GO:0045944,GO:0006351,GO:0045892,GO:0001708	CG3758-PA				SM00355,SM00355,SM00355,SM00355,SM00355		PF00096	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly1651.17	EGF domain-specific O-linked N-acetylglucosamine transferase	GO:0006493,GO:0008152,GO:0016262,GO:0097370,GO:0097363,GO:0005788,GO:0008363,GO:0016757	CG9867-PB						PF04577														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1651.18	Transcription factor Dp-1	GO:0007307,GO:0000082,GO:0097193,GO:0010628,GO:0003677,GO:0008069,GO:0043565,GO:0007219,GO:0005634,GO:0003713,GO:0005654,GO:0010467,GO:1900740,GO:0006367,GO:0048477,GO:0000981,GO:0045850,GO:0070345,GO:0000278,GO:0008283,GO:0008134,GO:0006915,GO:0005667,GO:0012501,GO:0019904,GO:0045476,GO:0007179,GO:0007113,GO:0008630,GO:0051726,GO:0003700,GO:0031523,GO:0006355,GO:0006357,GO:0045944,GO:0006351,GO:0005515,GO:0035189	CG4654-PA							PF08781,PF02319			G3DSA:1.10.10.10	SSF46785,SSF144074	258~285								
aly1651.19	Myeloma-overexpressed gene 2 protein homolog	GO:0005575,GO:0003674,GO:0051726	CG17059-PA						PF15004														
aly1651.2	Chromodomain-helicase-DNA-binding protein 7	GO:0019730,GO:0048752,GO:0030540,GO:0007614,GO:0060021,GO:0001501,GO:0021553,GO:0060324,GO:0003677,GO:0007411,GO:0007298,GO:0005875,GO:0050767,GO:0008026,GO:0007512,GO:0005634,GO:0007476,GO:0005654,GO:0042048,GO:0043584,GO:0006364,GO:0005524,GO:0030217,GO:0008015,GO:0046622,GO:0060429,GO:0016322,GO:0007628,GO:0003007,GO:0035116,GO:0045892,GO:0021772,GO:0007605,GO:0008340,GO:0007350,GO:0040011,GO:0060123,GO:0007031,GO:0007379,GO:0040018,GO:0050890,GO:0006355,GO:0006351,GO:0004386,GO:0000978,GO:0003682,GO:0048844,GO:0016568,GO:0060041	CG3696-PC				SM00592,SM00298,SM00298,SM00298,SM00487,SM00490		PF00176,PF07533,PF00271,PF00385	PS51194,PS50013,PS51192			G3DSA:3.40.50.300,G3DSA:2.40.50.40,G3DSA:2.40.50.40,G3DSA:2.40.50.40,G3DSA:3.40.50.300	SSF160481,SSF54160,SSF54160,SSF52540,SSF52540	1141~1164,2499~2519								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1651.20	tRNA-dihydrouridine (20) synthase [NAD(P)+]-like	GO:0005737,GO:0050660,GO:0008033,GO:0005783,GO:0065548,GO:0005739,GO:0004860,GO:0003824,GO:0003725,GO:0006469,GO:0017150,GO:0055114	CG1434-PA				SM00358		PF00035,PF01207				G3DSA:3.20.20.70,G3DSA:3.30.160.20	SSF54768,SSF51395									
aly1651.21	Protein big brother	GO:0035206,GO:0005634,GO:0003713,GO:0016513,GO:0006357,GO:0045944,GO:0046982,GO:0008134	CG7959-PB						PF02312				G3DSA:2.40.250.10	SSF50723	160~187								
aly1651.22	Protein crossbronx homolog	GO:0005575,GO:0016881,GO:0007291,GO:0003674,GO:0042742,GO:0007286	CG10536-PB				SM00212		PF00179	PS50127			G3DSA:3.10.110.10	SSF54495									
aly1651.23	UPF0598 protein C8orf82 homolog	GO:0005575,GO:0003674,GO:0042060	CG30010-PA						PF14956,PF14956														
aly1651.24	Katanin p80 WD40 repeat-containing subunit B1	GO:0007017,GO:0007420,GO:0051013,GO:0005813,GO:0008017,GO:0000922,GO:0030901,GO:0005515,GO:0008352,GO:0007067,GO:0005874,GO:0051301,GO:0046843	CG13956-PB	MF_03022			SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF13925	PS50082,PS50294,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678	G3DSA:2.130.10.10	SSF50978									
aly1651.25	M-phase phosphoprotein 6	GO:0005737,GO:0000460,GO:0000178,GO:0005730,GO:0005634,GO:0005575,GO:0003674,GO:0003723,GO:0022008	CG9250-PA						PF10175						16~36								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1651.26	Nucleolar protein 10	GO:0005634,GO:0005515,GO:0005730	CG7516-PA						PF08159				G3DSA:2.130.10.10	SSF50978									
aly1651.27	Unknown		CG3831-PC																				
aly1651.28	Sodium leak channel non-selective protein	GO:0005261,GO:0005272,GO:0043679,GO:0016021,GO:0016020,GO:0055085,GO:0048512,GO:0043025,GO:0005216,GO:0050975,GO:0007623,GO:0006811,GO:0034220,GO:0042752,GO:0005886,GO:0022008,GO:0086010,GO:0008344,GO:0072347,GO:0070588,GO:0070509,GO:0005245	CG1517-PF						PF00520,PF00520,PF00520,PF00520				G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350	SSF81324,SSF81324,SSF81324,SSF81324,SSF81324	1514~1546								
aly1651.29	WD repeat-containing protein 35	GO:0036064,GO:0030991,GO:0042384,GO:0035058,GO:0035091,GO:0005813,GO:0035721,GO:0031513,GO:0061512,GO:0003674,GO:0005515,GO:0005929,GO:0022008,GO:0005930	CG2069-PA				SM00320,SM00320,SM00320,SM00320			PS50294			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978									
aly1651.3	Phosphatidylserine synthase 1	GO:0016021,GO:0006659,GO:0005789,GO:0016740,GO:0003882,GO:0022008	CG4825-PA						PF03034														
aly1651.30	SelT-like protein	GO:0005575,GO:0045454,GO:0008430,GO:0012505	CG3887-PA					TIGR02174	PF10262				G3DSA:3.40.30.10,G3DSA:3.40.30.10	SSF52833,SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1651.31	PITH domain-containing protein 1	GO:0005575,GO:0006974,GO:0003674	CG6153-PA						PF06201	PS51532			G3DSA:2.60.120.470	SSF49785									
aly1651.32	Collagen alpha 1(IV) chain	GO:0007443,GO:0005201,GO:0005587,GO:0005581,GO:0002119,GO:0050714,GO:0005811,GO:0007519,GO:0007517,GO:0005604,GO:0030198,GO:0009792,GO:0061327	CG16858-PA				SM00111,SM00111		PF01413,PF01413,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391	PS51403			G3DSA:2.170.240.10	SSF56436,SSF56436			REACT_18266,REACT_16888,REACT_13552						
aly1651.33	Collagen alpha 1(IV) chain	GO:0005201,GO:0005587,GO:0055013,GO:0005581,GO:0007391,GO:0005604,GO:0035848	CG4145-PC				SM00111,SM00111		PF01413,PF01413,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF0139	PS51403			G3DSA:2.170.240.10	SSF56436,SSF56436	1972~1975		REACT_18266,REACT_16888,REACT_13552						
aly1651.34	Transmembrane protein 164	GO:0016021	CG14591-PA						PF14808														
aly1651.35	F-box/SPRY domain-containing protein 1	GO:0005737,GO:0007399,GO:0016567,GO:0005634,GO:0031594,GO:0045732,GO:0045886,GO:0005938,GO:0005515,GO:0007274,GO:0030054,GO:0045495	CG4643-PB				SM00449		PF00622	PS50188				SSF49899									
aly1651.36	Integrator complex subunit 10	GO:0016180,GO:0003674,GO:0032039	CG1120-PA								PR02106,PR02106,PR02106,PR02106												

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1651.37	Transcription initiation factor TFIID subunit 5	GO:0000124,GO:0007221,GO:0051123,GO:0006355,GO:0005634,GO:0001075,GO:0045944,GO:0006367,GO:0005669,GO:0022008	CG7704-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF04494,PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50294,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678	G3DSA:2.130.10.10	SSF160897,SSF50978,SSF50978									
aly1651.38	Dipeptidase 1	GO:0008239,GO:0006805,GO:0035690,GO:0044281,GO:0034235,GO:0008235,GO:0030054,GO:0031225,GO:0045177,GO:0050667,GO:0070062,GO:0016999,GO:0005634,GO:0016805,GO:0043066,GO:0070573,GO:0006508,GO:0043027,GO:0030336,GO:0006749,GO:0016324,GO:0071277,GO:0005886,GO:0005615,GO:0031528,GO:0072340,GO:0072341,GO:0071732,GO:0006691,GO:0043154,GO:0019369,GO:0008270	CG42750-PB						PF01244	PS51365		PS00869	G3DSA:3.20.20.140	SSF51556				PWY-7533					
aly1651.39	Unknown		n/a																				
aly1651.4	Alpha N-terminal protein methyltransferase 1	GO:0005737,GO:0042054,GO:0005634,GO:0035568,GO:0016571,GO:0018016,GO:0071885	CG1675-PA			PIRSF016958			PF05891			PS01131	G3DSA:3.40.50.150	SSF53335									
aly1651.40	Homocysteine S-methyltransferase 3	GO:0009086,GO:0008898,GO:0016205,GO:0005829,GO:0033528,GO:0005886,GO:0046872	CG10621-PA						PF02574	PS50970			G3DSA:3.20.20.330	SSF82282									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1651.41	Rho guanine nucleotide exchange factor 7	GO:0005089,GO:0030032,GO:0035023,GO:0005085,GO:0030426,GO:0042059,GO:0007165,GO:0048041,GO:0007411,GO:0005925,GO:0001726,GO:0043615,GO:2000394,GO:0043547,GO:1900026,GO:0043065,GO:0002244,GO:0043005,GO:0010763,GO:0097190,GO:0043025,GO:0051056,GO:0030027,GO:0050807,GO:0019901,GO:0007173,GO:0005938,GO:0048011,GO:0048013,GO:0007264,GO:0097482,GO:0043234,GO:0005829,GO:0005515	CG10043-PF				SM00326,SM00233,SM00325		PF00621,PF14604	PS50003,PS50010,PS50002	PR00452,PR00452,PR00452,PR00452		G3DSA:2.30.30.40,G3DSA:1.20.900.10,G3DSA:2.30.29.30	SSF50044,SSF48065,SSF50729	591~625									
aly1651.42	Ankyrin-2	GO:0042383,GO:0005200,GO:0031647,GO:0030507,GO:0072661,GO:0060307,GO:0003283,GO:0014704,GO:0036309,GO:0010628,GO:0007165,GO:0086046,GO:0086066,GO:0007411,GO:0035556,GO:0005622,GO:0060048,GO:0044325,GO:0030018,GO:0043268,GO:0005856,GO:0086005,GO:0051924,GO:0031430,GO:0045170,GO:0098907,GO:0070296,GO:0031672,GO:0034394,GO:0086036,GO:0016324,GO:0098904,GO:1901021,GO:0006874,GO:0048471,GO:0097481,GO:0010882,GO:0086004,GO:0002027,GO:1901019,GO:0030315,GO:0051117,GO:0015459,GO:0034613,GO:0055117,GO:0030674,GO:0016323,GO:0019901,GO:0045211,GO:0072659,GO:0070972,GO:0019899,GO:0005887,GO:0005886,GO:0033292,GO:0086070,GO:0086015,GO:0086014,GO:1901018,GO:0050821,GO:0007016,GO:0008092,GO:0036371,GO:0005829,GO:0051928,GO:0045169,GO:0086091,GO:0098910,GO:0010881,GO:2001259,GO:0033365,GO:0051279,GO:0043034	CG1651-PB				SM00969,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF07525,PF13606,PF12796,PF00023	PS50297,PS50088,PS50088,PS50088,PS50088,PS50297,PS50088,PS50225,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403,SSF158235					UPA00143					
aly1651.43	Ankyrin repeat domain-containing protein 39		CG44001-PA				SM00248,SM00248,SM00248,SM00248		PF12796	PS50088,PS50088,PS50297	PR01415,PR01415		G3DSA:1.25.40.20	SSF48403									
aly1651.44	Unknown		CG44000-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1651.45	Unknown	GO:0005575,GO:0008150,GO:0003674	CG33995-PA																				
aly1651.46	Orexin receptor type 1	GO:0017046,GO:0008528,GO:0004930,GO:0042277,GO:0006935,GO:0007631,GO:0007268,GO:0016021,GO:0016499,GO:0007218,GO:0004950,GO:0032870,GO:0045187,GO:1901652,GO:0005887,GO:0008188,GO:0007186	CG34381-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR01012,PR01012,PR01012,PR01012	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly1651.47	Unknown		n/a																				
aly1651.48	Unknown		n/a																				
aly1651.49	WD repeat-containing protein 35	GO:0006996,GO:0036064,GO:0030991,GO:0042384,GO:0035058,GO:0035091,GO:0005813,GO:0061512,GO:0035721,GO:0031513,GO:0097542,GO:0072372,GO:0003674,GO:0005515,GO:0005929,GO:0022008,GO:0005930	CG2069-PA										G3DSA:2.130.10.10	SSF50978									
aly1651.5	Protein AMN1 homolog		CG15412-PC				SM00367,SM00367,SM00367,SM00367						G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047,SSF52047									
aly1651.50	F-box/SPRY domain-containing protein 1	GO:0005737,GO:0007399,GO:0016567,GO:0005634,GO:0031594,GO:0045732,GO:0045886,GO:0005938,GO:0005515,GO:0007274,GO:0030054,GO:0045495	CG4643-PB				SM00256		PF12937	PS50181			G3DSA:1.20.1280.50	SSF81383									
aly1651.51	Unknown	GO:0005089,GO:0043547,GO:0005085,GO:0050807,GO:0035023,GO:0097482	CG10043-PF																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1651.6	Transmembrane protein 189	GO:0080132,GO:0016021,GO:0008150,GO:0005789	CG10723-PA						PF10520														
aly1651.7	Unknown		n/a												51~66								
aly1651.8	Golgin subfamily A member 2	GO:0005795,GO:0000137,GO:0007030,GO:0005783,GO:0048193,GO:0005801,GO:0032091,GO:0005634,GO:0017137,GO:0000139,GO:0019901,GO:0019905,GO:0005794,GO:0032580,GO:0030134,GO:0000278	CG11061-PA						PF15070,PF15070						248~268,341~375,407~441,562~596,199~233,164~191,625~652,1~28,108~135,470~504								
aly1651.9	60S ribosomal protein L35	GO:0005840,GO:0022625,GO:0005622,GO:0003735,GO:0007052,GO:0000022,GO:0006412,GO:0051298	CG4111-PA	MF_00374				TIGR00012	PF00831			PS00579	G3DSA:1.10.287.310	SSF46561	14~34								
aly16512.1	Unknown		n/a																				
aly16537.1	Kinesin-like protein KIF13A	GO:0050803,GO:0035371,GO:0032438,GO:0008333,GO:0035459,GO:0016887,GO:0005871,GO:0005874,GO:0010008,GO:0005813,GO:0006886,GO:0043001,GO:0005524,GO:0042803,GO:0051294,GO:0008017,GO:0032588,GO:0000235,GO:0008152,GO:0030496,GO:0000910,GO:0072383,GO:0007018,GO:0003777,GO:0005769	CG8183-PE						PF12423														
aly16540.1	Unknown		n/a																				
aly16540.2	Connectin	GO:0016200,GO:0007156,GO:0009986,GO:0044295,GO:0031594,GO:0005515,GO:0005886,GO:0007155,GO:0007413,GO:0031225	CG7503-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1656.1	Ribosome production factor 2 homolog	GO:0005730,GO:0019843,GO:0005575,GO:0000463,GO:0003674,GO:0022008,GO:0090307,GO:0000027	CG7993-PA				SM00879		PF04427	PS50833				SSF52954	285~305								
aly1656.10	E3 UFM1-protein ligase 1 homolog	GO:0016874	CG1104-PA						PF09743						85~105,728~748								
aly1656.11	Unknown	GO:1900074,GO:0008021,GO:0051124,GO:0005615,GO:0042051,GO:0007509,GO:0043410,GO:0007435,GO:0061177,GO:0061176,GO:0005515,GO:0007411,GO:0007522,GO:0030297,GO:0042694,GO:0005576	CG30040-PA				SM00192			PS50068		PS01209	G3DSA:4.10.400.10	SSF57424									
aly1656.12	Pancreatic lipase-related protein 2	GO:0009395,GO:0047714,GO:0004806,GO:0005615,GO:0032504,GO:0016042,GO:0005509,GO:0019376,GO:0004620,GO:0016298,GO:0047372	CG5162-PA						PF00151		PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly1656.13	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	GO:0005737,GO:0016614,GO:0005739,GO:0005654,GO:0005743,GO:0003858,GO:0008152,GO:0005759	CG8888-PA						PF00106		PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1656.14	Cell death activator CIDE-A	GO:0035634,GO:0005739,GO:0019915,GO:0008219,GO:0042981,GO:0005737,GO:0005634,GO:0005811,GO:0006309,GO:0010890,GO:1900118,GO:0043066,GO:0032720,GO:0042803,GO:0006629,GO:0006915,GO:0045476,GO:0001659,GO:1902510,GO:0030512,GO:0050710,GO:0050995,GO:0005622,GO:0006355,GO:0005740,GO:0006351	CG8357-PB				SM00266		PF02017,PF09033	PS51135			G3DSA:3.10.20.10	SSF54277										
aly1656.15	Guanine nucleotide-binding protein subunit gamma-1	GO:0007015,GO:0055059,GO:0045176,GO:0008360,GO:0007637,GO:0005834,GO:0003924,GO:0035050,GO:0007391,GO:0008152,GO:0061343,GO:0003015,GO:0004871,GO:0005886,GO:0007155,GO:0022008,GO:0007186	CG8261-PA				SM00224		PF00631	PS50058			G3DSA:4.10.260.10	SSF48670										
aly1656.16	Prefoldin subunit 3	GO:0005737,GO:0007017,GO:0016272,GO:0051297,GO:0051082,GO:0048487,GO:0090306,GO:0090307,GO:0006457	CG6719-PA			PIRSF016396			PF02996				G3DSA:1.10.287.370	SSF46579	72~92,136~156									
aly1656.17	Kelch-like protein 5	GO:0005737,GO:0005856,GO:0006909,GO:0005515	CG17754-PC			PIRSF037037	SM00875,SM00612,SM00612,SM00612,SM00612,SM00225		PF00651,PF01344,PF01344,PF01344,PF01344,PF07707	PS50097			G3DSA:3.30.710.10,G3DSA:2.130.10.80	SSF54695,SSF117281										
aly1656.18	T-complex protein 1 subunit theta	GO:0005737,GO:0006457,GO:0042623,GO:0051082,GO:0031122,GO:0007052,GO:0005832,GO:0005815,GO:0005875,GO:0005524	CG8258-PA					TIGR02346	PF00118		PR00304,PR00304,PR00304,PR00304,PR00304	PS00750,PS00995	G3DSA:1.10.560.10,G3DSA:1.10.560.10,G3DSA:3.50.7.10,G3DSA:3.30.260.10,G3DSA:3.30.260.10	SSF48592,SSF48592,SSF54849,SSF54849,SSF52029			REACT_17015						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1656.19	C-Myc-binding protein	GO:0005737,GO:0004054,GO:0005615,GO:0032504,GO:0005634,GO:0003713,GO:0006355,GO:0006351	CG4546-PA								PR02028,PR02028,PR02028				54~81								
aly1656.2	Organic cation transporter protein	GO:0015226,GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0016021	CG6006-PC						PF00083				G3DSA:1.20.1250.20	SSF103473									
aly1656.20	ATP synthase subunit O, mitochondrial	GO:0015986,GO:0015992,GO:0046933,GO:0005811,GO:0005739,GO:0005743,GO:0005756,GO:0008553	CG4307-PA	MF_01416				TIGR01145	PF00213		PR00125,PR00125,PR00125,PR00125		G3DSA:1.10.520.20	SSF47928	150~170								
aly1656.21	Eukaryotic translation initiation factor 2 subunit 3	GO:0003743,GO:0003924,GO:0005525	CG43665-PD						PF09173,PF00009,PF03144	PS51722	PR00315,PR00315,PR00315,PR00315		G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF50447,SSF50465									
aly1656.22	Cullin-5	GO:0005262,GO:0008582,GO:0000082,GO:0097193,GO:0007293,GO:0004872,GO:0007295,GO:0007281,GO:0005634,GO:0021799,GO:0042787,GO:0016360,GO:0008285,GO:0008283,GO:0007528,GO:0006970,GO:0005886,GO:0031461,GO:0031466,GO:0007050,GO:0031625,GO:0051726,GO:0051480,GO:0005829,GO:0070588,GO:0006511,GO:0016032,GO:0021942	CG1401-PA				SM00182,SM00884		PF10557,PF00888	PS50069		PS01256	G3DSA:4.10.1030.10,G3DSA:1.20.1310.10,G3DSA:1.10.10.10,G3DSA:1.20.13110.10,G3DSA:1.20.1310.10,G3DSA:1.10.10.10,G3DSA:1.20.1310.10	SSF75632,SSF46785,SSF74788	198~218				UPA00143				
aly1656.23	Unknown	GO:0000502	CG2046-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1656.24	Protein CREBRF homolog	GO:0043565,GO:0003700,GO:0005634,GO:0005575,GO:0006355,GO:0008150,GO:0006351,GO:0042803	CG13624-PE									PS00036	G3DSA:1.20.5.170										
aly1656.25	Peroxisomal N(1)-acetyl-spermine/spermidine oxidase	GO:0052899,GO:0005777,GO:0008215,GO:0052901,GO:0052902,GO:0052903,GO:0052904,GO:0055114,GO:0016491	CG8032-PA						PF01593,PF01593				G3DSA:3.90.660.10,G3DSA:3.90.660.10,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905,SSF51905										
aly1656.26	8-oxo-dGDP phosphatase NUDT18	GO:0016787,GO:0000287,GO:0044716,GO:0044717,GO:0044715,GO:0046712,GO:0006281,GO:0046057,GO:0046067,GO:0034656,GO:0005829,GO:0055086,GO:0044281	CG10898-PA						PF00293	PS51462		PS00893	G3DSA:3.90.79.10	SSF55811									
aly1656.27	Protein TAPT1 homolog	GO:0005575,GO:0008150,GO:0016021,GO:0003674	CG7218-PA						PF05346														
aly1656.28	Early growth response protein 3	GO:0033089,GO:0006909,GO:0045586,GO:0003676,GO:0003677,GO:0007274,GO:0007417,GO:0005737,GO:0071371,GO:0007517,GO:0042440,GO:0001938,GO:0005634,GO:0044344,GO:0043066,GO:0046872,GO:0035767,GO:0002042,GO:0016204,GO:0007525,GO:0007427,GO:0007398,GO:0003700,GO:0071320,GO:0007390,GO:0006355,GO:0006351,GO:0035924,GO:0007422	CG7847-PD				SM00355,SM00355,SM00355		PF00096	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly1656.29	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1656.3	Unknown	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG6131-PA							PS51155													
aly1656.30	Unknown		n/a																				
aly1656.31	Phosphatidylethanolamine-binding protein 1	GO:0005737,GO:0008289,GO:0005575,GO:0008150,GO:0004867,GO:0003674,GO:0005524	CG6180-PA						PF01161				G3DSA:3.90.280.10	SSF49777									
aly1656.32	Nuclear receptor-binding factor 2	GO:2000327,GO:0031410,GO:0006914,GO:0005776,GO:0045893,GO:0005634,GO:0006351	n/a						PF08961				G3DSA:1.20.5.10	SSF140361	69~89,167~194								
aly1656.33	Transmembrane protein 127	GO:0016021,GO:0005886	n/a																				
aly1656.34	Moricin-2	GO:0045087,GO:0005576,GO:0042742	n/a						PF06451				G3DSA:1.20.5.750										
aly1656.35	Unknown		n/a												53~108								
aly1656.36	Unknown	GO:0005576,GO:0042742	n/a						PF06451				G3DSA:1.20.5.750										
aly1656.37	Unknown		CG13408-PA																				
aly1656.38	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1656.39	Unknown		n/a																				
aly1656.4	Histone deacetylase complex subunit SAP18	GO:0016580,GO:0000122,GO:0071011,GO:0006342,GO:0005634,GO:0003714,GO:0008134,GO:0000398,GO:0007275,GO:0045892,GO:0006351,GO:0005515,GO:0071013	CG6046-PA			PIRSF037637			PF06487														
aly1656.40	Histone-lysine N-methyltransferase SUV39H2	GO:0018024,GO:0042054,GO:0030154,GO:0046974,GO:0008270,GO:0070868,GO:0051567,GO:0007049,GO:0036124,GO:0006306,GO:0006348,GO:0000122,GO:0030702,GO:0006342,GO:0005634,GO:0034968,GO:0036123,GO:0048511,GO:2001229,GO:0016571,GO:0016570,GO:0071456,GO:0048477,GO:0005525,GO:0003924,GO:0000792,GO:0042754,GO:0048132,GO:0000775,GO:0016458,GO:0031507,GO:0051276,GO:0006338,GO:0006333,GO:0005701,GO:0006325,GO:0000976,GO:0006351,GO:0000785,GO:0003682,GO:0045892	CG43664-PA			PIRSF009343	SM00298,SM00468,SM00317		PF00385,PF05033,PF00856	PS50867,PS50280,PS50013,PS50868		PS00598	G3DSA:2.170.270.10,G3DSA:2.170.270.10,G3DSA:2.40.50.40	SSF82199,SSF54160		00310+2.1.1.43							
aly1656.5	Protein sarah	GO:0005737,GO:0035039,GO:0007127,GO:0045924,GO:0019722,GO:0007616,GO:0005634,GO:0007343,GO:0007126,GO:0007275,GO:0046008,GO:0008597,GO:0070884,GO:0030431,GO:0005515,GO:0005759,GO:0050790,GO:0048477,GO:0007143,GO:0007005,GO:0008355	CG6072-PA						PF04847				G3DSA:3.30.70.330	SSF54928									
aly1656.6	Organic cation transporter protein	GO:0005215,GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0015101,GO:0016021	CG6126-PA						PF00083	PS50850		PS00216,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1656.7	Organic cation transporter protein	GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0015101,GO:0016021	CG6126-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly1656.8	Unknown		n/a											SSF103473									
aly1656.9	Monocarboxylate transporter 10	GO:0015349,GO:0008028,GO:0005215,GO:0016021,GO:0006727,GO:0034220,GO:0005887,GO:0005886,GO:0055085,GO:0015173	CG12286-PB						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly16576.1	ATP-binding cassette sub-family G member 1	GO:0043231,GO:0009897,GO:0034375,GO:0034374,GO:0005887,GO:0055037,GO:0017127,GO:0005789,GO:0034041,GO:0042157,GO:0055099,GO:0042987,GO:1901998,GO:0055091,GO:0005548,GO:0042626,GO:0033993,GO:0005543,GO:0005739,GO:0055085,GO:0005654,GO:0034436,GO:0034437,GO:0010745,GO:0010875,GO:0005524,GO:0033700,GO:0005794,GO:0005215,GO:0042803,GO:0043531,GO:0005886,GO:0010872,GO:0042632,GO:0043691,GO:0010033,GO:0008203,GO:0043190,GO:0019534,GO:0015485,GO:0032367,GO:0009720,GO:0000139,GO:0010887,GO:0006355,GO:0033344,GO:0045542,GO:0046983,GO:0046982,GO:0005768,GO:0044281	CG3164-PA				SM00382		PF00005,PF01061	PS50893		PS00211	G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly16576.2	Etoposide-induced protein 2.4 homolog	GO:0005737,GO:0005794,GO:0016020,GO:0005783,GO:0030308,GO:0006914,GO:0006915,GO:0031965,GO:0005789,GO:1901418,GO:0016021	CG15626-PB						PF07264														
aly16576.3	Equilibrative nucleoside transporter 3	GO:0005337,GO:0055085,GO:0016021,GO:0006810,GO:0015858,GO:0005765,GO:0031902	CG11907-PA						PF01733		PR01130,PR01130,PR01130,PR01130						REACT_1698,REACT_15518						
aly16576.4	Lysyl oxidase homolog 4	GO:0043235,GO:0070062,GO:0005044,GO:0016020,GO:0030246,GO:0004720,GO:0035002,GO:0005615,GO:0005507,GO:0005918	CG3921-PB				SM00202,SM00202,SM00202,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710		PF13229,PF00530,PF00530,PF00530,PF05473	PS50287,PS50287,PS50287	PR00258,PR00258,PR00258	PS00420	G3DSA:3.10.250.10,G3DSA:3.10.250.10,G3DSA:3.10.250.10,G3DSA:3.10.100.10,G3DSA:2.160.20.10,G3DSA:2.160.20.10,G3DSA:2.160.20.10,G3DSA:2.160.20.10,G3DSA:2.60.120.290	SSF56487,SSF51126,SSF56487,SSF51126,SSF51126,SSF56487,SSF51126,SSF51126,SSF49854,SSF56436	3056~3060,1468~1488									
aly16576.5	RNA-binding protein Rsf1	GO:0048025,GO:0005634,GO:0003729,GO:0003676,GO:0000166	CG5655-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly16576.6	Mediator of RNA polymerase II transcription subunit 17	GO:0033613,GO:0005634,GO:0009987,GO:0003713,GO:0006366,GO:0001104,GO:0045498,GO:0006357,GO:0045944,GO:0006367,GO:0007095,GO:0016592,GO:0005694	CG7957-PA						PF10156														
aly16576.7	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase classes I and II	GO:0004435,GO:0006651,GO:0007629,GO:0016042,GO:0005509,GO:0004871,GO:0006661,GO:0035556,GO:0005622	CG4574-PD											SSF50729									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly165819.1	Unknown		n/a																				
aly16590.1	Motile sperm domain-containing protein 2	GO:0005575,GO:0022008,GO:0016020,GO:0016021,GO:0005198	CG33523-PF						PF00635	PS50202			G3DSA:3.40.525.10,G3DSA:2.60.40.360	SSF52087,SSF49354									
aly166.1	Adenomatous polyposis coli protein	GO:1990090,GO:0016337,GO:0008258,GO:0031016,GO:0030426,GO:0030425,GO:0030424,GO:0046673,GO:0021550,GO:0030111,GO:0007163,GO:0031175,GO:0007411,GO:0005874,GO:0030178,GO:0005737,GO:0045177,GO:0044306,GO:0030951,GO:0007026,GO:0005813,GO:0006886,GO:0030720,GO:0000281,GO:0005875,GO:0043065,GO:0030877,GO:0032403,GO:0016477,GO:0043025,GO:0008285,GO:0006461,GO:2000211,GO:0019887,GO:0030027,GO:0031965,GO:0008017,GO:0051010,GO:0033134,GO:0008013,GO:0007050,GO:0005912,GO:0005886,GO:0070852,GO:0007405,GO:0035293,GO:0032587,GO:0000776,GO:0032886,GO:0043234,GO:0006974,GO:0007017,GO:0007447,GO:0007420,GO:0097305,GO:0016055,GO:0042493,GO:0045736,GO:0005515,GO:0044295,GO:0005634,GO:0005938	CG1451-PA				SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185		PF05923,PF05923,PF05923,PF05923,PF05923,PF00514,PF05972,PF05972	PS50176			G3DSA:1.25.10.10	SSF48371									
aly166.2	UPF0565 protein C2orf69 homolog	GO:0005576,GO:0015271,GO:0005267,GO:0016021,GO:0071805	CG10864-PA						PF07885,PF07885,PF10561		PR01333,PR01333		G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324,SSF81324	313~333								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly166.3	Glucosidase 2 subunit beta	GO:0017177,GO:0005783,GO:0006491,GO:0006487,GO:0005515,GO:0004558	CG7685-PA						PF12999				G3DSA:4.10.400.10,G3DSA:4.10.400.10										
aly166.4	ATP-binding cassette sub-family G member 1	GO:0043231,GO:0009897,GO:0034375,GO:0034374,GO:0005887,GO:0055037,GO:0017127,GO:0005789,GO:0034041,GO:0042157,GO:0016887,GO:0042987,GO:1901998,GO:0055091,GO:0005548,GO:0042626,GO:0055099,GO:0033993,GO:0005543,GO:0005739,GO:0055085,GO:0005654,GO:0034436,GO:0034437,GO:0010745,GO:0010875,GO:0005524,GO:0033700,GO:0005794,GO:0005215,GO:0042803,GO:0043531,GO:0005886,GO:0010872,GO:0042632,GO:0022008,GO:0043691,GO:0010033,GO:0008203,GO:0043190,GO:0019534,GO:0015485,GO:0032367,GO:0009720,GO:0000139,GO:0010887,GO:0006355,GO:0033344,GO:0045542,GO:0046983,GO:0046982,GO:0005768,GO:0044281	CG2969-PA				SM00382		PF01061,PF00005	PS50893		PS00211	G3DSA:3.40.50.300	SSF52540									
aly166.5	Slit homolog 3 protein	GO:0008285,GO:0009887,GO:0035385,GO:0005515,GO:0030308,GO:0048846,GO:0051414,GO:0010629,GO:0042059,GO:0048495,GO:0070100,GO:0032870,GO:0005739,GO:0005509,GO:0005887,GO:0050919,GO:0007411,GO:0061364,GO:0005615	CG4977-PA				SM00082,SM00369,SM00369,SM00369,SM00369,SM00369		PF00560,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly166.6	Unknown		n/a																				
aly166.7	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly166.8	Paired box protein Pax-2-A	GO:0048666,GO:0007517,GO:0007367,GO:0042676,GO:0003700,GO:0005634,GO:0000122,GO:0003705,GO:0001158,GO:0045676,GO:0006355,GO:0048813,GO:0045944,GO:0006351,GO:0003677,GO:0042682,GO:0042673	CG11049-PA				SM00351		PF00292	PS51057	PR00027,PR00027,PR00027,PR00027	PS00034	G3DSA:1.10.10.10,G3DSA:1.10.10.10	SSF46689	196~217								
aly166.9	Potassium voltage-gated channel protein Shal	GO:0043204,GO:0071805,GO:0006813,GO:0016021,GO:0005886,GO:0051260,GO:0008076,GO:0030425,GO:0005249,GO:0007268,GO:0005250,GO:0005251,GO:0055085	CG9262-PB						PF11879		PR01497,PR01497												
aly1660.1	Unknown		n/a																				
aly1660.10	Succinate dehydrogenase [ubiqui] iron-sulfur subunit, mitochondrial	GO:0046872,GO:0051538,GO:0051539,GO:0051537,GO:0006121,GO:0005743,GO:0006099,GO:0008177,GO:0048039,GO:0005749,GO:0005875,GO:0009055	CG3283-PA					TIGR00384	PF13085,PF13534	PS51085,PS51379		PS00198,PS00197	G3DSA:1.10.1060.10,G3DSA:3.10.20.30	SSF46548,SSF54292		00720+1.3.5.1,00190+1.3.5.1,00020+1.3.5.1,00650+1.3.5.1		PWY-561,PWY-4302,PWY-3781,PWY-7279,PWY-6969,PWY-6728,PWY-7254,PWY-5690					
aly1660.11	Unknown		n/a																				
aly1660.12	ABC transporter G family member 23	GO:0043190,GO:0042626,GO:0006810,GO:0005215,GO:0016021,GO:0016020,GO:0016887,GO:0005886,GO:0005524	CG9990-PA				SM00382		PF00005,PF01061	PS50893,PS51012	PR00164,PR00164,PR00164	PS00211	G3DSA:3.40.50.300	SSF52540									
aly1660.13	RNA-binding protein 34	GO:0005730,GO:0008143,GO:0005634,GO:0044822,GO:0000166,GO:0005875,GO:0003729	CG12288-PA				SM00360,SM00360		PF14259,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1660.14	Unknown		CG14905-PA												26~51								
aly1660.15	Unknown		n/a																				
aly1660.2	Translocator protein	GO:0071222,GO:0030325,GO:0006869,GO:0060242,GO:0048678,GO:0006821,GO:0010042,GO:0010940,GO:0048266,GO:0048265,GO:0008503,GO:0071294,GO:0070062,GO:0014012,GO:0016021,GO:0071476,GO:0005739,GO:0045019,GO:0043065,GO:0032720,GO:2000379,GO:0006811,GO:0031965,GO:0060253,GO:0060252,GO:0050810,GO:0007268,GO:0005497,GO:0008347,GO:0007568,GO:0010266,GO:0051928,GO:0042493,GO:0033574,GO:0005740,GO:0005741,GO:0051901,GO:0006694,GO:0032570	CG2789-PA						PF03073															
aly1660.3	Translocator protein	GO:0071222,GO:0030325,GO:0006869,GO:0060242,GO:0048678,GO:0006821,GO:0010042,GO:0010940,GO:0048266,GO:0048265,GO:0008503,GO:0071294,GO:0070062,GO:0014012,GO:0016021,GO:0071476,GO:0005739,GO:0045019,GO:0043065,GO:0032720,GO:2000379,GO:0006811,GO:0031965,GO:0060253,GO:0060252,GO:0050810,GO:0007268,GO:0005497,GO:0008347,GO:0007568,GO:0010266,GO:0051928,GO:0042493,GO:0033574,GO:0005740,GO:0005741,GO:0051901,GO:0006694,GO:0032570	CG2789-PA			PIRSF005859			PF03073															
aly1660.4	Nucleolar protein 14 homolog	GO:0032040,GO:0005730,GO:0030490,GO:0042274,GO:0006364,GO:0030692,GO:0030515	CG5824-PA						PF04147,PF04147						269~297,186~213								
aly1660.5	Unknown		n/a						PF08766				G3DSA:1.10.10.60	SSF109715	60~80								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1660.6	UPF0704 protein C6orf165 homolog		CG13436-PA						PF12018														
aly1660.7	Unknown		n/a												42~92,149~169,114~134								
aly1660.8	Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial	GO:0030956,GO:0050567,GO:0030717,GO:0032543,GO:0070681,GO:0005739,GO:0048477,GO:0006412,GO:0005524	CG6007-PA	MF_00120					PF01425				G3DSA:3.90.1300.10	SSF75304		00970+6.3.5.7		PWY-5921					
aly1660.9	Biorientation of chromosomes in cell division protein 1	GO:0005737,GO:0007067,GO:0005815,GO:0051301,GO:0000777	CG5514-PE						PF05205						1109~1129,725~755								
aly166012.1	Cytochrome P450 4d2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG3466-PA										G3DSA:1.10.630.10				REACT_13433						
aly1661.1	Unknown		n/a																				
aly1661.2	Unknown		n/a																				
aly1661.3	Unknown	GO:0007424,GO:0005201,GO:0051539,GO:0040005,GO:0007475,GO:0008362,GO:0046331,GO:0005509,GO:0031012,GO:0005578	CG33196-PQ																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1661.4	Protein phosphatase 1 regulatory subunit 37	GO:0019902,GO:0010923,GO:0004864	CG31635-PC				SM00368,SM00368,SM00368,SM00368						G3DSA:3.80.10.10	SSF52047									
aly1661.5	Unknown		n/a																				
aly1664.1	Leucine-rich repeat-containing protein 15	GO:0043236,GO:0070062,GO:0016021,GO:0046813,GO:0030335,GO:0005622,GO:0005515,GO:0008056,GO:0090005,GO:0005518,GO:0001968	CG15151-PB				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF13855,PF00560	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly166451.1	ATP-citrate synthase	GO:0006633,GO:0016020,GO:0015936,GO:0031325,GO:0003878,GO:0035338,GO:0044281,GO:0005737,GO:0044262,GO:0070062,GO:0005811,GO:0005739,GO:0005654,GO:0006112,GO:0004775,GO:0046872,GO:0005524,GO:0048037,GO:0005886,GO:0044255,GO:0008610,GO:0006084,GO:0006085,GO:0005829,GO:0019432,GO:0006101,GO:0009346	CG8322-PD											SSF56059									
aly16648.1	Dipeptidyl peptidase 8	GO:0005737,GO:0005654,GO:0016020,GO:0008239,GO:0006955,GO:0006508,GO:0008236	CG3744-PD						PF00930				G3DSA:2.140.10.30										
aly1667.1	Unknown		n/a																				
aly1667.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1667.3	Unknown		n/a																				
aly166716.1	THO complex subunit 6	GO:0009408,GO:0003674,GO:0006406,GO:0000347,GO:0008283	CG5632-PA										G3DSA:2.130.10.10	SSF50998									
aly167.1	Zinc finger and BTB domain-containing protein 24	GO:0005737,GO:0005819,GO:0003700,GO:0005634,GO:0006355,GO:0002244,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0005876,GO:0006351	CG8474-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028		SSF57667,SSF57667										
aly167.2	Orexin receptor type 2	GO:0007268,GO:0007631,GO:0004930,GO:0042277,GO:0007200,GO:0016021,GO:0008261,GO:0007218,GO:0016499,GO:0032870,GO:0045187,GO:1901652,GO:0022410,GO:0005887,GO:0008188,GO:0007186	CG2872-PB						PF00001	PS50262			G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly167107.1	Anoctamin-8	GO:0005229,GO:1902476,GO:0016021,GO:0005622,GO:0034220,GO:0006821,GO:0005886,GO:0055085	CG15270-PA						PF04547														
aly1672.1	RNA pseudouridylate synthase domain-containing protein 2	GO:0044822,GO:0009982,GO:0009231,GO:0003723,GO:0008835,GO:0009451,GO:0001522	CG31719-PA					TIGR00005	PF00849	PS50889		PS01129		SSF55120,SSF55120									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1672.10	Endonuclease/exonuclease/phosphatase family domain containing protein 1	GO:0006281,GO:0003677	n/a						PF12836,PF12836				G3DSA:1.10.150.310,G3DSA:1.10.150.280,G3DSA:3.60.10.10	SSF47781,SSF47781			REACT_216						
aly1672.11	Cytoplasmic dynein 1 light intermediate chain 2	GO:0000226,GO:0030286,GO:0007067,GO:0005874,GO:0051028,GO:0042623,GO:0005813,GO:0016020,GO:0008088,GO:0005875,GO:0048477,GO:0003774,GO:0005524,GO:0019886,GO:0006810,GO:0003777,GO:0007052,GO:0007409,GO:0005868,GO:0051642,GO:0005829,GO:0007018,GO:0048813,GO:0048814	CG1938-PD						PF05783				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									
aly1672.12	Coiled-coil and C2 domain-containing protein 1-like	GO:0048749,GO:0005737,GO:0007219,GO:0007423,GO:0000122,GO:0007472,GO:0016197,GO:0006886,GO:0005543,GO:0008586,GO:0000281,GO:0045746,GO:0045732,GO:0008593,GO:0036257,GO:0048132,GO:0005634,GO:0030100,GO:0045035,GO:0000981,GO:0016324	CG4713-PB				SM00685,SM00685																
aly1672.13	Unknown		n/a																				
aly1672.14	Unknown		n/a				SM00249			PS50016		PS01359	G3DSA:3.30.40.10	SSF57903	144~164,108~135								
aly1672.2	Unknown	GO:0016021	CG3625-PB						PF04750														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1672.3	Protein asteroid	GO:0007476,GO:0008586,GO:0005575,GO:0003674,GO:0007173,GO:0001745,GO:0007526,GO:0001752	CG4426-PA						PF00752,PF12813		PR00853,PR00853,PR00853		G3DSA:3.40.50.1010	SSF88723									
aly1672.4	La protein homolog	GO:0005634,GO:0008098,GO:0030529,GO:0003676,GO:0003677,GO:0000166,GO:0006396,GO:0003729	CG10922-PA				SM00360,SM00715		PF14259,PF08777,PF05383	PS50102,PS50961	PR00302,PR00302,PR00302,PR00302		G3DSA:1.10.10.10,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF46785									
aly1672.5	Protein SAAL1	GO:0006953,GO:0005576,GO:0005488,GO:0005615	CG30467-PA										G3DSA:1.25.10.10	SSF48371									
aly1672.6	TBC1 domain family member 24	GO:0032313,GO:0031594,GO:0043195,GO:0005097,GO:0005096	CG9339-PJ				SM00164,SM00584		PF07534,PF00566					SSF47923									
aly1672.7	Maestro heat-like repeat-containing protein family member 1	GO:0005575,GO:0003674,GO:0008150	CG12132-PA										G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371	1635~1640								
aly1672.8	Unknown		n/a																				
aly1672.9	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly167232.1	Spectrin beta chain, non-erythrocytic 5	GO:0032432,GO:0019894,GO:0032029,GO:0030036,GO:0000281,GO:0007009,GO:0007041,GO:0007411,GO:0030507,GO:0005737,GO:0016020,GO:0045505,GO:0005543,GO:0051260,GO:0030707,GO:0003779,GO:0051693,GO:0034452,GO:0032391,GO:0032509,GO:0016324,GO:0008017,GO:0016327,GO:0042060,GO:0010797,GO:0045186,GO:0005912,GO:0006897,GO:0043621,GO:0070062,GO:0097381,GO:0007030,GO:0008091,GO:0008092,GO:0005829,GO:0005515	CG12008-PE				SM00150,SM00150		PF00435,PF00435				G3DSA:1.20.58.60,G3DSA:1.20.58.60	SSF46966,SSF46966	1~25								
aly16739.1	Unknown		n/a																				
aly167498.1	Solanesyl diphosphate synthase 3, chloroplastic/mitochondrial	GO:0052924,GO:0009536,GO:0000010,GO:0004659,GO:0006744,GO:0009793,GO:0005739,GO:0008299,GO:0050347,GO:0046872,GO:0009507	CG10585-PA										G3DSA:1.10.600.10	SSF48576	41~61								
aly1675.1	Acyl-CoA dehydrogenase family member 9, mitochondrial	GO:0050660,GO:0005615,GO:0032504,GO:0032981,GO:0005634,GO:0030425,GO:0004466,GO:0005739,GO:0003995,GO:0001745,GO:0006979,GO:0055114	CG9006-PA										G3DSA:2.40.110.10	SSF56645									
aly1675.10	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005576,GO:0005886,GO:0006508	CG40160-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1675.2	Glutamate receptor	GO:0043235,GO:0016021,GO:0007608,GO:0004970,GO:0071683,GO:0006811,GO:0016020,GO:0015277,GO:0015276,GO:0005234,GO:0045211,GO:0004872,GO:0005886,GO:0005216,GO:0030054,GO:0050907	CG32704-PA				SM00079,SM00918		PF10613,PF00060		PR00177,PR00177,PR00177		G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:1.10.287.70	SSF81324,SSF53850,SSF53850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1675.3	Unknown	GO:0043235,GO:0007608,GO:0071683,GO:0006811,GO:0016020,GO:0015277,GO:0015276,GO:0005234,GO:0050907,GO:0005886,GO:0016021	CG32704-PA																				
aly1675.4	Single-stranded DNA binding protein 4	GO:0006355,GO:0005634,GO:0048812,GO:0003697,GO:0035220	CG7187-PD						PF04503														
aly1675.5	Single-stranded DNA binding protein 3	GO:0060322,GO:2000744,GO:0006351,GO:0005634,GO:0006461,GO:0002244,GO:0035220,GO:0021501,GO:0008284,GO:0006355,GO:0060323,GO:0048812,GO:0045944,GO:0021547,GO:0005515,GO:0043234,GO:0003697,GO:0045893	CG7187-PD				SM00667		PF04503	PS50896	PR01743,PR01743,PR01743,PR01743,PR01743												
aly1675.6	60S ribosomal protein L32	GO:0005737,GO:0005840,GO:0022625,GO:0005730,GO:0005622,GO:0003735,GO:0007052,GO:0000022,GO:0000228,GO:0006412	CG7939-PC						PF01655			PS00580		SSF52042	114~134								
aly1675.7	DNA/RNA-binding protein KIN17	GO:0006310,GO:0005737,GO:0016363,GO:0043231,GO:0006281,GO:0071011,GO:0005634,GO:0000398,GO:0006974,GO:0006260,GO:0003723,GO:0003676,GO:0003690,GO:0046872,GO:0006397	CG5649-PA						PF10357					SSF57667	150~184,238~265								
aly1675.8	Unknown		n/a												95~115,66~86								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1675.9	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005576,GO:0005886,GO:0006508	CG40160-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly16764.1	Unknown		n/a																				
aly16766.1	Unknown		n/a												1~21								
aly167753.1	Zinc transporter 8	GO:0016324,GO:0006812,GO:0016021,GO:0008324,GO:0005622,GO:0030658,GO:0005886,GO:0005385,GO:0010043,GO:0046873,GO:0006829,GO:0055085	CG3994-PA										G3DSA:1.20.1510.10										
aly168.1	Mediator of RNA polymerase II transcription subunit 1	GO:0005634,GO:0001104,GO:0006357,GO:0006351,GO:0006367,GO:0006366,GO:0016592	CG7162-PA						PF10744						24~44								
aly168.10	Conserved oligomeric Golgi complex subunit 8	GO:0015031,GO:0017119,GO:0000139	CG6488-PA						PF04124,PF04124														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly168.11	DNA repair protein RAD50	GO:0000723,GO:0000781,GO:0046872,GO:0051321,GO:0006302,GO:0006281,GO:0004518,GO:0016233,GO:0005634,GO:0006974,GO:0000793,GO:0008104,GO:0030870,GO:0008270,GO:0016887,GO:0003690,GO:0002168,GO:0000722,GO:0005524,GO:0051276	CG6339-PD					TIGR00606	PF04423,PF13476	PS51131			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.287.510	SSF52540,SSF75712,SSF52540,SSF52540	466~533,303~330,389~430,253~294,229~249,191~225,795~815,537~564,589~609,1001~1021,644~664,747~767,1031~1051,825~911,712~732,1070~1097,435~455								
aly168.12	Transmembrane protein 47	GO:0016021,GO:0007163,GO:0060857,GO:0005918	CG45049-PD																				
aly168.13	Replication protein A 70 kDa DNA-binding subunit	GO:0006310,GO:0006281,GO:0005634,GO:0005875,GO:0007052,GO:0048812,GO:0006260,GO:0006261,GO:0005662,GO:0007095,GO:0046872,GO:0003697	CG9633-PA					TIGR00617	PF08646,PF16900,PF04057,PF01336				G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:2.40.50.140	SSF50249,SSF50249,SSF50249,SSF50249										
aly168.14	Gamma-glutamyltranspeptidase 1	GO:0016021,GO:0036374,GO:0031638,GO:0006536,GO:0003840,GO:0006749,GO:0005886,GO:0006750,GO:0006751	CG17636-PC						PF01019		PR01210,PR01210,PR01210,PR01210,PR01210,PR01210,PR01210,PR01210,PR01210,PR01210			SSF56235		00460+2.3.2.2,00430+2.3.2.2,00480+2.3.2.2+3.4.19.13		PWY-4041,PWY-5826					
aly168.15	UPF0454 protein C12orf49 homolog	GO:0005576	CG15643-PA						PF10218														
aly168.16	Unknown		n/a																				
aly168.17	Conserved oligomeric Golgi complex subunit 8	GO:0015031,GO:0017119,GO:0000139	CG6488-PA						PF04124														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly168.2	Unknown		n/a												57~77								
aly168.3	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG4797-PB						PF00083	PS50850		PS00217,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	270~290								
aly168.4	General transcription factor IIH subunit 2	GO:0006468,GO:0001113,GO:0005634,GO:0005675,GO:0006289,GO:0006355,GO:0004439,GO:0008270,GO:0006367,GO:0006366,GO:0000990,GO:0001111	CG11115-PB				SM00327	TIGR00622	PF04056	PS50234			G3DSA:3.40.50.410	SSF53300									
aly168.5	SUMO-conjugating enzyme UBC9 A	GO:0035204,GO:0035207,GO:0031072,GO:0000780,GO:0007059,GO:0007067,GO:0007143,GO:0051301,GO:0005737,GO:0006959,GO:0016567,GO:0005634,GO:0000940,GO:0031099,GO:0019789,GO:0007275,GO:0007088,GO:0005524,GO:0035172,GO:0006606,GO:0016321,GO:0006464,GO:0007352,GO:0016925,GO:0016874,GO:0061484,GO:0007391,GO:0071560,GO:0045751,GO:0005515,GO:0007095	CG3018-PD				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly168.6	Heterochromatin protein 1	GO:0042393,GO:0035064,GO:0000182,GO:0000781,GO:0000780,GO:0007067,GO:0005701,GO:0042981,GO:0000723,GO:0005819,GO:0006355,GO:0030702,GO:0005813,GO:0005634,GO:0007552,GO:0005654,GO:0016458,GO:1900111,GO:0005694,GO:0006351,GO:0005721,GO:0000090,GO:0000792,GO:0000793,GO:0007052,GO:0000791,GO:0045892,GO:0045893,GO:0044026,GO:0051310,GO:0007059,GO:0022008,GO:0000775,GO:0005720,GO:0034773,GO:0031507,GO:0051276,GO:0003696,GO:0005704,GO:0005705,GO:0005703,GO:0005700,GO:0006343,GO:0006325,GO:0035012,GO:0003723,GO:0006342,GO:0007094,GO:0031060,GO:0003682,GO:0033697,GO:0003729	CG10712-PB				SM00298		PF00385	PS50013		PS00598	G3DSA:2.40.50.40	SSF54160										
aly168.7	BET1 homolog	GO:0031985,GO:0006888,GO:0016192,GO:0005801,GO:0016021,GO:0016020,GO:0000139,GO:0048280,GO:0019905,GO:0005515,GO:0015031,GO:0005484,GO:0022008,GO:0005789,GO:0031201	CG14084-PA				SM00397			PS50192			G3DSA:1.20.5.110	SSF58038									
aly168.8	Unknown		n/a																				
aly168.9	Zinc finger protein 467	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG7987-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1680.1	Connectin	GO:0016200,GO:0007156,GO:0009986,GO:0044295,GO:0031594,GO:0005886,GO:0007155,GO:0007413,GO:0031225	CG7503-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly1681.1	Neurogenic protein big brain	GO:0009992,GO:0044719,GO:0005261,GO:0007498,GO:0016337,GO:0007219,GO:0031410,GO:0016021,GO:0016020,GO:0030707,GO:0015250,GO:0015254,GO:0006812,GO:0005372,GO:0015793,GO:0005215,GO:0005216,GO:0006810,GO:0034220,GO:0006833,GO:0046331,GO:0005912,GO:0005887,GO:0005886,GO:0055085,GO:0007399,GO:0007398,GO:0015267,GO:0098655	CG4722-PB						PF00230				G3DSA:1.20.1080.10	SSF81338									
aly16812.1	mRNA-capping enzyme	GO:0004484,GO:0008138,GO:0006470,GO:0004725,GO:0004651,GO:0006370,GO:0050355,GO:0005634,GO:0005525	CG1810-PA						PF00782	PS50056		PS00383	G3DSA:3.90.190.10	SSF52799									
aly16812.2	Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1	GO:0016791,GO:0070062,GO:0006470,GO:0005634,GO:0008420,GO:0045665,GO:0006357,GO:2000134,GO:0001933,GO:0046872	CG5830-PB				SM00577	TIGR02251	PF03031	PS50969			G3DSA:3.40.50.1000	SSF56784									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly16812.3	Alsin	GO:0008104,GO:0043087,GO:0007626,GO:0030426,GO:0030425,GO:0030424,GO:0007041,GO:0071902,GO:0008219,GO:0001881,GO:0035249,GO:0001662,GO:0005737,GO:0007032,GO:0001726,GO:0001701,GO:0031982,GO:0016601,GO:0007528,GO:0005813,GO:0005634,GO:0016020,GO:0051260,GO:0043025,GO:0042802,GO:0042803,GO:0016197,GO:0030027,GO:0005096,GO:0017137,GO:0017112,GO:0032483,GO:0014069,GO:0007409,GO:0051036,GO:0043234,GO:0006979,GO:0043539,GO:0043547,GO:0030676,GO:0035011,GO:0043197,GO:0005829,GO:0016050,GO:0048365,GO:0048812,GO:0045860,GO:0005769	CG7158-PA				SM00233,SM00698,SM00698,SM00698,SM00698,SM00698,SM00698,SM00698,SM00698		PF00415,PF02493,PF02493,PF02493,PF02493,PF02493,PF02493,PF02493,PF02204	PS51205,PS50012,PS50012			G3DSA:2.30.29.30,G3DSA:2.130.10.30,G3DSA:2.130.10.30,G3DSA:2.20.110.10,G3DSA:2.20.110.10	SSF109993,SSF109993,SSF50985,SSF50729,SSF82185,SSF82185										
aly16812.4	Eukaryotic translation initiation factor 3 subunit H	GO:0005852,GO:0016282,GO:0005829,GO:0045747,GO:0005515,GO:0033290,GO:0022008,GO:0006413,GO:0001731,GO:0003743	CG9124-PA	MF_03007			SM00232		PF01398						216~243								
aly16816.1	Unknown		n/a																				
aly1689.1	Protein NDRG3	GO:0005737,GO:0070062,GO:0030308,GO:0030154,GO:0046579,GO:0005575,GO:0007283,GO:0003674,GO:0007165	CG15669-PI						PF03096				G3DSA:3.40.50.1820	SSF53474									
aly1689.10	Unknown	GO:0035070,GO:0005634,GO:0046716,GO:0003779,GO:0003012,GO:0010623,GO:0048471	CG42610-PI																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1689.11	Paramyosin, long form	GO:0032982,GO:0030239,GO:0007498,GO:0030016,GO:0008307,GO:0016459,GO:0008152,GO:0005863,GO:0003774	CG5939-PB						PF01576					SSF90257,SSF90257,SSF90257	230~292,541~561,738~800,815~849,604~638,297~539,118~159,695~729,653~687,33~74,174~222								
aly1689.12	Unknown		n/a																				
aly1689.13	Unknown		n/a																				
aly1689.14	Unknown		n/a																				
aly1689.15	Paramyosin, short form	GO:0032982,GO:0030239,GO:0007498,GO:0030016,GO:0008152,GO:0003774	n/a												273~293,128~158								
aly1689.2	Syntaxin-7	GO:0016021,GO:0016334,GO:0055037,GO:0006906,GO:0030139,GO:0048227,GO:0035264,GO:0005484,GO:0031201,GO:0035088,GO:0070820,GO:0070062,GO:0000149,GO:0005770,GO:0051640,GO:0006886,GO:0048471,GO:0031901,GO:1902685,GO:0008285,GO:0035073,GO:0016081,GO:1903076,GO:0048278,GO:0042582,GO:0012505,GO:0007269,GO:0005886,GO:0070925,GO:0034058,GO:0019869,GO:0050678,GO:0016192,GO:0005765,GO:0001916,GO:0005515,GO:0045807,GO:0005769,GO:0001772	CG5081-PA				SM00503,SM00397		PF05739,PF14523	PS50192		PS00914	G3DSA:1.20.58.70	SSF47661	153~190		REACT_11184							
aly1689.3	PAB-dependent poly(A)-specific ribonuclease subunit PAN3	GO:0005737,GO:0006468,GO:0000289,GO:0010606,GO:0016772,GO:0044822,GO:0000932,GO:0031251,GO:0005515,GO:0004672,GO:0005524,GO:0006397	CG11486-PG	MF_03181						PS50011			G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112,SSF56112	487~514								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1689.4	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	GO:0005168,GO:0030307,GO:0042059,GO:0051281,GO:0004871,GO:0032868,GO:0007298,GO:0035556,GO:0008180,GO:0009395,GO:0001726,GO:0001701,GO:0030971,GO:0045766,GO:0005509,GO:0016477,GO:0005737,GO:0050852,GO:0019722,GO:0030027,GO:0035254,GO:0019901,GO:0045596,GO:0007173,GO:0005911,GO:0005886,GO:0042995,GO:0010634,GO:0004435,GO:0071364,GO:0043536,GO:0005829	CG4200-PA			PIRSF000952	SM00233,SM00233,SM00239,SM00149,SM00148,SM00326,SM00252,SM00252		PF00388,PF09279,PF00017,PF00017,PF00018,PF00387,PF00168	PS50007,PS50001,PS50002,PS50003,PS50222,PS50008,PS50004,PS50001	PR00452,PR00452,PR00452,PR00452,PR00390,PR00390,PR00390,PR00390,PR00390,PR00390,PR00401,PR00401,PR00401,PR00401		G3DSA:2.60.40.150,G3DSA:3.30.505.10,G3DSA:1.10.238.10,G3DSA:2.30.29.30,G3DSA:2.30.29.30,G3DSA:3.20.20.190,G3DSA:3.20.20.190,G3DSA:2.30.29.30,G3DSA:2.30.30.40,G3DSA:1.10.238.10,G3DSA:3.30.505.10	SSF50729,SSF55550,SSF51695,SSF51695,SSF50044,SSF49562,SSF55550,SSF55550,SSF47473		00562+3.1.4.11	REACT_604	PWY-6367,PWY-6351,PWY-7039					
aly1689.5	TGF-beta receptor type-1	GO:2001235,GO:2001237,GO:0032924,GO:0008584,GO:0001501,GO:0007165,GO:0051897,GO:0070723,GO:0007455,GO:0016021,GO:0001824,GO:0001822,GO:0051491,GO:0032331,GO:0005024,GO:0046872,GO:0060017,GO:0048762,GO:0070411,GO:0046332,GO:0060317,GO:0030513,GO:0007179,GO:0048179,GO:0043235,G	CG8224-PB				SM00220,SM00467		PF01064,PF08515,PF07714	PS51256,PS50011	PR00653,PR00653,PR00653	PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:2.10.60.10,G3DSA:1.10.510.10	SSF57302,SSF56112									
aly1689.6	Unknown		CG43780-PA																				
aly1689.7	Unknown	GO:0005515	n/a				SM00256		PF12937	PS50181			G3DSA:1.20.1280.50	SSF81383									
aly1689.8	Tetratricopeptide repeat protein 37	GO:0005737,GO:0005634,GO:0000956,GO:0035327,GO:0005515,GO:0055087	CG8777-PA				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF13424,PF13181,PF00515	PS50005,PS50005,PS50005,PS50293,PS50005,PS50293,PS50005,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452,SSF48452,SSF48452									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1689.9	FH1/FH2 domain-containing protein 3	GO:0005856,GO:0055003,GO:0035070,GO:0005634,GO:0030837,GO:0051639,GO:0046716,GO:0003779,GO:0003012,GO:0005488,GO:0010623,GO:0048471,GO:0030018	CG32030-PA				SM00498		PF02181	PS51232,PS51444			G3DSA:1.25.10.10	SSF48371,SSF101447,SSF101447									
aly16916.1	Syntaxin	GO:0008021,GO:0016020,GO:0006906,GO:0007349,GO:0061025,GO:0005484,GO:0005622,GO:0007274,GO:0031201,GO:0042335,GO:0016021,GO:0006887,GO:0000281,GO:0005886,GO:0017157,GO:0007482,GO:0006936,GO:0016081,GO:0000149,GO:0007317,GO:0007269,GO:0007268,GO:0043195,GO:0016192,GO:0031629,GO:0005515,GO:0006836,GO:0006886	CG31136-PB				SM00397			PS50192		PS00914	G3DSA:1.20.5.110	SSF58038	5~25		REACT_11184						
aly169556.1	Dynein heavy chain, cytoplasmic	GO:0016319,GO:0045198,GO:0034501,GO:0045197,GO:0007301,GO:0008088,GO:0007294,GO:0005524,GO:0030286,GO:0007067,GO:0030723,GO:0005874,GO:0005875,GO:0005737,GO:0040003,GO:0005938,GO:0040001,GO:0042623,GO:0006886,GO:0047497,GO:0007349,GO:0005739,GO:0030529,GO:0048134,GO:0007098,GO:0048477,GO:0003774,GO:0003777,GO:0005794,GO:0007298,GO:0048311,GO:0034063,GO:0035011,GO:0007051,GO:0046604,GO:0007282,GO:0007312,GO:0005868,GO:0051237,GO:0007405,GO:0051642,GO:0000776,GO:0050658,GO:0007279,GO:0045172,GO:0007018,GO:0007052,GO:0045169,GO:0030071,GO:0048813,GO:0008298,GO:0045478,GO:0043148,GO:0051683,GO:2001019	CG7507-PI						PF03028													
aly1698.1	Aminopeptidase N	GO:0004177,GO:0070062,GO:0005793,GO:0009897,GO:0016021,GO:0030154,GO:0005765,GO:0008270,GO:0006508,GO:0001525,GO:0008237,GO:0005615	CG40470-PA						PF11838,PF01433		PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF55486,SSF63737	696~716,939~941								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1698.2	Puromycin-sensitive aminopeptidase	GO:0004046,GO:0004177,GO:0070062,GO:0002474,GO:0005829,GO:0000209,GO:1903955,GO:0046331,GO:0008270,GO:0071456,GO:0006508,GO:0005634,GO:0008237	CG11956-PC						PF01433,PF01433,PF11838		PR00756,PR00756,PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF63737,SSF63737,SSF55486									
aly17.1	Unknown		n/a				SM00409,SM00409,SM00409						G3DSA:2.60.40.10	SSF48726									
aly17.10	UPF0518 protein CG3558	GO:0005575,GO:0003674,GO:0008150	CG3558-PC						PF10257						686~706								
aly17.11	Eukaryotic translation initiation factor 2-alpha kinase 3	GO:0005783,GO:0007595,GO:0005788,GO:0005789,GO:0048009,GO:0031642,GO:0045444,GO:0001525,GO:0030282,GO:0031018,GO:0045943,GO:0032092,GO:0006986,GO:0006983,GO:0007029,GO:0016021,GO:0019722,GO:0051260,GO:0046777,GO:0004674,GO:0010508,GO:0043066,GO:0010998,GO:0004672,GO:0002063,GO:0004694,GO:0051879,GO:0005524,GO:0006468,GO:0032933,GO:0019217,GO:0006919,GO:0032055,GO:0032057,GO:1902237,GO:1990737,GO:0042149,GO:0010389,GO:0004686,GO:0030968,GO:0070059,GO:0010575,GO:0005623,GO:0001503,GO:0017148,GO:0006412	CG2087-PA				SM00220		PF00069,PF00069	PS50011		PS00107,PS00108	G3DSA:2.140.10.10,G3DSA:2.140.10.10,G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF50998,SSF56112,SSF56112										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly17.12	Nischarin	GO:0030336,GO:0055037,GO:0016020,GO:0016601,GO:0035091,GO:0005829,GO:0006915,GO:0030036,GO:0032228,GO:0008217,GO:0005515,GO:0005886,GO:0006006,GO:0007186,GO:0005769,GO:0042802,GO:0048243	CG11807-PA				SM00312		PF00787	PS51450,PS51450,PS51450,PS50195,PS51450			G3DSA:3.80.10.10,G3DSA:3.30.1520.10	SSF52075,SSF64268										
aly17.13	DNA replication licensing factor Mcm2	GO:0003682,GO:0042555,GO:0008283,GO:0046872,GO:0005634,GO:0006270,GO:0030261,GO:0006267,GO:0005656,GO:0046331,GO:0006260,GO:0007049,GO:0051301,GO:0003677,GO:0003678,GO:0022008,GO:0043138,GO:0032508,GO:0005524	CG7538-PA				SM00350		PF12619,PF14551,PF00493	PS50051	PR01658,PR01658,PR01658,PR01658,PR01658,PR01657,PR01657,PR01657,PR01657,PR01657	PS00847	G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:3.30.1640.10,G3DSA:3.40.50.300	SSF52540,SSF50249			REACT_152,REACT_383,REACT_1538							
aly17.14	Zinc finger CCHC domain containing protein 10	GO:0008270,GO:0003676	CG5516-PA						PF13917					SSF57756									
aly17.15	Mitochondrial import inner membrane translocase subunit Tim16	GO:0001700,GO:0030150,GO:0005575,GO:0003674,GO:0005744,GO:0022008,GO:0002168	CG5268-PB						PF03656														
aly17.16	Transmembrane protein 169	GO:0016021	CG4596-PA						PF15052														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly17.17	3-hydroxyacyl-CoA dehydrogenase type-2	GO:0016229,GO:0006631,GO:0006637,GO:0005829,GO:0005811,GO:0008210,GO:0047015,GO:0005739,GO:0004303,GO:0047035,GO:0018454,GO:0008209,GO:0047022,GO:0008033,GO:0008205,GO:0003857,GO:0030283,GO:0005875,GO:0008202	CG7113-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly17.18	F-box/LRR-repeat protein 7	GO:0005737,GO:0008283,GO:0000086,GO:0005813,GO:0031146,GO:0000151,GO:0016567,GO:0006511,GO:0019005,GO:0005515,GO:0007067,GO:0004842,GO:0051301	CG4221-PA				SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00256		PF00646,PF13516,PF13516,PF13516	PS50181			G3DSA:3.80.10.10	SSF52047,SSF81383									
aly17.19	Thioredoxin domain-containing protein 12	GO:0045454,GO:0019153,GO:0005788	n/a						PF13899				G3DSA:3.40.30.10	SSF52833									
aly17.2	Trypsin, alkaline A	GO:0004252,GO:0005576,GO:0005615,GO:0006508	CG18681-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly17.20	PIN2/TERF1-interacting telomerase inhibitor 1	GO:0005654,GO:0005819,GO:0005730,GO:0005739,GO:0000781,GO:0007080,GO:0003676,GO:0070034,GO:0022008,GO:0007004,GO:0000228,GO:0000777	CG11180-PA				SM00443		PF01585	PS50174													
aly17.21	Unknown		n/a												80~100,45~65								
aly17.22	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly17.23	Eukaryotic translation initiation factor 2-alpha kinase	GO:0006468,GO:0006986,GO:0005783,GO:0006983,GO:0016021,GO:0017148,GO:0004686,GO:0005788,GO:0005789,GO:0004674,GO:0010508,GO:0004672,GO:0006417,GO:0010389,GO:0005524	CG2087-PA																				
aly17.3	Unknown		n/a																				
aly17.4	Another transcription unit protein	GO:0035206,GO:0005575,GO:0003674,GO:0016570,GO:0016593,GO:0006368	CG1433-PA						PF04004														
aly17.5	Tight junction protein ZO-2	GO:0035147,GO:0016337,GO:0006921,GO:0060439,GO:0030155,GO:0035220,GO:0030424,GO:0009790,GO:0007163,GO:0090559,GO:0050892,GO:0046328,GO:0090557,GO:0001745,GO:0005923,GO:0030054,GO:0005737,GO:0007254,GO:0046939,GO:0005654,GO:0048812,GO:0016476,GO:0035156,GO:0006915,GO:0004385,GO:0045177,GO:0016323,GO:0005917,GO:0036059,GO:0046331,GO:0005913,GO:0005912,GO:0005886,GO:0035329,GO:0050839,GO:0010033,GO:0007424,GO:0030674,GO:0012501,GO:0005829,GO:0007391,GO:0022416,GO:0019904	CG43140-PO				SM00228,SM00228,SM00228,SM00072		PF00625,PF00595,PF00595,PF07653	PS50106,PS50052,PS50106,PS50106			G3DSA:3.40.50.300,G3DSA:2.30.42.10,G3DSA:2.30.30.40,G3DSA:2.30.42.10,G3DSA:1.10.533.10,G3DSA:2.30.42.10	SSF50156,SSF50044,SSF50156,SSF47986,SSF52540,SSF50156										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly17.6	Tight junction protein ZO-1	GO:0035147,GO:0016337,GO:0060439,GO:0030155,GO:0035220,GO:0030424,GO:0009790,GO:0007163,GO:0046328,GO:0001745,GO:0005923,GO:0005921,GO:0007254,GO:0031410,GO:0048812,GO:0016476,GO:0035156,GO:0009986,GO:0004385,GO:0045177,GO:0071277,GO:0016323,GO:0005917,GO:0036059,GO:0046331,GO:0005913,GO:0005912,GO:0005911,GO:0005886,GO:0050839,GO:0007424,GO:0070830,GO:0007391,GO:0022416	CG43140-PO				SM00218		PF00791	PS51145					755~775									
aly17.7	S-antigen protein	GO:0006030,GO:0005576,GO:0008061,GO:0020003	CG14607-PB				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly17.8	Leucine-rich repeat-containing protein 71	GO:0005515	n/a				SM00368,SM00368,SM00368,SM00368		PF00560	PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047									
aly17.9	Leucine-rich repeat-containing protein 71		n/a				SM00368,SM00368,SM00368						G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047,SSF52047									
aly17014.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1702.1	Unknown		n/a																				
aly17040.1	Unknown		n/a																				
aly17040.2	Unknown		n/a																				
aly17055.1	Unknown	GO:0007346,GO:0006909,GO:0017053,GO:0003714,GO:0007476,GO:0005700,GO:0045746,GO:0045892,GO:0005515,GO:0003677,GO:0003682	CG4013-PG										G3DSA:1.10.10.60										
aly1706.1	Cytochrome P450 6B7	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0070330,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly1706.2	Cytochrome P450 6B6	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0070330,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1706.3	Poly(U)-binding-splicing factor half pint	GO:0043234,GO:0000381,GO:0000380,GO:0051726,GO:0071011,GO:0005634,GO:0000398,GO:0000166,GO:0008266,GO:0007282,GO:0006376,GO:0005515,GO:0022008,GO:0003729,GO:0048477,GO:0071013,GO:0001558	CG12085-PA				SM00360,SM00360	TIGR01645	PF00076,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928	191~211								
aly1706.4	Unknown		n/a																				
aly1708.1	DNA ligase 1	GO:0006310,GO:0005737,GO:0007049,GO:0071897,GO:0006281,GO:0005634,GO:0051103,GO:0043596,GO:0006260,GO:0003910,GO:0051301,GO:0003677,GO:0046872,GO:0005524	CG5602-PA					TIGR00574	PF04675,PF04675,PF01068	PS50160		PS00697	G3DSA:1.10.3260.10,G3DSA:1.10.3260.10,G3DSA:3.30.470.30,G3DSA:3.30.1490.70,G3DSA:3.30.1490.70	SSF56091,SSF117018			REACT_216						
aly1708.2	Non-canonical poly(A) RNA polymerase PAPD5	GO:0005737,GO:0071044,GO:0046872,GO:0005730,GO:0044822,GO:0004652,GO:0003887,GO:0003916,GO:0006364,GO:0003677,GO:0043630,GO:0007067,GO:0006397,GO:0051301,GO:0007062	CG11265-PC						PF03828,PF01909				G3DSA:3.30.460.10	SSF81631,SSF81301									
aly1708.3	Unknown		n/a																				
aly1708.4	Lipase 3	GO:0004806,GO:0006629,GO:0016788,GO:0016042	CG6113-PC			PIRSF000862			PF04083				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1708.5	Lipase 1	GO:0004806,GO:0006629,GO:0007586,GO:0016788,GO:0016042,GO:0005576	CG6113-PC			PIRSF000862			PF04083				G3DSA:3.40.50.1820	SSF53474									
aly1708.6	Unknown	GO:0005515	n/a				SM00249		PF00628	PS50016		PS01359	G3DSA:3.30.40.10	SSF57903	133~153								
aly17085.1	Deoxynucleoside kinase	GO:0005737,GO:0006230,GO:0016773,GO:0016310,GO:0019136,GO:0016301,GO:0046939,GO:0005739,GO:0009157,GO:0071897,GO:0006165,GO:0004797,GO:0005524	CG5452-PA			PIRSF000705			PF01712				G3DSA:3.40.50.300	SSF52540									
aly17085.2	NADH dehydrogenase [ubiqui] iron-sulfur protein 8, mitochondrial	GO:0051539,GO:0032981,GO:0008137,GO:0016020,GO:0005739,GO:0006120,GO:0016651,GO:0006979,GO:0046872,GO:0003954,GO:0055114,GO:0005747	CG3944-PA	MF_01351				TIGR01971	PF12838	PS51379,PS51379		PS00198,PS00198	G3DSA:1.10.1060.10	SSF54862									
aly17085.3	Pyridoxal-dependent decarboxylase domain-containing protein 1	GO:0016831,GO:0019752,GO:0030170	CG1486-PA										G3DSA:3.40.640.10	SSF53383									
aly1709.1	Unknown		n/a						PF01094				G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300	SSF53822									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1709.2	Arrestin homolog	GO:0005737,GO:0016028,GO:0006897,GO:0016060,GO:0016059,GO:0007602,GO:0007165,GO:0002046,GO:0045494	CG5711-PA				SM01017		PF02752,PF00339		PR00309,PR00309,PR00309,PR00309	PS00295	G3DSA:2.60.40.640,G3DSA:2.60.40.840	SSF81296,SSF81296									
aly1709.3	Neural cell adhesion molecule 1-B	GO:0016021,GO:0005575,GO:0003674,GO:0005515,GO:0005886,GO:0007155,GO:0008150	CG42313-PA				SM00408,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409		PF13927,PF13927,PF07679,PF07686,PF08205	PS50835,PS50853,PS50835,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726									
aly1709.4	Unknown		n/a																				
aly1709.5	Unknown		n/a																				
aly1709.6	Unknown		n/a																				
aly171.1	Membrane-bound alkaline phosphatase	GO:0016791,GO:0004035,GO:0035094,GO:0008152,GO:0005886,GO:0046872,GO:0031225	CG8147-PA				SM00098		PF00245		PR00113,PR00113,PR00113,PR00113,PR00113	PS00123	G3DSA:3.40.720.10	SSF53649		00627+3.1.3.1,00790+3.1.3.1		PWY-5491					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly171.10	Protein deadpan	GO:0045840,GO:0007549,GO:0007540,GO:0000122,GO:0003700,GO:0001078,GO:0005634,GO:0002052,GO:0006355,GO:0048813,GO:0007219,GO:0045892,GO:0006351,GO:0003677,GO:0046983,GO:0008345,GO:0008344,GO:0007530	CG8704-PA				SM00511,SM00353		PF00010,PF07527	PS51054,PS50888			G3DSA:4.10.280.10	SSF158457,SSF47459										
aly171.11	Mitochondrial ribosome-associated GTPase 2	GO:0044065,GO:0000287,GO:0003924,GO:0042254,GO:0070129,GO:0005743,GO:0005761,GO:0008152,GO:0005759,GO:0005525	CG13390-PA			PIRSF002401		TIGR02729	PF01018,PF01926	PS51710	PR00326,PR00326,PR00326,PR00326		G3DSA:2.70.210.12,G3DSA:3.40.50.300	SSF52540,SSF82051									
aly171.12	Centrosomal protein of 131 kDa	GO:0035869,GO:0000242,GO:0042384,GO:0035082,GO:0042073,GO:0007283,GO:0035735,GO:0048935,GO:0008344	CG1625-PD												1283~1310,1008~1042,1107~1149,245~265,865~935,1078~1105,1160~1180,1240~1271,1211~1231,1045~1065								
aly171.13	Perilipin-4	GO:0005737,GO:0005811,GO:0005886	CG1648-PB												761~829								
aly171.14	28S ribosomal protein S18a, mitochondrial	GO:0032543,GO:0005840,GO:0005622,GO:0003735,GO:0005743,GO:0005763,GO:0006412	CG31450-PA						PF01084				G3DSA:4.10.640.10	SSF46911									
aly171.15	Ubiquitin carboxyl-terminal hydrolase 5	GO:0071108,GO:0032436,GO:0048812,GO:0043161,GO:0008242,GO:0004221,GO:0005764,GO:0006511,GO:0008270,GO:0005515,GO:0004197,GO:0016579,GO:0004843,GO:0043130	CG12082-PA				SM00165,SM00165		PF00443,PF00627,PF00627	PS50030,PS50030,PS50235		PS00973	G3DSA:1.10.8.10,G3DSA:1.10.8.10	SSF46934,SSF54001,SSF54001,SSF54001									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly171.16	Troponin C, isoform 2	GO:0005509	CG6514-PA				SM00054,SM00054,SM00054,SM00054		PF13499,PF13499	PS50222,PS50222,PS50222,PS50222			G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly171.17	Unknown		n/a																				
aly171.18	Unknown		n/a																				
aly171.2	Calmodulin	GO:0051383,GO:0042052,GO:0046716,GO:0031476,GO:0031475,GO:0005875,GO:0005737,GO:0016028,GO:0016062,GO:0016061,GO:0016060,GO:0005814,GO:0000922,GO:0005509,GO:0007099,GO:0032036,GO:0006468,GO:0007605,GO:0072499,GO:0030048,GO:0007052,GO:0005819,GO:2001020,GO:0031489,GO:0070855,GO:0016059,GO:0016056,GO:0030496,GO:0051533,GO:0005513,GO:0046331,GO:0005516,GO:0005515	CG8472-PA				SM00054,SM00054,SM00054,SM00054		PF13499,PF13499	PS50222,PS50222,PS50222,PS50222		PS00018,PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly171.3	von Willebrand factor A domain-containing protein 8	GO:0005575,GO:0008150,GO:0016887,GO:0005524	CG12149-PB				SM00382,SM00382,SM00327		PF13519,PF07728,PF07728,PF07728	PS50234			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF53300,SSF52540,SSF52540,SSF52540,SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly171.4	RWD domain-containing protein 2B	GO:0005575,GO:0008150,GO:0003674,GO:0005515	CG30338-PA			PIRSF038021	SM00591		PF06544,PF05773	PS50908			G3DSA:3.10.110.10	SSF54495									
aly171.5	Zinc finger protein 808	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	306~326								
aly171.6	Arginine-glutamic acid dipeptide repeats protein	GO:0008586,GO:0042059,GO:0048755,GO:0008270,GO:0003677,GO:0035282,GO:0070491,GO:0043565,GO:0004407,GO:0005634,GO:0003714,GO:0021930,GO:0021691,GO:0009880,GO:0007480,GO:0006607,GO:0000118,GO:0001105,GO:0001106,GO:0045892,GO:0006338,GO:0008267,GO:0007379,GO:0005705,GO:0003700,GO:0048813,GO:0001654,GO:0003682,GO:0021942	CG6964-PJ				SM00717		PF03154	PS51293,PS51156				SSF46689	1772~1792,1454~1483									
aly171.7	Unknown		CG13449-PA																				
aly171.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly171.9	Unknown		n/a												253~301,155~175,200~241								
aly171361.1	PiggyBac transposable element-derived protein 3		n/a						PF13843														
aly171496.1	Unknown		n/a																				
aly172.1	Unknown		n/a																				
aly172.10	Y+L amino acid transporter 2	GO:1902475,GO:0031594,GO:0015297,GO:0007635,GO:0006868,GO:0007619,GO:0015813,GO:0003333,GO:0016020,GO:0015734,GO:0016323,GO:0014047,GO:0015807,GO:0015179,GO:0005887,GO:0008049,GO:0015171	CG6070-PA			PIRSF006060			PF13520														
aly172.11	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly172.12	Serine/threonine-protein kinase tricorner	GO:0030425,GO:0030424,GO:0071944,GO:0007165,GO:0070593,GO:0035556,GO:0035317,GO:0005737,GO:0005634,GO:0007476,GO:0004674,GO:0048800,GO:0004672,GO:0070451,GO:0005524,GO:0006468,GO:0044297,GO:0022416,GO:0005938,GO:0046872,GO:0050773,GO:0048813,GO:0048814,GO:0005515	CG8637-PB				SM00220		PF00069,PF00433	PS50011,PS51285		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10	SSF56112,SSF56112	91~121								
aly172.13	Nuclear hormone receptor E75	GO:0043565,GO:0003700,GO:0005634,GO:0003707,GO:0006355,GO:0002165,GO:0008270,GO:0043401,GO:0004879,GO:0006351	CG18023-PA				SM00399,SM00430		PF00105,PF00104	PS51030	PR00047,PR00047,PR00047,PR00047,PR00546,PR00546,PR00546,PR00398,PR00398,PR00398,PR00398,PR00398	PS00031	G3DSA:1.10.565.10,G3DSA:1.10.565.10,G3DSA:3.30.50.10	SSF48508,SSF48508,SSF57716			REACT_71						
aly172.14	Nitrogen permease regulator 2-like protein	GO:0015840,GO:0033673,GO:0006468,GO:0005096,GO:0048813,GO:0015824,GO:0004672,GO:0016247,GO:0035859	CG9104-PA						PF06218,PF06218														
aly172.15	PHD finger protein 12	GO:0070822,GO:0001222,GO:0016580,GO:0017053,GO:0000122,GO:0003700,GO:0005634,GO:0005654,GO:0035091,GO:0001106,GO:0045892,GO:0008270,GO:0006351	CG3815-PA				SM00249,SM00249		PF00628,PF00628,PF16737	PS50016,PS50016,PS50006		PS01359	G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:2.60.200.20	SSF49879,SSF57903,SSF57903	127~180								
aly172.16	Proton-coupled amino acid transporter 4	GO:0008021,GO:0015495,GO:0016021,GO:0015293,GO:0003333,GO:0006865,GO:0022008,GO:0015171	CG16700-PA						PF01490														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly172.17	Coatomer subunit beta'	GO:0048194,GO:0005795,GO:0006891,GO:0006890,GO:0006888,GO:0005794,GO:0005215,GO:0006886,GO:1901998,GO:0005198,GO:0010883,GO:0005515,GO:0030126,GO:0005829	CG6699-PA			PIRSF005567	SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF04053,PF00400,PF00400,PF00400,PF00400	PS50294,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320		G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50969	886~906		REACT_11123						
aly172.18	Transcription initiation factor TFIID subunit 4	GO:0007517,GO:0001092,GO:0006355,GO:0003700,GO:0008134,GO:0006366,GO:0001075,GO:0048813,GO:0045944,GO:0006367,GO:0003677,GO:0005669,GO:0051123,GO:0022008,GO:0046982,GO:0005634	CG5444-PE				SM00549		PF05236,PF07531	PS51119			G3DSA:1.10.20.10	SSF47113,SSF158553	769~794		REACT_71,REACT_6185,REACT_1788						
aly172.19	H(+)/Cl(-) exchange transporter 3	GO:0005794,GO:0015297,GO:0005770,GO:1903959,GO:0030554,GO:0016021,GO:0016020,GO:0031902,GO:0005769,GO:0030658,GO:0030165,GO:0006821,GO:0031901,GO:0012506,GO:0005247,GO:0005254,GO:0055085,GO:0005524	CG5284-PC				SM00116,SM00116		PF00571,PF00571,PF00654	PS51371,PS51371	PR00762,PR00762,PR00762,PR00762,PR00762,PR00762		G3DSA:3.10.580.10,G3DSA:1.10.3080.10,G3DSA:1.10.3080.10,G3DSA:1.10.3080.10	SSF54631,SSF81340,SSF81340,SSF81340									
aly172.2	Unknown		n/a																				
aly172.20	Protein furry	GO:0005737,GO:0006351,GO:0045177,GO:0045860,GO:0042052,GO:0050773,GO:0007476,GO:0016055,GO:0044297,GO:0048601,GO:0030425,GO:0008407,GO:0048800,GO:0045893,GO:0048814,GO:0005515,GO:0070593,GO:0030424,GO:0035316,GO:0035317,GO:0005938	CG32045-PG						PF14225,PF14228,PF14228,PF14228														
aly172.21	Neuropeptides capa receptor	GO:0004930,GO:0007589,GO:0001607,GO:0016021,GO:0051928,GO:0007218,GO:0016323,GO:0071465,GO:0008188,GO:0007186	CG16726-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly172.22	Unknown		n/a																				
aly172.23	Unknown		n/a																				
aly172.3	Potassium voltage-gated channel protein Shaker	GO:0048675,GO:0007619,GO:0060025,GO:0007611,GO:0048047,GO:0001508,GO:0050909,GO:0071805,GO:0016021,GO:0007637,GO:0051260,GO:0006813,GO:0022843,GO:0005251,GO:0009584,GO:0048150,GO:0008076,GO:0007629,GO:0045187,GO:0030431,GO:0008345,GO:0055085,GO:0005249	CG12348-PE				SM00225		PF00520,PF02214		PR01491,PR01491,PR01491,PR01491,PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR01496,PR01496,PR01496,PR01496,PR01496		G3DSA:3.30.710.10,G3DSA:1.10.287.70,G3DSA:1.20.120.350	SSF54695,SSF81324,SSF81324	513~540								
aly172.4	Unknown		n/a																				
aly172.5	Protein angel homolog 2	GO:0005575,GO:0003674,GO:0008150	CG12273-PA						PF03372				G3DSA:3.60.10.10,G3DSA:3.60.10.10	SSF56219,SSF56219									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly172.6	Vacuolar protein sorting associated protein 13B	GO:0015031	CG15523-PA						PF12624						3856~3856								
aly172.7	Proton-coupled amino acid transporter 4	GO:0003333,GO:0006865,GO:0016021,GO:0015171,GO:0015293	CG7888-PB						PF01490														
aly172.8	E3 ubiquitin-protein ligase UHRF1	GO:0042393,GO:0035064,GO:0032776,GO:0010390,GO:0031493,GO:0008270,GO:0007049,GO:0010216,GO:0000381,GO:0000122,GO:0061630,GO:0005634,GO:0006281,GO:0040029,GO:0016574,GO:0010467,GO:0005657,GO:0032270,GO:0000987,GO:0042787,GO:0016363,GO:0042802,GO:0008283,GO:0008327,GO:2000373,GO:0000792,GO:0044729,GO:0000791,GO:0004842,GO:0016874,GO:0003700,GO:0000790,GO:0051865,GO:0045944,GO:0006351	CG2926-PA				SM00213,SM00249,SM00466,SM00184,SM00184		PF00628,PF00240,PF12148,PF00097,PF02182	PS50089,PS50089,PS51015,PS50016,PS50053		PS00518	G3DSA:2.30.280.10,G3DSA:3.10.20.90,G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:2.30.30.30	SSF54236,SSF88697,SSF57903,SSF57850	644~664				UPA00143				
aly172.9	Unknown		n/a																				
aly1720.1	COMM domain-containing protein 2	GO:0005737,GO:0006355,GO:0006351	CG7168-PA						PF07258	PS51269													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1720.10	EF-hand domain-containing protein 1	GO:0008022,GO:0051124,GO:0043195,GO:0043025,GO:0005929,GO:0030425,GO:0043065,GO:0005813,GO:0072686,GO:0048814,GO:0006874,GO:0005874,GO:0005930,GO:0021795,GO:0005509	CG8959-PA																				
aly1720.11	Prostaglandin E synthase	GO:0005737,GO:0008285,GO:0004364,GO:0043231,GO:0016021,GO:0005811,GO:0001516,GO:0005741,GO:0050220,GO:0005641,GO:0043295	CG1742-PA						PF01124				G3DSA:1.20.120.550	SSF161084									
aly1720.12	Microsomal glutathione S-transferase 1	GO:0005783,GO:0033327,GO:0005789,GO:0032496,GO:0045177,GO:0005778,GO:0016021,GO:0005811,GO:0005739,GO:0006749,GO:0042802,GO:0042803,GO:0070207,GO:0004364,GO:0043231,GO:0010243,GO:0042493,GO:0005743,GO:0005741,GO:0071449,GO:0005634,GO:0004602,GO:0043295	CG1742-PA						PF01124				G3DSA:1.20.120.550	SSF161084									
aly1720.13	EF-hand domain-containing protein 1	GO:0008022,GO:0072686,GO:0005813,GO:0042384,GO:0005509,GO:0043025,GO:0005930,GO:0021795	CG11048-PA				SM00676		PF06565	PS51336,PS51336					226~250								
aly1720.14	Golgi SNAP receptor complex member 2	GO:0006909,GO:0060439,GO:0006906,GO:0005789,GO:0061025,GO:0005484,GO:0031201,GO:0044267,GO:0006888,GO:0007430,GO:0000149,GO:0016020,GO:0031902,GO:0005795,GO:0005794,GO:0005215,GO:0006623,GO:0036498,GO:0042147,GO:0012507,GO:0006896,GO:0006891,GO:0016192,GO:0030968,GO:0000139,GO:0048280,GO:0016021	CG4780-PA						PF12352				G3DSA:1.20.5.110										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1720.2	AP-3 complex subunit delta	GO:0006887,GO:0005783,GO:0005488,GO:0007041,GO:0007040,GO:0030131,GO:0030123,GO:0008565,GO:0006886,GO:0005770,GO:0005795,GO:0030665,GO:0005798,GO:0006727,GO:0006726,GO:0060967,GO:0008055,GO:0008057,GO:0008340,GO:0048072,GO:0007220,GO:0006897,GO:0046907,GO:0006895	CG10986-PB						PF06375,PF01602				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371										
aly1720.3	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	GO:0070062,GO:0006104,GO:0043209,GO:0005813,GO:0007052,GO:0005739,GO:0006105,GO:0010824,GO:0006099,GO:0009361,GO:0004774,GO:0004775,GO:0046872,GO:0005875,GO:0005524	CG11963-PC			PIRSF001554		TIGR01016	PF00549,PF08442	PS50975		PS01217	G3DSA:3.30.470.20,G3DSA:3.40.50.261,G3DSA:3.30.1490.20	SSF52210,SSF56059		00640+6.2.1.5,00660+6.2.1.5,00020+6.2.1.5,00720+6.2.1.5	REACT_1046	PWY-5913,PWY-7384,PWY-5392,PWY-6969,PWY-5537,PWY-6728,PWY-5538,PWY-5690	UPA00223				
aly1720.4	Unknown	GO:0006390,GO:0005739	CG7175-PA																				
aly1720.5	Unknown	GO:0035159,GO:0016021,GO:0019991,GO:0060857,GO:0005919,GO:0005918	CG1298-PA						PF13903														
aly1720.6	Unknown	GO:0007424,GO:0035151,GO:0016021,GO:0019991,GO:0007391,GO:0061343,GO:0060857,GO:0003015,GO:0005886,GO:0005918	CG10624-PA						PF13903														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1720.7	Unknown	GO:0007424,GO:0035151,GO:0016021,GO:0019991,GO:0035002,GO:0060857,GO:0005918	CG14779-PA						PF13903														
aly1720.8	CD82 antigen	GO:0003674,GO:0016021,GO:0008150,GO:0070062	CG9033-PB						PF00335					SSF48652									
aly1720.9	Pseudouridine 5'-phosphate glycosidase	GO:0016773,GO:0016798,GO:0005575,GO:0004730,GO:0008150,GO:0046113,GO:0046872	CG2794-PA						PF04227					SSF110581		00240+4.2.1.70		PWY-6019					
aly172192.1	Proteasome-associated protein ECM29 homolog	GO:0005737,GO:0016020,GO:0005770,GO:0005783,GO:0005793,GO:0016023,GO:0005813,GO:0005634,GO:0030433,GO:0005769,GO:0030139,GO:0005771,GO:0008150,GO:0000502,GO:0003674,GO:0030134	CG8858-PA						PF13001				G3DSA:1.25.10.10										
aly172286.1	Serine/threonine-protein kinase ATR	GO:0009314,GO:0030261,GO:0004672,GO:0003677,GO:0000723,GO:0007126,GO:0000075,GO:0005634,GO:0007348,GO:0007349,GO:0000706,GO:0004674,GO:0016310,GO:0007088,GO:0048477,GO:0005524,GO:0033314,GO:0006468,GO:0006281,GO:0016301,GO:0016321,GO:0031000,GO:0006974,GO:0008360,GO:0001700,GO:0007133,GO:0007131,GO:0007015,GO:0000077,GO:0000076,GO:0045003,GO:0045002,GO:0007444,GO:0007095,GO:0046983,GO:0007093	CG4252-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1723.1	Unknown	GO:0007157,GO:0005576,GO:0003674,GO:0005515	CG14390-PA							PS50835,PS50835			G3DSA:2.60.40.10										
aly1727.1	Unknown		n/a																				
aly1727.2	Unknown		n/a																				
aly1727.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1727.4	Neuroligin-3	GO:0048675,GO:0007416,GO:0050808,GO:0060077,GO:2000463,GO:0060024,GO:0060076,GO:0007612,GO:0061002,GO:0030425,GO:0050804,GO:0030139,GO:0008065,GO:0004872,GO:0002087,GO:0060080,GO:0007298,GO:0008542,GO:0030054,GO:0019991,GO:0097105,GO:0097104,GO:0060999,GO:0048515,GO:2000310,GO:2000311,GO:0043025,GO:0061001,GO:2000331,GO:0035151,GO:0042043,GO:0071625,GO:0097151,GO:0035176,GO:0009986,GO:1902474,GO:0048709,GO:0016321,GO:0008039,GO:0035321,GO:0052689,GO:0005887,GO:0005886,GO:0060079,GO:2000969,GO:0050839,GO:0005918,GO:0030534,GO:1900271,GO:0090394,GO:0060291,GO:0006898,GO:0061343,GO:0097110,GO:0051966,GO:0051965,GO:2000809,GO:0007158,GO:0051968,GO:0045202	CG3903-PA						PF00135			PS00941	G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474										
aly1727.5	Armadillo repeat-containing protein 3	GO:0005737,GO:0070062	n/a				SM00185,SM00185,SM00185,SM00185,SM00185						G3DSA:1.25.10.10	SSF48371,SSF48371									
aly1727.6	17-beta-hydroxysteroid dehydrogenase 13	GO:0005576,GO:0005811,GO:0046889,GO:0008152,GO:0016491	CG2254-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly1727.7	Oxysterol-binding protein-related protein 1	GO:0007016,GO:0005200,GO:0045170,GO:0008092,GO:0005770,GO:0008289,GO:0045169,GO:0006869,GO:0007165,GO:0005886	CG1651-PB				SM00233,SM00248,SM00248,SM00248,SM00248,SM00248		PF13857,PF12796	PS50088,PS50297,PS50088,PS50003,PS50088	PR01415,PR01415		G3DSA:2.30.29.30,G3DSA:1.25.40.20	SSF50729,SSF48403	456~476,134~154								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1728.1	Muscle segmentation homeobox	GO:0043565,GO:0007517,GO:0009953,GO:0007420,GO:0021782,GO:0007398,GO:0003700,GO:0007450,GO:0005634,GO:0007400,GO:0035222,GO:0007485,GO:0035309,GO:0006355,GO:0010629,GO:0042659,GO:0007389,GO:0003677,GO:0007476,GO:0007419,GO:0007417	CG1897-PA												222~224									
aly1728.10	Unknown		n/a																				
aly1728.11	Probable isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	GO:0016616,GO:0051287,GO:0000287,GO:0005739,GO:0006099,GO:0004449,GO:0005875,GO:0055114	CG6439-PB					TIGR00175	PF00180			PS00470	G3DSA:3.40.718.10	SSF53659		00020+1.1.1.41	REACT_1046	PWY-6549,PWY-5690					
aly1728.12	Sideroflexin-1	GO:0008324,GO:0016021,GO:0030218,GO:0006812,GO:0006811,GO:0016020,GO:0005739,GO:0015075,GO:0005743,GO:0055072,GO:0006826,GO:0055085,GO:0005371	CG11739-PC						PF03820														
aly1728.13	Homeobox protein MSH-C	GO:0021782,GO:0007476,GO:0035222,GO:0007419,GO:0010629,GO:0003677,GO:0007275,GO:0007417,GO:0043565,GO:0007517,GO:0005634,GO:0007450,GO:0007485,GO:0007389,GO:0035309,GO:0042659,GO:0007400,GO:0009953,GO:0007420,GO:0007398,GO:0003700,GO:0006355	CG1897-PA							PS50071			G3DSA:1.10.10.60	SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1728.2	Unknown		n/a																				
aly1728.3	Unknown		n/a																				
aly1728.4	Homeobox protein MSH-C	GO:0021782,GO:0007476,GO:0035222,GO:0007419,GO:0010629,GO:0003677,GO:0007275,GO:0007417,GO:0043565,GO:0007517,GO:0005634,GO:0007450,GO:0007485,GO:0007389,GO:0035309,GO:0042659,GO:0007400,GO:0009953,GO:0007420,GO:0007398,GO:0003700,GO:0006355	CG1897-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly1728.5	Unknown		n/a																				
aly1728.6	General transcription factor IIH subunit 3	GO:0008094,GO:0001113,GO:0001111,GO:0005675,GO:0006289,GO:0006355,GO:0000439,GO:0009411,GO:0006367,GO:0006366,GO:0008353,GO:0046872,GO:0005634	CG5041-PA						PF03850														
aly1728.7	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1728.8	E3 ubiquitin-protein ligase MARCH5	GO:0070585,GO:0090141,GO:0090344,GO:0005783,GO:0004842,GO:0016021,GO:0016020,GO:0051020,GO:0005789,GO:0051020,GO:0005741,GO:0008270,GO:0090140,GO:0016874,GO:0000209,GO:0051865	CG9855-PA				SM00744		PF12906	PS51292			G3DSA:3.30.40.10	SSF57850					UPA00143				
aly1728.9	Solute carrier family 10 member 6	GO:0016020,GO:0015721,GO:0008508,GO:0006814,GO:0005887,GO:0043250,GO:0043251	CG11655-PA						PF01758														
aly173.1	Protein daughter of sevenless	GO:0005070,GO:0005737,GO:0042169,GO:0042461,GO:0019730,GO:0045500,GO:0009967,GO:0046578,GO:0035220,GO:0008595,GO:0005515,GO:0005886,GO:0008293	CG1044-PA				SM00233		PF00169	PS50003			G3DSA:2.30.29.30	SSF50729									
aly173.10	3-hydroxyacyl CoA dehydrogenase type-2	GO:0016229,GO:0006631,GO:0006637,GO:0005829,GO:0005811,GO:0008210,GO:0047015,GO:0005739,GO:0004303,GO:0047035,GO:0018454,GO:0008209,GO:0047022,GO:0008033,GO:0008205,GO:0003857,GO:0030283,GO:0005875,GO:0008202	CG7113-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735									
aly173.11	Fibrinogen C domain-containing protein 1-A	GO:0016021,GO:0046872,GO:0008061	CG1791-PA				SM00186		PF00147	PS51406		PS00514	G3DSA:3.90.215.10,G3DSA:4.10.530.10	SSF56496									
aly173.12	Polyhomeotic-proximal chromatin protein	GO:0030708,GO:0000070,GO:0035186,GO:0005730,GO:0044547,GO:0035102,GO:0005634,GO:0051087,GO:0035075,GO:0016458,GO:0045892,GO:0008270,GO:0005515,GO:0006342,GO:0001047,GO:0021954,GO:0003682,GO:0003677,GO:0030713	CG18412-PA				SM00454		PF00536	PS50105			G3DSA:1.10.150.50	SSF47769									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.13	Polyhomeotic-proximal chromatin protein	GO:0030708,GO:0000070,GO:0035186,GO:0005730,GO:0044547,GO:0035102,GO:0005634,GO:0051087,GO:0035075,GO:0016458,GO:0045892,GO:0008270,GO:0005515,GO:0006342,GO:0001047,GO:0021954,GO:0003682,GO:0003677,GO:0030713	CG18412-PA																				
aly173.14	Sperm-associated antigen 17	GO:0005737,GO:0035082,GO:0005654,GO:0031514,GO:1990716,GO:0003341,GO:0005874	n/a												1599~1619								
aly173.15	Lysophospholipase-like protein 1	GO:0005737,GO:0016787,GO:0070062,GO:0005829,GO:0002084,GO:0004622,GO:0042997	CG6567-PB						PF02230				G3DSA:3.40.50.1820	SSF53474									
aly173.16	Unknown		n/a																				
aly173.17	Membrane-bound transcription factor site-1 protease	GO:0005795,GO:0004252,GO:0034976,GO:0006629,GO:0030968,GO:0005794,GO:0035103,GO:0016021,GO:0036500,GO:0000139,GO:0044281,GO:0005788,GO:0007040,GO:0031293,GO:0006508,GO:0005789,GO:0044267,GO:0008203	CG7169-PA						PF00082		PR00723,PR00723,PR00723	PS00137,PS00138	G3DSA:3.40.50.200	SSF52743									
aly173.18	Acetyl-coenzyme A synthetase	GO:0005737,GO:0048149,GO:0016208,GO:0019427,GO:0008152,GO:0003987,GO:0005524	CG9390-PA					TIGR02188	PF13193,PF16177,PF00501			PS00455	G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.30.300.30	SSF56801		00680+6.2.1.1,00010+6.2.1.1,00620+6.2.1.1,00720+6.2.1.1,00640+6.2.1.1	REACT_13433	PWY-7118,PWY-6672						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.19	Unknown		n/a																				
aly173.2	Unknown		n/a																				
aly173.20	SURF1-like protein	GO:0007632,GO:0015232,GO:0042331,GO:0016021,GO:0016020,GO:0033617,GO:0008535,GO:0005743,GO:0009060,GO:0022008,GO:0002168	CG9943-PA						PF02104	PS50895													
aly173.21	Ankyrin repeat domain-containing protein 12	GO:0005737,GO:0005654,GO:0005575,GO:0003674,GO:0005515,GO:0008150	CG10984-PB				SM00248,SM00248,SM00248		PF12796,PF13637	PS50088,PS50088,PS50297,PS50088	PR01415,PR01415		G3DSA:1.25.40.20	SSF48403									
aly173.22	Prostaglandin E synthase 2	GO:0046903,GO:0050220,GO:0020037,GO:0005829,GO:0016829,GO:0005634,GO:0005739,GO:0000139,GO:0001516,GO:0045893,GO:0003677,GO:0045454,GO:0043295,GO:0015035,GO:0016021,GO:0009055	CG4086-PA						PF14497,PF00462	PS51354		PS00195	G3DSA:3.40.30.10,G3DSA:1.20.1050.10,G3DSA:1.20.1050.10	SSF47616,SSF52833									
aly173.23	Unknown		CG13313-PA						PF00431	PS01180			G3DSA:2.60.120.290	SSF49854									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.24	Unknown	GO:0043565,GO:0046872,GO:0048814,GO:0050774	CG12029-PB																				
aly173.25	Sodium-dependent noradrenaline transporter	GO:0051610,GO:0015222,GO:0015844,GO:0006837,GO:0008504,GO:0016021,GO:0005886,GO:0005261,GO:0030424,GO:0005887,GO:0006836,GO:0005328,GO:0048265,GO:0006909,GO:0043679	CG4545-PA						PF00209	PS50267				SSF161070,SSF161070									
aly173.26	Unknown		n/a																				
aly173.27	Multidrug resistance protein homolog 49	GO:0015893,GO:0042626,GO:0042623,GO:0016021,GO:0031427,GO:0006855,GO:0015238,GO:0008559,GO:0005524,GO:0005887,GO:0005886,GO:0001666,GO:0055085,GO:0008354	CG3879-PA				SM00382,SM00382		PF00664,PF00664,PF00005,PF00005,PF00005	PS50893,PS50929,PS50929,PS50893		PS00211,PS00211	G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF90123,SSF90123,SSF90123,SSF52540,SSF52540									
aly173.28	Circadian locomoter output cycles protein kaput	GO:0032922,GO:0008062,GO:0048148,GO:0007165,GO:0004871,GO:0003677,GO:0005737,GO:0000122,GO:0005634,GO:0000977,GO:0007623,GO:0007622,GO:0008134,GO:0045187,GO:0045475,GO:0009649,GO:0009266,GO:0006351,GO:0003700,GO:0045944,GO:0005515,GO:0005667,GO:0046982,GO:0045893	CG7391-PD				SM00091,SM00091,SM00086		PF14598,PF00989	PS50112,PS50112	PR00785,PR00785,PR00785		G3DSA:3.30.450.20,G3DSA:3.30.450.20,G3DSA:3.30.450.20	SSF55785,SSF55785	488~519								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.29	LON peptidase N-terminal domain and RING finger protein 3	GO:0004176,GO:0006508,GO:0008270,GO:0005515	CG32369-PA				SM00184,SM00184,SM00464		PF02190,PF13920	PS50089		PS00518	G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57850,SSF88697									
aly173.3	Unknown		n/a						PF14924														
aly173.30	Probable palmitoyltransferase ZDHHC16	GO:0005794,GO:0018345,GO:0016021,GO:0006915,GO:0005789,GO:0008270,GO:0019706	CG5880-PA						PF01529	PS50216													
aly173.31	Helix-loop-helix protein 13	GO:0005737,GO:0048699,GO:0003700,GO:0008134,GO:0005634,GO:0030154,GO:0043054,GO:0008286,GO:0006355,GO:0010628,GO:0045475,GO:0003677,GO:0046983,GO:0006979,GO:0006351	CG5952-PD				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459									
aly173.32	Peptide transporter family 1	GO:0006857,GO:0006810,GO:0005427,GO:0005215,GO:0016020,GO:0005887,GO:0015031,GO:0035672	CG2930-PE						PF00854								REACT_19419,REACT_15518						
aly173.33	Esterase E4	GO:0052689	CG6414-PA						PF00135				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.34	Peptide transporter family 1	GO:0006857,GO:0006810,GO:0005427,GO:0005215,GO:0016020,GO:0005887,GO:0015031,GO:0035672	CG2930-PE						PF00854			PS01023,PS01022	G3DSA:1.20.1250.20	SSF103473,SSF103473			REACT_19419,REACT_15518						
aly173.35	Odorant receptor 13a	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG12697-PA						PF02949														
aly173.36	Tissue factor pathway inhibitor	GO:0005201,GO:0005604,GO:0004222,GO:0005615,GO:0009986,GO:0007596,GO:0030198,GO:0008270,GO:0004867,GO:0005578	CG33103-PE				SM00131,SM00131		PF00014,PF00014	PS50279,PS50279	PR00759,PR00759,PR00759	PS00280	G3DSA:4.10.410.10,G3DSA:4.10.410.10	SSF57362,SSF57362									
aly173.37	SPARC-related modular calcium-binding protein 1	GO:0009897,GO:0005604,GO:0060173,GO:0030718,GO:0010811,GO:0030154,GO:0007165,GO:0045667,GO:0043395,GO:0005576,GO:0001654,GO:0005509,GO:0030198,GO:0050840,GO:0008340,GO:0030513,GO:0005578,GO:0030510	CG2264-PA				SM00280,SM00211,SM00211		PF10591,PF10591,PF07648,PF00086,PF00086	PS51162,PS51465,PS50222,PS50222,PS50222,PS50222,PS51162		PS00484,PS00018,PS00484,PS00018,PS00018	G3DSA:4.10.800.10,G3DSA:4.10.800.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:3.30.60.30	SSF57610,SSF47473,SSF47473,SSF57610										
aly173.38	Centrosome-associated protein 350	GO:0005737,GO:0034453,GO:0005819,GO:0005813,GO:0016020,GO:0005654	n/a												1269~1270,1058~1081								
aly173.39	Ubiquitin carboxyl-terminal hydrolase 38	GO:0043161,GO:0004843,GO:0061136,GO:0004197,GO:0006511,GO:0016579,GO:0036459	CG8830-PB						PF00443	PS50235		PS00972	G3DSA:2.20.210.10	SSF48371,SSF48371,SSF48371,SSF54001,SSF54001									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.4	Unknown		n/a																				
aly173.40	Unknown		CG5928-PC																				
aly173.41	Cytochrome b-c1 complex subunit Rieske, mitochondrial	GO:0005743,GO:0016021,GO:0051537,GO:0008121,GO:0006122,GO:0005739,GO:0005750,GO:0070469,GO:0046872,GO:0005875,GO:0055114,GO:0016491	CG7361-PB					TIGR01416	PF00355,PF02921	PS51296	PR00162,PR00162,PR00162		G3DSA:2.102.10.10,G3DSA:1.20.5.270	SSF81502,SSF50022		00190+1.10.2.2		PWY-7279,PWY-6692,PWY-7082,PWY-3781					
aly173.42	Polypeptide N-acetylgalactosaminyltransferase 35A	GO:0005795,GO:0007424,GO:0046872,GO:0006486,GO:0016021,GO:0004653,GO:0030246,GO:0000139,GO:0009312	CG7480-PA				SM00458		PF00535,PF00535,PF00652	PS50231			G3DSA:3.90.550.10,G3DSA:3.90.550.10,G3DSA:3.90.550.10,G3DSA:2.80.10.50	SSF53448,SSF53448,SSF50370									
aly173.43	Discoidin domain-containing receptor 2	GO:0038063,GO:0048146,GO:0031214,GO:0018108,GO:0001503,GO:0007165,GO:0030500,GO:0007169,GO:0005925,GO:0046777,GO:0070062,GO:0016021,GO:0004714,GO:0004713,GO:0038062,GO:0010763,GO:0003416,GO:0045669,GO:0005524,GO:0090091,GO:0006468,GO:0016324,GO:0035988,GO:0005887,GO:0005886,GO:0007155,GO:0051091,GO:0045860,GO:0010715,GO:0030199,GO:0030198,GO:0005518	CG33531-PF				SM00231		PF00754,PF07714	PS50022,PS50011	PR00109,PR00109,PR00109	PS01286	G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:2.60.120.260	SSF49785,SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.44	Unknown		n/a						PF00078					SSF56672									
aly173.45	Lipase 3	GO:0004806,GO:0006629,GO:0032504,GO:0016788,GO:0016042,GO:0016298,GO:0005615	CG8093-PA						PF04083				G3DSA:3.40.50.1820	SSF53474	46~66								
aly173.46	Unknown		n/a																				
aly173.47	Unknown	GO:0033181,GO:0000220,GO:0015991,GO:0046961,GO:0005886	CG18617-PB																				
aly173.48	Unknown	GO:0015991,GO:0033181,GO:0033179,GO:0000220,GO:0046961,GO:0005886,GO:0015078	CG18617-PB						PF01496														
aly173.49	V-type proton ATPase 116 kDa subunit a isoform 1	GO:0005737,GO:0005794,GO:0070072,GO:0015986,GO:0070062,GO:0015991,GO:0051117,GO:0016021,GO:0005654,GO:1901998,GO:0033181,GO:0030659,GO:0000220,GO:0007035,GO:0046961,GO:0005886,GO:0016471,GO:0042470,GO:0043231	CG18617-PB						PF01496						94~114								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.5	Unknown		n/a																				
aly173.50	Unknown		n/a												195~229								
aly173.51	Flightin	GO:0030241,GO:0031672,GO:0071688,GO:0008307,GO:0045214,GO:0014703,GO:0043292,GO:0005863,GO:0097493,GO:0007527	CG7445-PA																				
aly173.52	Unknown		n/a																				
aly173.53	Unknown		n/a																				
aly173.54	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.55	Unknown	GO:0005575,GO:0008150,GO:0003674	CG10176-PB																				
aly173.56	Period circadian protein	GO:0004871,GO:0007619,GO:0007616,GO:0007617,GO:0042745,GO:0009416,GO:0007165,GO:0008062,GO:0060086,GO:0005737,GO:0000122,GO:0005634,GO:0003714,GO:0003712,GO:0048511,GO:0048512,GO:0048148,GO:0042803,GO:0007624,GO:0007623,GO:0007622,GO:0007620,GO:0008134,GO:0042752,GO:0045187,GO:0045892,GO:0045475,GO:0009649,GO:0009266,GO:0008340,GO:0006979,GO:0001306,GO:0045433,GO:0006355,GO:0005515,GO:0043153,GO:0046982,GO:2000678	CG2647-PA				SM00091,SM00091		PF14598,PF12114,PF00989	PS50112,PS50112			G3DSA:3.30.450.20,G3DSA:3.30.450.20,G3DSA:1.20.5.770,G3DSA:3.30.450.20	SSF55785,SSF55785,SSF55785	903~923								
aly173.57	Coatomer subunit gamma	GO:0035147,GO:0007424,GO:0006890,GO:0006909,GO:0005783,GO:0008362,GO:0005794,GO:0009306,GO:0006886,GO:0000281,GO:0035149,GO:0005198,GO:0005801,GO:0048812,GO:0010883,GO:0030198,GO:0007112,GO:0007436,GO:0030126,GO:0035158,GO:0016192	CG1528-PA			PIRSF037093			PF08752,PF16381,PF01602				G3DSA:3.30.310.30,G3DSA:2.60.40.1480,G3DSA:1.25.10.10	SSF49348,SSF48371,SSF55711										
aly173.58	Unknown	GO:0005575,GO:0003674,GO:0008150	CG43901-PA																				
aly173.59	RING finger and SPRY domain-containing protein 1	GO:0005576,GO:0008270,GO:0005515	CG6752-PA				SM00449,SM00184		PF00622,PF13920	PS50089,PS50188			G3DSA:3.30.40.10	SSF57850,SSF49899									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.6	Proton-coupled amino acid transporter 4	GO:0040007,GO:0015293,GO:0003333,GO:0006865,GO:0040008,GO:0015171,GO:0016021	CG3424-PA						PF01490														
aly173.60	Flotillin-1	GO:0005737,GO:0016600,GO:0005198,GO:0008150,GO:0005886,GO:0007275	CG8200-PB				SM00244		PF15975,PF01145					SSF117892	245~265,181~205								
aly173.61	Sulfhydryl oxidase 1	GO:0016971,GO:0045171,GO:0070062,GO:0003756,GO:0030173,GO:0045454,GO:0016242,GO:0055114,GO:0005615	CG4670-PA						PF00085,PF04777	PS51324,PS51352		PS00194	G3DSA:3.40.30.10,G3DSA:1.20.120.310	SSF52833,SSF69000				PWY-7533					
aly173.62	Transcription factor 25	GO:0007507,GO:0000122,GO:0003700,GO:0005634,GO:0006351,GO:0003677	CG7927-PA						PF04910				G3DSA:1.25.10.10										
aly173.63	Solute carrier family 15 member 1	GO:0006857,GO:0015293,GO:0005427,GO:0016021,GO:0005903,GO:0005887,GO:0015031,GO:0035672	CG44402-PD																				
aly173.64	Solute carrier family 15 member 2	GO:0006857,GO:0015293,GO:0005427,GO:0016021,GO:0016020,GO:0015198,GO:0015031	CG2930-PE						PF00854,PF00854					SSF103473			REACT_19419,REACT_15518						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.65	Trypsin epsilon	GO:0004252,GO:0005576,GO:0005615,GO:0006508	CG18681-PA				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly173.66	Unknown		n/a																				
aly173.67	Protein scabrous	GO:0048749,GO:0016318,GO:0007219,GO:0007399,GO:0007460,GO:0005770,GO:0008587,GO:0008407,GO:0016321,GO:0005577,GO:0046331,GO:0004871,GO:0045468,GO:0097305,GO:0005576	CG17579-PA				SM00186		PF00147	PS51406			G3DSA:4.10.530.10,G3DSA:3.90.215.10	SSF56496	181~201,245~265,221~241								
aly173.68	Unknown		n/a																				
aly173.69	Intraflagellar transport protein 122 homolog	GO:0005737,GO:0005856,GO:0030991,GO:0042384,GO:0035058,GO:0050954,GO:0045879,GO:0031513,GO:0072372,GO:0005515,GO:0035721,GO:0007275	CG7161-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400	PS50082,PS50294			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978									
aly173.7	USP6 N-terminal-like protein	GO:1903358,GO:0005794,GO:0007030,GO:0043547,GO:0048227,GO:0032313,GO:0031410,GO:0019068,GO:0005096,GO:0005097,GO:0017137,GO:0016023,GO:0035526,GO:0005886,GO:0007298	CG8085-PA				SM00164		PF00566	PS50086			G3DSA:1.10.8.270	SSF47923,SSF47923									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.70	Fork head domain-containing protein crocodile	GO:0043565,GO:0051090,GO:0000122,GO:0003700,GO:0005634,GO:0003705,GO:0009888,GO:0007380,GO:0006355,GO:0048513,GO:0008301,GO:0006357,GO:0005667,GO:0003677,GO:0030154,GO:0003690,GO:0009653,GO:0008134,GO:0000981,GO:0006351	CG5069-PA				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00657,PS00658	G3DSA:1.10.10.10	SSF46785	155~185								
aly173.71	Zinc finger CCCH domain containing protein 10	GO:0044822,GO:0046872	n/a							PS50103,PS50103					296~330							
aly173.72	Unknown		n/a												206~226								
aly173.73	OCIA domain-containing protein 1	GO:0005794,GO:0035167,GO:0046425,GO:0031410,GO:0055037,GO:0035162,GO:0005764,GO:0003674,GO:0048542,GO:0005769,GO:0016021	CG13533-PB						PF07051														
aly173.74	OCIA domain-containing protein 1	GO:0005794,GO:0035167,GO:0046425,GO:0031410,GO:0055037,GO:0035162,GO:0005764,GO:0003674,GO:0048542,GO:0005769,GO:0016021	CG13533-PB						PF07051														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.75	Protein cycle	GO:0032922,GO:0042594,GO:0048148,GO:0007165,GO:0004871,GO:0003677,GO:0005737,GO:0000122,GO:0005634,GO:0000977,GO:0007623,GO:0007622,GO:0045187,GO:0045475,GO:0008062,GO:0003700,GO:0006355,GO:0045944,GO:0006351,GO:0005667,GO:0046982,GO:0045893	CG8727-PA				SM00091,SM00091,SM00353		PF14598,PF00010,PF00989	PS50112,PS50112,PS50888	PR00785,PR00785,PR00785,PR00785,PR00785,PR00785,PR00785,PR00785		G3DSA:3.30.450.20,G3DSA:4.10.280.10,G3DSA:3.30.450.20	SSF55785,SSF55785,SSF55785,SSF47459									
aly173.76	Unknown		n/a																				
aly173.77	G-protein-signaling modulator 2	GO:0008105,GO:0055059,GO:0008277,GO:0008356,GO:0045175,GO:0045177,GO:0040001,GO:0045179,GO:0007186,GO:0042802,GO:0005737,GO:0005092,GO:0051294,GO:0030695,GO:0005938,GO:0007405,GO:0060487,GO:0007400,GO:0045167,GO:0000132,GO:0045185,GO:0005515,GO:0019904	CG5692-PA				SM00390,SM00390,SM00390,SM00390,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF00515,PF07721,PF02188,PF02188,PF02188,PF13424,PF13176	PS50005,PS50005,PS50877,PS50877,PS50293,PS50293,PS50877,PS50005,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452	254~274								
aly173.78	LIM/homeobox protein Awh	GO:0048749,GO:0043565,GO:0007444,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0010468,GO:0006351	CG1072-PC				SM00132,SM00132,SM00389		PF00412,PF00412,PF00046	PS50023,PS50023,PS50071		PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:1.10.10.60,G3DSA:2.10.110.10	SSF57716,SSF57716,SSF46689									
aly173.79	Protein henna	GO:0004510,GO:0004505,GO:0006909,GO:0006559,GO:0007616,GO:0016714,GO:0005811,GO:0006726,GO:0042427,GO:0005506,GO:0016597,GO:0055114	CG7399-PA			PIRSF000336		TIGR01268	PF01842,PF00351	PS51410,PS51671	PR00372,PR00372,PR00372,PR00372,PR00372,PR00372		G3DSA:1.10.800.10	SSF56534,SSF55021	439~456	00400+1.14.16.1,00360+1.14.16.1		PWY-7158,PWY-6134	UPA00139				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.8	Probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial	GO:0050660,GO:0006635,GO:0005811,GO:0005739,GO:0003995,GO:0005759,GO:0005875	CG12262-PA						PF02771,PF00441,PF02770			PS00072,PS00073	G3DSA:2.40.110.10,G3DSA:1.20.140.10,G3DSA:1.10.540.10	SSF56645,SSF47203										
aly173.80	ATP synthase subunit gamma, mitochondrial	GO:0045261,GO:0015986,GO:0015992,GO:0046933,GO:0000275,GO:0005811,GO:0005739,GO:0005743,GO:0046961,GO:0006909,GO:0008553	CG7610-PC					TIGR01146	PF00231		PR00126,PR00126,PR00126,PR00126	PS00153	G3DSA:1.10.287.80,G3DSA:3.40.1380.10	SSF52943										
aly173.81	Amino acid transporter ANTL1	GO:0003333,GO:0006865,GO:0016021,GO:0015171,GO:0005886	CG13646-PA						PF01490														
aly173.82	Protein furry homolog-like	GO:0005737,GO:0006351,GO:0045177,GO:0045860,GO:0042052,GO:0050773,GO:0007476,GO:0016055,GO:0044297,GO:0048601,GO:0030425,GO:0008407,GO:0006355,GO:0048800,GO:0048814,GO:0005515,GO:0070593,GO:0030424,GO:0035316,GO:0035317,GO:0005938	CG32045-PG						PF14222				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371	224~244									
aly173.83	Unknown		n/a																				
aly173.84	Putative oligosaccharyltransferase complex subunit CG9662	GO:0005575,GO:0008150,GO:0016021,GO:0003674	CG9662-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly173.85	Unknown		n/a												113~133								
aly173.86	Histone-lysine N-methyltransferase SETMAR	GO:0090305,GO:0044774,GO:0046975,GO:0051568,GO:0097676,GO:2001034,GO:0043566,GO:0004803,GO:0006303,GO:0000729,GO:0008270,GO:0003690,GO:0031297,GO:0003697,GO:0042803,GO:0008283,GO:2000373,GO:0035861,GO:0000014,GO:0006313,GO:0044547,GO:0004519,GO:0010452,GO:0000737,GO:0015074,GO:0042800,GO:0071157,GO:0005634,GO:2001251	n/a																				
aly173.9	Nuclear hormone receptor FTZ-F1	GO:0016319,GO:0002165,GO:0001077,GO:0008270,GO:0043401,GO:0003677,GO:0035626,GO:0008219,GO:0004879,GO:0005737,GO:0043565,GO:0007365,GO:0005634,GO:0007552,GO:0003712,GO:0045944,GO:0035075,GO:0035074,GO:0035073,GO:0035071,GO:0007480,GO:0042048,GO:0008134,GO:0055088,GO:0040034,GO:0003700,GO:0009725,GO:0003707,GO:0006355,GO:0048813,GO:0006357,GO:0000976,GO:0006351,GO:0046982	CG4059-PB				SM00430,SM00399		PF00104,PF00105	PS51030	PR00398,PR00398,PR00398,PR00398,PR00398,PR00047,PR00047,PR00047,PR00047	PS00031	G3DSA:1.10.565.10,G3DSA:3.30.50.10	SSF48508,SSF48508,SSF48508,SSF57716			REACT_71							
aly1730.1	Irregular chiasm C-roughest protein	GO:0061321,GO:0001745,GO:0046666,GO:0045177,GO:0046667,GO:1901739,GO:0097206,GO:0016021,GO:0007156,GO:0050839,GO:0042802,GO:0048749,GO:0016202,GO:0009986,GO:0005917,GO:0036059,GO:0030165,GO:0005913,GO:0005912,GO:0005886,GO:0007520,GO:0007157,GO:0007523,GO:0036058,GO:0046331,GO:0005515	CG3653-PB				SM00409,SM00409,SM00409,SM00408,SM00408,SM00408		PF07679,PF07679,PF13895	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1730.2	Irregular chiasm C-roughest protein	GO:0048749,GO:0016202,GO:0045177,GO:0001745,GO:0046667,GO:0016021,GO:0030165,GO:0046331,GO:0005913,GO:0007409,GO:0005886,GO:0007520,GO:0046666,GO:0007156,GO:0042802	CG4125-PA				SM00408,SM00409		PF07679	PS50835			G3DSA:2.60.40.10	SSF48726									
aly1730.3	Unknown		n/a																				
aly1732.1	GTP-binding protein REM 1	GO:0016020,GO:0005622,GO:0005575,GO:0006184,GO:0007264,GO:0005525	CG34397-PE				SM00175,SM00173		PF00071	PS51421	PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540									
aly1732.2	Beta-1,3-glucan-binding protein	GO:0045087,GO:0005975,GO:0045088,GO:0008329,GO:0009620,GO:0009986,GO:0002758,GO:0005576,GO:0005515,GO:0004553,GO:0052736,GO:0032491,GO:0001872	CG5008-PA						PF00722,PF15886			PS01159	G3DSA:2.60.120.200	SSF49899,SSF49899									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly17330.1	Catenin alpha-1	GO:0017166,GO:0015629,GO:0034332,GO:0008584,GO:0014704,GO:0043627,GO:0060323,GO:0007163,GO:0001669,GO:0045880,GO:0007406,GO:0031103,GO:0005925,GO:0030055,GO:0008013,GO:0071681,GO:0016600,GO:0030720,GO:0005198,GO:0003779,GO:0043066,GO:2001241,GO:2001240,GO:0042127,GO:0016264,GO:0016342,GO:0030027,GO:0051291,GO:2001045,GO:0034613,GO:0044822,GO:0051015,GO:0005915,GO:0005914,GO:0005913,GO:0005912,GO:0005911,GO:0005886,GO:0007155,GO:0090136,GO:0001541,GO:0007015,GO:0007016,GO:0007568,GO:0008092,GO:0005829,GO:0045295,GO:0045296,GO:0005515,GO:2000146,GO:0043297,GO:0042475	CG17947-PA						PF01044,PF01044		PR00805,PR00805,PR00805		G3DSA:1.20.120.230,G3DSA:1.20.120.230	SSF47220,SSF47220	73~93,42~62								
aly1734.1	Cytochrome P450 6k1	GO:0004497,GO:0016020,GO:0043231,GO:0020037,GO:0016705,GO:0005789,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG8859-PA						PF00067,PF00067		PR00465,PR00465,PR00465,PR00465,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264,SSF48264			REACT_13433						
aly17342.1	Unknown		n/a																				
aly1735.1	Leucine-rich repeat-containing protein 15	GO:0043236,GO:0070062,GO:0016021,GO:0046813,GO:0030335,GO:0005622,GO:0090005,GO:0005518,GO:0001968	CG6749-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00365,SM00365,SM00365,SM00365		PF13855,PF13855,PF00560	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1735.10	Unknown	GO:0005634,GO:0008270,GO:0003676,GO:0003677	CG14710-PB				SM00868,SM00384,SM00384,SM00355		PF07776	PS50157		PS00028	G3DSA:3.30.160.60	SSF57667,SSF57716									
aly1735.11	Zinc finger protein 431	GO:0046872,GO:0000122,GO:0005634,GO:0030154,GO:0043433,GO:0008270,GO:0001046,GO:0003677,GO:0003682,GO:0042826,GO:0045668,GO:0006351	CG14711-PA				SM00355,SM00355,SM00355,SM00355		PF00096,PF12874	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly1735.12	Unknown		n/a												88~122,35~55								
aly1735.13	Homeobox protein slou	GO:0043565,GO:0007517,GO:0007399,GO:0000122,GO:0003700,GO:0005634,GO:0007501,GO:0006355,GO:0003677,GO:0007521,GO:0007525	CG6534-PB				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly1735.14	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG1213-PA						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171		G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						
aly1735.15	Gastrula zinc finger protein XlCGF17.1 (Fragment)	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG10959-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1735.2	Unknown		n/a												41~61								
aly1735.3	Unknown	GO:0008150,GO:0003674,GO:0005887	CG15189-PA						PF07898														
aly1735.4	Unknown	GO:0003674,GO:0008150,GO:0005887	CG15188-PA						PF07898														
aly1735.5	Equilibrative nucleoside transporter 3	GO:0090281,GO:0016021,GO:0006810,GO:0015858,GO:0005765,GO:0008306,GO:0005886,GO:0007268,GO:0005337,GO:0031902	CG31911-PB			PIRSF016379			PF01733								REACT_1698,REACT_15518							
aly1735.6	Transmembrane protein 216	GO:0005737,GO:0005856,GO:0036038,GO:0042384,GO:0060271,GO:0016021,GO:0005929	CG8116-PA						PF09799														
aly1735.7	Unknown	GO:0005634,GO:0008270,GO:0003676	CG4936-PA				SM00868		PF07776					SSF57716									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1735.8	PR domain zinc finger protein 15	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0008168,GO:0046872,GO:0006351	CG15436-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667,SSF57667,SSF57667										
aly1735.9	Phosphatidylinositide phosphatase SAC2	GO:0042578	CG7956-PF						PF12456,PF02383	PS50275													
aly173522.1	Unknown		n/a																				
aly17356.1	Antichymotrypsin-1	GO:0060570,GO:0005783,GO:0005576,GO:0030162,GO:0004867,GO:0010951,GO:0004869,GO:0010955,GO:0005615	CG9453-PB				SM00093		PF00079			PS00284	G3DSA:2.30.39.10,G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574										
aly17356.2	Kelch repeat and BTB domain-containing protein 8	GO:0035183,GO:0007300,GO:0005819,GO:0045172,GO:0005794,GO:0007349,GO:0030717,GO:0030723,GO:0003779,GO:0007301,GO:0007303,GO:0007297,GO:0030036,GO:0035324,GO:0048477,GO:0005938	CG7210-PB				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695										
aly17356.3	Peptide-N(4)-(N-acetyl-beta-glucosaminyl) asparagine amidase	GO:0005737,GO:0016787,GO:0005829,GO:0030246,GO:0006516,GO:0000224,GO:0046872	CG7865-PA				SM00460		PF04721,PF01841	PS51398				SSF54001,SSF49785,SSF143503										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly17356.4	Bardet-Biedl syndrome 4 protein homolog	GO:0034452,GO:0000242,GO:0042384,GO:0035058,GO:0060170,GO:0005813,GO:0051297,GO:0034451,GO:0008152,GO:0005929,GO:0003777,GO:0034464	CG13232-PA						PF07719	PS50293			G3DSA:1.25.40.10	SSF48452									
aly173633.1	Unknown		n/a										G3DSA:3.30.1050.10										
aly1738.1	Unknown		n/a																				
aly173937.1	Transposable element Tcb2 transposase	GO:0004803,GO:0006313,GO:0005634,GO:0007476,GO:0015074,GO:0003677,GO:0002121	CG14478-PA						PF13384,PF13358,PF01498				G3DSA:1.10.10.10	SSF46689									
aly17394.1	Calsyntenin-1	GO:0016339,GO:0045211,GO:0005576,GO:0005509,GO:0005887,GO:0007268,GO:0044331,GO:0007156	CG11059-PC																				
aly1743.1	Unknown		n/a						PF01826,PF01826				G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57567,SSF57567									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1743.2	Unknown		n/a																				
aly17441.1	Protein CASC1		CG15373-PB						PF12366														
aly17441.2	Unknown		n/a																				
aly174549.1	Uncharacterized protein KIAA1109	GO:0016021,GO:0016020,GO:0005575,GO:0001558,GO:0003674,GO:0030856,GO:0005634,GO:0048488	CG42555-PJ																				
aly174550.1	Uncharacterized protein KIAA1109	GO:0051647,GO:0006629,GO:0016021,GO:0019915,GO:0005575,GO:0007283,GO:0001558,GO:0003674,GO:0060612,GO:0045444,GO:0005634,GO:0048488	CG42555-PJ																				
aly1748.1	Unknown	GO:0005515	n/a				SM00280		PF07648	PS51257,PS51465		PS00282	G3DSA:3.30.60.30	SSF100895									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1748.2	Trypsin epsilon	GO:0004252,GO:0005615,GO:0006508	CG13430-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1748.3	Unknown		n/a																				
aly1748.4	Unknown		n/a																				
aly174899.1	Unknown		n/a																				
aly17494.1	Unknown	GO:0003676	n/a						PF00075	PS50879			G3DSA:3.30.420.10	SSF53098									
aly1750.1	Neurotrimin	GO:0050767,GO:0016337,GO:0043005,GO:0009986,GO:0007606,GO:0008038,GO:0005575,GO:0003674,GO:0005911,GO:0005886,GO:0007155,GO:0043025,GO:0031225	CG33202-PB				SM00408,SM00408,SM00409,SM00409		PF13927,PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1755.1	Odorant receptor coreceptor	GO:0005549,GO:0007608,GO:0048149,GO:0008527,GO:0042048,GO:0016021,GO:0016020,GO:0051291,GO:0030425,GO:0050911,GO:0050912,GO:0007610,GO:0005886,GO:0004984,GO:0050909,GO:0019236,GO:0042803	CG10609-PA						PF02949														
aly1755.2	Aquaporin AQPAe.a	GO:0006810,GO:0005215,GO:0016021,GO:0016020,GO:0015250,GO:0015267,GO:0003014,GO:0055085	CG17664-PC						PF00230		PR00783,PR00783,PR00783,PR00783,PR00783,PR00783		G3DSA:1.20.1080.10	SSF81338									
aly176.1	Protein couch potato	GO:0035206,GO:0007422,GO:0042048,GO:0005634,GO:0009987,GO:0000166,GO:0003676,GO:0007268,GO:0022611,GO:0007275,GO:0003729	CG43738-PS				SM00360		PF00076,PF00076	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									
aly176.10	Ubiqui biosynthesis O methyltransferase, mitochondrial	GO:0008689,GO:0042060,GO:0004395,GO:0031314,GO:0006071,GO:0008425,GO:0006744,GO:0006743	CG9249-PA					TIGR01983	PF08241	PS51257			G3DSA:3.40.50.150	SSF53335		00130+2.1.1.222+2.1.1.64		PWY-7233,PWY-7230,PWY-6708,PWY-5855,PWY-5857,PWY-5856,PWY-5873,PWY-5872,PWY-5871,PWY-5870	UPA00232				
aly176.11	Unknown		n/a																				
aly176.12	Alkaline phosphatase, tissue-nonspecific isozyme	GO:0016791,GO:0004035,GO:0008152,GO:0005886,GO:0046872,GO:0031225	CG3290-PA				SM00098		PF00245		PR00113,PR00113,PR00113,PR00113,PR00113		G3DSA:3.40.720.10	SSF53649		00627+3.1.3.1,00790+3.1.3.1		PWY-5491					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly176.13	Unknown		n/a																				
aly176.14	Unknown		CG9812-PD																				
aly176.15	Unknown		n/a																				
aly176.16	Unknown		n/a																				
aly176.17	Juvenile hormone epoxide hydrolase	GO:0008096,GO:0043231,GO:0033961,GO:0016021,GO:0005789,GO:0004301,GO:0019439,GO:0006719	CG15102-PA			PIRSF001112			PF06441		PR00412,PR00412,PR00412,PR00412,PR00412,PR00412		G3DSA:3.40.50.1820	SSF53474		00980+3.3.2.9							
aly176.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly176.3	PRADC1-like protein	GO:0007521,GO:0005576,GO:0003674	CG9849-PA																				
aly176.4	Endoribonuclease Dicer	GO:0009597,GO:0033227,GO:0008026,GO:0030423,GO:0030422,GO:0031054,GO:0016887,GO:0070868,GO:0005737,GO:0004525,GO:0006342,GO:0005634,GO:0035087,GO:0003725,GO:0016246,GO:0046872,GO:0070578,GO:0005524,GO:0007626,GO:0004386,GO:0016442,GO:0051607,GO:0035197,GO:0002230,GO:0003723,GO:0006379	CG6493-PA				SM00490,SM00949,SM00535,SM00535,SM00487		PF00271,PF02170,PF00636,PF00636,PF03368,PF04851	PS51192,PS51194,PS50821,PS50142,PS51327,PS50142,PS50137		PS00517	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.1520.10,G3DSA:1.10.1520.10,G3DSA:1.10.1520.10	SSF54768,SSF52540,SSF52540,SSF69065,SSF69065,SSF69065									
aly176.5	60S ribosomal protein L18a	GO:0005840,GO:0022625,GO:0003735,GO:0007052,GO:0000022,GO:0006412,GO:0051298	CG6510-PA	MF_00273		PIRSF002190			PF01775				G3DSA:3.10.20.10	SSF160374									
aly176.6	Uncharacterized aarF domain-containing protein kinase 1	GO:0006468,GO:0005739,GO:0004674,GO:0005576,GO:0004672,GO:0005524	CG3608-PB						PF03109	PS50011			G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF56112									
aly176.7	Ubiquinone biosynthesis O-methyltransferase, mitochondrial	GO:0008689,GO:0042060,GO:0004395,GO:0031314,GO:0008171,GO:0006071,GO:0005739,GO:0008425,GO:0006744,GO:0006743	CG9249-PA					TIGR01983	PF13489				G3DSA:3.40.50.150	SSF53335		00130+2.1.1.222+2.1.1.64		PWY-7233,PWY-7230,PWY-6708,PWY-5855,PWY-5857,PWY-5856,PWY-5873,PWY-5872,PWY-5871,PWY-5870	UPA00232				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly176.8	Ubiqui biosynthesis O methyltransfer ase, mitochondrial	GO:0008689,GO:0042060,GO:0004395,GO:0031314,GO:0006071,GO:0008425,GO:0006744,GO:0006743	CG9249-PA					TIGR01983	PF08241				G3DSA:3.40.50.150	SSF53335		00130+2.1.1.222+2.1.1.64		PWY-7233,PWY-7230,PWY-6708,PWY-5855,PWY-5857,PWY-5856,PWY-5873,PWY-5872,PWY-5871,PWY-5870	UPA00232				
aly176.9	Unknown		n/a																				
aly176055.1	Unknown		n/a																				
aly1761.1	Unknown		n/a																				
aly1761.2	Polypyrimidin e tract-binding protein 2	GO:0033119,GO:0008103,GO:0008587,GO:0008586,GO:0007291,GO:0003676,GO:0008187,GO:0030529,GO:0005737,GO:0007219,GO:0000900,GO:0005634,GO:0000166,GO:2000177,GO:0003730,GO:0044822,GO:0006974,GO:0007286,GO:2001020,GO:0007319,GO:0000398,GO:0006376,GO:0005681,GO:0003729	CG31000-PY				SM00360,SM00360,SM00360,SM00360	TIGR01649	PF13893,PF13893,PF14259,PF14259	PS50102,PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928,SSF54928	660~660								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1761.3	RPII140-upstream gene protein	GO:0005575,GO:0016021,GO:0003674,GO:0007275	CG9852-PA						PF02466														
aly1761.4	Twinfilin	GO:0010591,GO:0016319,GO:0048488,GO:0030837,GO:0005856,GO:0008407,GO:0005622,GO:0003779,GO:0004713,GO:0007298,GO:0030042,GO:0007274,GO:0005737,GO:0005938	CG3172-PA				SM00102,SM00102		PF00241,PF00241	PS51263,PS51263			G3DSA:3.40.20.10,G3DSA:3.40.20.10	SSF55753,SSF55753									
aly1761.5	Serine protease inhibitor 3/4 (Fragment)	GO:0005615,GO:0032504,GO:0030162,GO:0004867,GO:0010951,GO:0045861	CG6717-PA				SM00093		PF00079				G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:2.30.39.10	SSF56574									
aly1761.6	Unknown		n/a																				
aly176237.1	Lipase 1	GO:0004806,GO:0006629,GO:0007586,GO:0016788,GO:0016042,GO:0048812,GO:0005576	CG31871-PA			PIRSF000862			PF00561				G3DSA:3.40.50.1820	SSF53474									
aly1763.1	Unknown		n/a				SM00249			PS50081			G3DSA:3.30.60.20	SSF57903	121~155								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1763.2	Unknown		n/a												33~53								
aly1763.3	Unknown		n/a																				
aly1763.4	Unknown		n/a																				
aly17669.1	Unknown		n/a																				
aly1770.1	Putative fatty acyl-CoA reductase CG5065	GO:0005737,GO:0045177,GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0035149,GO:0035002,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG1443-PA						PF07993,PF07993,PF03015				G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735,SSF51735			REACT_22258						
aly1772.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1772.10	Zinc finger and BTB domain-containing protein 17	GO:0001702,GO:0006351,GO:0007398,GO:0003700,GO:0005634,GO:1903955,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:1903146,GO:0045893	CG3032-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF00096	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667										
aly1772.11	Unknown		n/a																				
aly1772.12	Unknown	GO:0046872	n/a							PS50157		PS00028	G3DSA:3.30.160.60	SSF57667									
aly1772.13	PR domain zinc finger protein 12	GO:0048666,GO:0003700,GO:0005634,GO:0006357,GO:0000977,GO:0003676,GO:0008168,GO:0022008,GO:0046872,GO:0006351	CG3998-PA				SM00355,SM00355		PF12874	PS50157,PS50157		PS00028	G3DSA:3.30.160.60	SSF57667									
aly1772.14	Unknown		n/a																				
aly1772.2	U1 small nuclear ribonucleoprotein 70 kDa	GO:0016607,GO:0000381,GO:0030619,GO:0030532,GO:0071011,GO:0005634,GO:0043484,GO:0005692,GO:0000398,GO:0000166,GO:0007052,GO:0003723,GO:0005515,GO:0048025,GO:0022008,GO:0071013,GO:0005685,GO:0005681,GO:0003729	CG8749-PA				SM00360		PF12220,PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1772.3	KRAB-A domain-containing protein 2	GO:0015074,GO:0006355,GO:0003676,GO:0005622	n/a							PS50994			G3DSA:3.30.420.10	SSF53098									
aly1772.4	Serine/threonine-protein kinase ULK3	GO:0005737,GO:0006468,GO:0006914,GO:0045879,GO:0004674,GO:0045880,GO:0004672,GO:0046777,GO:0005524	CG8866-PA				SM00220,SM00745		PF04212,PF00069,PF00069	PS50011		PS00108,PS00107	G3DSA:1.20.58.280,G3DSA:1.10.510.10,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF56112,SSF116846									
aly1772.5	Unknown		n/a																				
aly1772.6	Unknown	GO:0046872	n/a				SM00355,SM00355,SM00355			PS50157,PS50157		PS00028,PS00028,PS00028		SSF57667,SSF57667									
aly1772.7	WD repeat domain-containing protein 83	GO:0071011,GO:0005737,GO:0071013,GO:0000398,GO:0005515	CG4935-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400	PS50082,PS50082,PS50294,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678	G3DSA:2.130.10.10	SSF50978									
aly1772.8	Sorting nexin-16	GO:0005770,GO:0035091,GO:0005771,GO:0008333,GO:0031902,GO:0006622,GO:0045022,GO:0005764,GO:0045887,GO:0031313,GO:0005515,GO:0005769,GO:0031901	CG6410-PA				SM00312		PF00787	PS50195			G3DSA:3.30.1520.10,G3DSA:1.10.287.510	SSF64268	259~279								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1772.9	Zinc finger and BTB domain-containing protein 41	GO:0045931,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF05605	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667									
aly17732.1	Pickpocket protein 28	GO:0050975,GO:0005272,GO:0042756,GO:0015280,GO:0016021,GO:0009415,GO:0030425,GO:0006814,GO:0035002,GO:0035725,GO:0071462,GO:0005886,GO:0030424,GO:0043025	CG1058-PB						PF00858				G3DSA:2.60.470.10,G3DSA:2.60.470.10										
aly17732.2	EF-hand domain-containing protein D2 homolog	GO:0007498,GO:0005927,GO:0005509,GO:0005886	CG10641-PA				SM00054,SM00054		PF13499	PS50222,PS50222		PS00018	G3DSA:1.10.238.10	SSF47473	152~189								
aly17732.3	Unknown		n/a																				
aly17732.4	Ankyrin repeat family A protein 2	GO:0005856,GO:0005829,GO:0016020,GO:0003712,GO:0006357,GO:0005515,GO:0005634,GO:0030169	CG5846-PA				SM00248,SM00248,SM00248		PF12796	PS50088,PS50297,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403									
aly17732.5	2-hydroxyacyl-CoA lyase 1	GO:0051259,GO:0030976,GO:0006629,GO:0016830,GO:0008949,GO:0000287,GO:0005777,GO:0001561,GO:0048037,GO:0005102,GO:0016829,GO:0042802	CG11208-PA						PF02776,PF00205,PF02775				G3DSA:3.40.50.970,G3DSA:3.40.50.970,G3DSA:3.40.50.970,G3DSA:3.40.50.1220	SSF52518,SSF52518,SSF52467									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly17732.6	Sialin	GO:0006865,GO:0006820,GO:0030054,GO:0005737,GO:0044267,GO:0015992,GO:0006488,GO:0016021,GO:0016020,GO:0043687,GO:0018279,GO:0015739,GO:0005351,GO:0006811,GO:0005316,GO:0005887,GO:0005886,GO:0055085,GO:0030672,GO:0015136,GO:0005764,GO:0005765	CG9864-PA						PF07690	PS51257,PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473										
aly17732.7	Vesicular glutamate transporter 1	GO:0030672,GO:0015293,GO:0035435,GO:0005316,GO:0043005,GO:0006836,GO:0006814,GO:0016021,GO:0030054	CG10207-PA						PF07690				G3DSA:1.20.1250.20	SSF103473									
aly1775.1	Protein I'm not dead yet	GO:0071422,GO:0015744,GO:0006848,GO:1901475,GO:0006814,GO:0015137,GO:0050833,GO:0016323,GO:0005887,GO:0005886,GO:0015141,GO:0008340,GO:0015142,GO:0055085,GO:0010889	CG3979-PB						PF00939,PF00939			PS01271					REACT_20633,REACT_15518						
aly1775.2	Protein I'm not dead yet	GO:0071422,GO:0015142,GO:1901475,GO:0006848,GO:0005215,GO:0016020,GO:0015137,GO:0050833,GO:0016323,GO:0015746,GO:0005887,GO:0005886,GO:0015141,GO:0008340,GO:0006814,GO:0055085,GO:0010889,GO:0015744	CG3979-PB						PF00939			PS01271					REACT_20633,REACT_15518						
aly1775.3	Solute carrier family 13 member 5	GO:0006810,GO:0005215,GO:0016021,GO:0016020,GO:0006814,GO:0016323,GO:0005886,GO:0015137,GO:0015141,GO:0017153,GO:0055085	CG33934-PE						PF00939								REACT_20633,REACT_15518						
aly1775.4	Voltage-dependent calcium channel gamma-5 subunit	GO:0032281,GO:0005262,GO:0016021,GO:0005198,GO:0045211,GO:0014069,GO:0051966,GO:0016247,GO:2000311,GO:0005244,GO:0005923,GO:0030054	CG32514-PA						PF13903			PS01346					REACT_20676						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly17777.1	Integrin alpha-4	GO:0009897,GO:0016020,GO:0007494,GO:0048149,GO:0034446,GO:0060710,GO:0007614,GO:0005886,GO:0050901,GO:0007613,GO:0034113,GO:0007611,GO:0007160,GO:0050900,GO:0035001,GO:0090074,GO:0004872,GO:0050904,GO:0007411,GO:0005925,GO:0003344,GO:0008355,GO:0003366,GO:0070062,GO:0007431,GO:0035987,GO:0016021,GO:0005055,GO:0005198,GO:0030198,GO:0030183,GO:0016477,GO:0016339,GO:0006909,GO:0005178,GO:0007596,GO:2000406,GO:0016340,GO:0007507,GO:0009986,GO:0042060,GO:0008305,GO:0050776,GO:0007159,GO:0005911,GO:0043277,GO:0007155,GO:0007157,GO:0050839,GO:0072678,GO:0043113,GO:0040011,GO:0007424,GO:0046872,GO:0071345,GO:0007391,GO:0007229,GO:0007508,GO:0001974,GO:0045886,GO:1903238,GO:0098657,GO:0034669,GO:0046982,GO:0060324	CG8095-PB				SM00191,SM00191,SM00191,SM00191		PF01839,PF01839	PS51470,PS51470,PS51470,PS51470,PS51470	PR01185,PR01185,PR01185,PR01185,PR01185,PR01185		G3DSA:2.130.10.130,G3DSA:2.60.40.1460	SSF69318			REACT_13552						
aly1779.1	Slowpoke-binding protein	GO:0005737,GO:0042391,GO:0006468,GO:0005515,GO:0050804,GO:0042594,GO:0004672,GO:0007274	CG43756-PJ										G3DSA:1.10.510.10	SSF56112									
aly1779.10	Unknown		CG13868-PA																				
aly1779.11	Unknown		CG13868-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1779.12	Unknown		n/a																				
aly1779.13	Unknown		CG7781-PA											SSF57302									
aly1779.14	Nucleosome-remodeling factor subunit NURF301	GO:0035064,GO:0008270,GO:0003677,GO:0046426,GO:0042766,GO:0006325,GO:0045747,GO:0070577,GO:0045824,GO:0048515,GO:0010468,GO:0035076,GO:0035073,GO:0046331,GO:0030097,GO:0016922,GO:0006338,GO:0016589,GO:0048813,GO:0006357,GO:0006351,GO:0005515,GO:0007095	CG7781-PA				SM00297		PF00439	PS50014			G3DSA:1.20.920.10	SSF47370										
aly1779.15	Unknown	GO:0019028	CG42598-PB						PF03067														
aly1779.16	ATPase family AAA domain-containing protein 1-A	GO:0048190,GO:0005783,GO:0005777,GO:0008568,GO:0031122,GO:0008152,GO:0045211,GO:0005741,GO:0030054,GO:0016887,GO:0007286,GO:0005524	CG5395-PA				SM00382		PF00004			PS00674	G3DSA:3.40.50.300,G3DSA:1.10.8.60	SSF52540										
aly1779.17	Nucleolar MIF4G domain-containing protein 1 homolog	GO:0022008,GO:0005730,GO:0005488,GO:0003723	CG9004-PA				SM00544		PF02847	PS51366				SSF48371	81~124								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1779.18	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN	GO:2001235,GO:0006470,GO:0048679,GO:0007613,GO:0007611,GO:0051898,GO:0019915,GO:0010043,GO:0031658,GO:0002902,GO:0051895,GO:0005654,GO:0051717,GO:0045786,GO:0097107,GO:0097105,GO:0060997,GO:0033032,GO:2000060,GO:0031104,GO:1901888,GO:0035176,GO:0050680,GO:0019901,GO:0008361,GO:0030165,GO:2000808,GO:0010975,GO:0050771,GO:0042995,GO:0045792,GO:0090175,GO:0090071,GO:0032228,GO:0033555,GO:0032535,GO:0060179,GO:0090344,GO:0030336,GO:0061002,GO:0009898,GO:0050821,GO:0048008,GO:0002164,GO:0043220,GO:0043542,GO:0016605,GO:0003779,GO:0035749,GO:0046856,GO:0046855,GO:0071456,GO:0016477,GO:0007584,GO:0007626,GO:0009887,GO:0006629,GO:0009888,GO:0021542,GO:0060070,GO:0060074,GO:2000134,GO:0007425,GO:0035011,GO:0004726,GO:0004725,GO:0031647,GO:0004722,GO:0036294,GO:0004438,GO:0031642,GO:0000287,GO:0030308,GO:0016314,GO:0019899,GO:0035335,GO:0007416,GO:0007417,GO:0005737,GO:0050765,GO:0060341,GO:0005634,GO:0007552,GO:0005739,GO:0043005,GO:0021955,GO:0010997,GO:0008284,GO:0008285,GO:0008286,GO:0008138,GO:0030534,GO:0009987,GO:0016322,GO:0045211,GO:0040015,GO:0051091,GO:0007568,GO:0042711,GO:0050773,GO:0060291,GO:0060292,GO:0042493,GO:0048738,GO:0043491,GO:0033198,GO:0070374,GO:0032286,GO:0045926,GO:0042052,GO:0035206,GO:0051726,GO:0060024,GO:0030036,GO:0060736,GO:0060134,GO:0004721,GO:0042594,GO:0007270,GO:0001525,GO:0032355,GO:0008283,GO:0043066,GO:0048681,GO:0046685,GO:0010506,GO:0007436,GO:0046620,GO:0046621,GO:0006914,GO:0006915,GO:2000463,GO:0046627,GO:0045471,GO:0045475,GO:0005	CG5671-PD						PF10409	PS51182			G3DSA:2.60.40.1110	SSF49562									
aly1779.19	Methyltransferase-like protein 14 homolog	GO:0006139,GO:0080009,GO:0003700,GO:0005634,GO:0016422,GO:0001510	CG7818-PA						PF05063	PS51592,PS51143				SSF53335									
aly1779.2	Mitochondrial 2-oxoglutarate/malate carrier protein	GO:0016021,GO:0006810,GO:0044822,GO:0022857,GO:0005739,GO:0005743,GO:0005740,GO:0015367,GO:0006839,GO:0005634,GO:0015743,GO:0015742	CG18418-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1779.20	Cysteine-rich venom protein 6	GO:0005576	n/a						PF01826,PF01826				G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57567,SSF57567,SSF57567									
aly1779.21	Non-specific lipid-transfer protein (Fragment)	GO:0005737,GO:0005548,GO:0006869,GO:0015914,GO:0005811,GO:0005777,GO:0008289,GO:0005739,GO:0016747,GO:0008152,GO:0033814	CG17320-PA						PF02036,PF00108,PF02803			PS00098	G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.30.1050.10	SSF53901,SSF55718,SSF53901			REACT_22258						
aly1779.22	Protein Dok-7	GO:0007528,GO:0035091,GO:0031594,GO:0019901,GO:0005886,GO:0061098,GO:0043113,GO:0001934,GO:0030054	n/a						PF02174	PS51064			G3DSA:2.30.29.30,G3DSA:2.30.29.30	SSF50729,SSF50729									
aly1779.23	Cysteine-rich venom protein 6	GO:0005576	CG42259-PA						PF01826,PF01826,PF01826				G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57567,SSF57567,SSF57567									
aly1779.24	Unknown		n/a																				
aly1779.25	Unknown	GO:0003677	n/a				SM00595		PF02944,PF10545	PS51031,PS51029													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1779.3	Ski oncogene	GO:0048666,GO:0005737,GO:0000122,GO:0090099,GO:0005634,GO:0046332,GO:0048813,GO:0006351,GO:0030512	CG34421-PB				SM01046		PF08782,PF02437				G3DSA:3.10.390.10,G3DSA:3.10.260.20	SSF63763,SSF46955	372~417								
aly1779.4	Unknown	GO:0005575,GO:0008150,GO:0003674	CG42557-PA						PF14989						30~57								
aly1779.5	Sepiapterin reductase	GO:0006729,GO:0016265,GO:0070062,GO:0006558,GO:0048667,GO:0019889,GO:0005654,GO:0050882,GO:0005739,GO:0006809,GO:0042417,GO:0042415,GO:0042428,GO:0004757,GO:0055114,GO:0040014	CG12117-PA					TIGR01500	PF00106		PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735		00790+1.1.1.153		PWY-5663					
aly1779.6	Unknown		n/a																				
aly1779.7	Non-specific lipid-transfer protein (Fragment)	GO:0005737,GO:0005548,GO:0006869,GO:0015914,GO:0005811,GO:0005777,GO:0008289,GO:0005739,GO:0016747,GO:0008152,GO:0033814	CG17320-PA						PF00108,PF02036,PF02803			PS00098,PS00737	G3DSA:3.30.1050.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10	SSF55718,SSF53901,SSF53901			REACT_22258							
aly1779.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1779.9	Myeloid leukemia factor	GO:0005737,GO:2000495,GO:0005705,GO:0050821,GO:0006355,GO:0048471,GO:0005634	CG8295-PD						PF10248														
aly17793.1	Stomatin-4	GO:0003674,GO:0016021,GO:0006909	CG33253-PB						PF01145		PR00721,PR00721,PR00721			SSF117892									
aly177958.1	Bromodomain containing protein 8	GO:0006351,GO:0030522,GO:0043967,GO:0006325,GO:0005634,GO:0006355,GO:0005739,GO:0000812,GO:0005654,GO:0043968,GO:0010629,GO:0006357,GO:0035267,GO:0007166,GO:0003700,GO:0004887,GO:0040008,GO:0007165	CG14514-PA												42~62								
aly17797.1	Unknown		n/a																				
aly17797.2	Unknown		n/a																				
aly17803.1	Antichymotrypsin-1	GO:0005615,GO:0032504,GO:0002784,GO:0050832,GO:0030162,GO:0004867,GO:0010951,GO:0045861	CG9456-PB				SM00093		PF00079				G3DSA:3.30.497.10	SSF56574									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly17803.2	Antichymotrypsin-1	GO:0060570,GO:0005783,GO:0005576,GO:0030162,GO:0004867,GO:0010951,GO:0004869,GO:0010955,GO:0005615	CG9453-PB				SM00093		PF00079			PS00284	G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:2.30.39.10,G3DSA:2.30.39.10	SSF56574										
aly17803.3	Antichymotrypsin-1	GO:0060570,GO:0005783,GO:0005576,GO:0030162,GO:0004867,GO:0010951,GO:0004869,GO:0010955,GO:0005615	CG9453-PB				SM00093		PF00079			PS00284	G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:2.30.39.10,G3DSA:2.30.39.10	SSF56574										
aly17803.4	Antichymotrypsin-1	GO:0060570,GO:0005783,GO:0005576,GO:0030162,GO:0004867,GO:0010951,GO:0004869,GO:0010955,GO:0005615	CG9453-PB				SM00093		PF00079				G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:2.30.39.10	SSF56574										
aly17805.1	Insulin-like growth factor-binding protein complex acid labile subunit	GO:0007424,GO:0070062,GO:0035151,GO:0035159,GO:0005654,GO:0042567,GO:0005515,GO:0008045,GO:0007155	CG8561-PB				SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00369		PF13306,PF13855,PF13855,PF13855,PF13855	PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52058,SSF52058,SSF52058,SSF52058									
aly17805.2	Unknown		n/a																				
aly17809.1	Methyltransferase-like protein 9		CG5339-PA						PF05219														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1781.1	Sodium-dependent dopamine transporter	GO:0005328,GO:0005329,GO:0032809,GO:0015872,GO:0051583,GO:0006821,GO:0015837,GO:0032590,GO:0005275,GO:0016021,GO:0019811,GO:0090494,GO:0005254,GO:0005330,GO:1902476,GO:0030431,GO:0005887,GO:0006836,GO:0072488,GO:0030673,GO:0042734,GO:0042745,GO:0098655	CG8380-PB						PF00209	PS50267	PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176	PS00754		SSF161070,SSF161070									
aly1781.2	Ankyrin repeat and MYND domain-containing protein 2	GO:0046872,GO:0005929	CG8003-PA				SM00248,SM00248		PF13637,PF01753	PS50297,PS50088,PS50865,PS50088		PS01360	G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF144232									
aly1781.3	T-box-containing protein TBX6L (Fragment)	GO:0007507,GO:0001700,GO:0061327,GO:0003700,GO:0005634,GO:0035051,GO:0003705,GO:0001158,GO:0006355,GO:0045944,GO:0006351,GO:0003677,GO:0007275,GO:0035294,GO:0010468	CG5133-PA				SM00425		PF00907	PS50252	PR00937,PR00937,PR00937,PR00937,PR00937,PR00937,PR00937		G3DSA:2.60.40.820	SSF49417									
aly1781.4	Unknown	GO:0007507,GO:0001700,GO:0061327,GO:0003700,GO:0005634,GO:0035051,GO:0003705,GO:0001158,GO:0006355,GO:0045944,GO:0035294,GO:0010468	CG5133-PA						PF00907	PS50252			G3DSA:2.60.40.820	SSF49417									
aly1781.5	Ubiquitin-protein ligase E3B	GO:0005737,GO:0016874,GO:0005634,GO:0042787,GO:0005515,GO:0004842	CG5087-PA				SM00015,SM00119		PF00612,PF00632	PS50096,PS50237			G3DSA:3.30.2160.10	SSF56204					UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1781.6	Serine/threonine kinase NLK	GO:0048749,GO:0016318,GO:0006468,GO:0042332,GO:0005634,GO:0016055,GO:0007476,GO:0008586,GO:0007474,GO:0001736,GO:0004674,GO:0004707,GO:0045887,GO:0005938,GO:0004672,GO:0007275,GO:0046872,GO:0030178,GO:0005524	CG7892-PE																				
aly1781.7	Serine/threonine-protein kinase NLK	GO:0016318,GO:0018107,GO:0033136,GO:0008586,GO:0045887,GO:0046777,GO:0005737,GO:0042332,GO:0005634,GO:0000287,GO:0007476,GO:0007474,GO:0030178,GO:0004674,GO:0004672,GO:0005524,GO:0048749,GO:0006468,GO:0001736,GO:0007179,GO:0016055,GO:0006355,GO:0004707,GO:0006351	CG7892-PE				SM00220		PF00069	PS50011		PS01351,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly1781.8	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246	n/a				SM00034		PF00059,PF00059	PS50041			G3DSA:3.10.100.10,G3DSA:3.10.100.10	SSF56436,SSF56436									
aly17828.1	Unknown		n/a																				
aly1785.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1785.2	Unknown		n/a																				
aly17865.1	Unknown		n/a																				
aly178698.1	Protein toll	GO:0009897,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0035007,GO:0008063,GO:0006955,GO:0007416,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0002229,GO:0006952,GO:0042802,GO:0016201,GO:0009880,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005887,GO:0005886,GO:0007155,GO:0007352,GO:0043234,GO:0007507,GO:0009950,GO:0009620,GO:0004888,GO:0045944,GO:0005515,GO:0030097,GO:0045610,GO:0005769,GO:0007165	CG5490-PC				SM00255		PF01582	PS50104			G3DSA:3.80.10.10,G3DSA:3.40.50.10140	SSF52200										
aly178705.1	4-hydroxyphenylpyruvate dioxygenase	GO:0006572,GO:0006559,GO:0003868,GO:0055114,GO:0046872,GO:0009072	CG11796-PA										G3DSA:3.10.180.10	SSF54593	23~43								
aly178732.1	Cleavage and polyadenylation specificity factor subunit 1	GO:0005847,GO:0031124,GO:0006366,GO:0019899,GO:0017022,GO:0008380,GO:0005654,GO:0010467,GO:0003730,GO:0098789,GO:0006369,GO:0000398,GO:0022008,GO:0006379,GO:0035925,GO:0006378,GO:0006406,GO:0003729	CG10110-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly178960.1	Speract receptor	GO:0006468,GO:0004383,GO:0016849,GO:0005622,GO:0004672,GO:0035556,GO:0009190,GO:0016021,GO:0005524,GO:0005525	CG42637-PA						PF00211	PS50125		PS00452	G3DSA:3.30.70.1230	SSF55073									
aly17967.1	Unknown		n/a																				
aly179672.1	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase	GO:0033857,GO:0000832,GO:0000827,GO:0005829,GO:0003993,GO:0006020,GO:0052723,GO:0052724,GO:0005524	CG14616-PK																				
aly17970.1	Unknown		n/a																				
aly179819.1	Choline kinase A2	GO:0004103,GO:0006646,GO:0006657,GO:0016310,GO:0004305,GO:0046872,GO:0005524	CG2201-PB						PF01633				G3DSA:3.10.450.110,G3DSA:3.10.450.110	SSF56112,SSF56112									
aly17992.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly180098.1	Unknown		n/a																				
aly18020.1	Serine/threonine-protein kinase Genghis Khan	GO:0008154,GO:0006468,GO:0046872,GO:0030833,GO:0019992,GO:0005083,GO:0030426,GO:0008039,GO:0030424,GO:0008064,GO:0004674,GO:0031532,GO:0004672,GO:0035556,GO:0005622,GO:0005524	CG4012-PA												72~92,101~139,1~42								
aly18031.1	Unknown		n/a																				
aly18087.1	PiggyBac transposable element-derived protein 3		n/a						PF13843														
aly18087.2	Unknown		n/a																				
aly18087.3	Uncharacterized protein K02A2.6	GO:0015074,GO:0008270,GO:0003676	n/a				SM00343,SM00343						G3DSA:4.10.60.10	SSF50630									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly180894.1	Pyruvate carboxylase	GO:0046872,GO:0005811,GO:0004736,GO:0009374,GO:0003824,GO:0003677,GO:0005759,GO:0004075,GO:0006090,GO:0005875,GO:0005524,GO:0006094	CG1516-PI						PF02786				G3DSA:3.30.1490.20	SSF56059									
aly1811.1	Zinc finger protein 500	GO:0009649,GO:0042051,GO:0003700,GO:0005634,GO:0003705,GO:0035271,GO:0006355,GO:0045944,GO:0006351,GO:0043153,GO:0003677,GO:0007605,GO:0010114,GO:0046872,GO:0001752	CG7672-PC				SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF00096,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:2.170.270.10,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly1811.10	Unknown		n/a																				
aly1811.11	Lachesin	GO:0007424,GO:0016331,GO:0019991,GO:0035151,GO:0050767,GO:0009986,GO:0007606,GO:0035160,GO:0005575,GO:0042803,GO:0005918,GO:0061343,GO:0003674,GO:0043005,GO:0005886,GO:0016337,GO:0007156,GO:0043025,GO:0031225	CG32600-PA				SM00408,SM00408,SM00409,SM00409		PF07686,PF00047	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly1811.12	Unknown		n/a																				
aly1811.13	Sodium-dependent nutrient amino acid transporter 1	GO:0002009,GO:0005328,GO:0003333,GO:0016021,GO:0006814,GO:0015804,GO:0005283,GO:1903825,GO:0005887,GO:0006836,GO:0042940,GO:0042943,GO:0015175,GO:0005326	CG3897-PD						PF00209	PS50267	PR00176,PR00176,PR00176,PR00176			SSF161070									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1811.14	Unknown		n/a						PF16009		PR00334,PR00334,PR00334												
aly1811.15	Cytochrome P450 6B1	GO:0070330,GO:0043231,GO:0020037,GO:0016705,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG8687-PD						PF00067		PR00385,PR00385,PR00385,PR00385,PR00465,PR00465,PR00465,PR00465	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly1811.2	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG14205-PA				SM00703		PF01757,PF01757						142~162								
aly1811.3	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG14205-PA				SM00703		PF01757														
aly1811.4	Unknown	GO:0016747	CG16723-PB																				
aly1811.5	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG14205-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1811.6	Nose resistant to fluoxetine protein 6	GO:0006869,GO:0016021,GO:0008289,GO:0035220,GO:0022416,GO:0016747,GO:0007275	CG14204-PA						PF01757														
aly1811.7	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG14205-PA				SM00703		PF01757														
aly1811.8	Lachesin	GO:0007424,GO:0016331,GO:0019991,GO:0035151,GO:0043005,GO:0050767,GO:0009986,GO:0007606,GO:0035160,GO:0005575,GO:0042803,GO:0005918,GO:0061343,GO:0003674,GO:0005515,GO:0005886,GO:0016337,GO:0007156,GO:0043025,GO:0031225	CG32600-PA				SM00408,SM00408,SM00409,SM00409		PF07679,PF07686	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly1811.9	Unknown		n/a																				
aly1814.1	Shootin-1	GO:0005829,GO:0007409,GO:0030424	n/a										G3DSA:1.20.5.490		366~407,120~140,336~363,64~112,239~276,200~227								
aly1814.2	Aminopeptidase N	GO:0004046,GO:0004177,GO:0016021,GO:0030154,GO:0001618,GO:0046331,GO:0008270,GO:0006508,GO:0001525,GO:0008237	CG11956-PC						PF11838,PF01433,PF01433		PR00756,PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF55486,SSF63737									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1814.3	Unknown		n/a																				
aly1814.4	Unknown		n/a												25~54,80~111								
aly1816.1	Cytochrome P450 6B7	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0070330,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly1816.10	Unknown		n/a												53~73								
aly1816.11	Unknown		CG3386-PA				SM00595		PF10545	PS51029					61~81								
aly1816.12	Coiled-coil domain-containing protein 42A		CG17564-PB						PF13863						151~171,123~146,33~53								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1816.13	Odorant receptor 83a	GO:0005549,GO:0008104,GO:0007608,GO:0042048,GO:0016021,GO:0016020,GO:0030425,GO:0050911,GO:0005886,GO:0004984,GO:0032590,GO:0043025	CG10612-PA						PF02949														
aly1816.14	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	GO:0032922,GO:0030324,GO:0006470,GO:0048754,GO:0050829,GO:0016791,GO:0072357,GO:0051301,GO:0005737,GO:0070062,GO:0005730,GO:0005981,GO:0005634,GO:0000164,GO:0007049,GO:0043005,GO:0070688,GO:0032403,GO:0046872,GO:0043025,GO:0016787,GO:0045089,GO:0043021,GO:0042752,GO:0008157,GO:0042587,GO:0005886,GO:0043204,GO:0005977,GO:0043197,GO:0005979,GO:2001241,GO:0005829,GO:0004722,GO:0004721,GO:0043153	CG6593-PA				SM00156		PF16891,PF00149		PR00114,PR00114,PR00114,PR00114,PR00114,PR00114,PR00114	PS00125	G3DSA:3.60.21.10	SSF56300									
aly1816.15	Coiled-coil domain-containing protein 63		CG14905-PA												355~375,162~182,127~154								
aly1816.16	Bicaudal D-related protein homolog	GO:0005575,GO:0048812,GO:0003674	CG32137-PB												416~450,462~482,222~298,105~172,504~524								
aly1816.17	Coiled-coil domain-containing protein 63		CG14905-PA												10~30,141~161,356~376,96~123,261~281,317~344								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1816.18	Unknown	GO:0006508,GO:0005634,GO:0008233	n/a						PF03568														
aly1816.2	Cytochrome P450 6B2	GO:0070330,GO:0020037,GO:0016705,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG7249-PB						PF00067,PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086,PS00086	G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264,SSF48264			REACT_13433						
aly1816.3	Cytochrome P450 6k1	GO:0004497,GO:0020037,GO:0016705,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG7249-PB						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly1816.4	Protein unc-93 homolog A	GO:0005575,GO:0003674,GO:0016021,GO:0008150,GO:0005886	CG3078-PB										G3DSA:1.20.1250.20										
aly1816.5	Proline dehydrogenase 1, mitochondrial	GO:0007626,GO:0006562,GO:0042331,GO:0004657,GO:0005739,GO:0006537,GO:0010133,GO:0071949,GO:0005759,GO:0055114	CG1417-PD						PF01619				G3DSA:3.20.20.220,G3DSA:3.20.20.220,G3DSA:3.20.20.220	SSF51730,SSF51730,SSF51730		00330+1.5.5.2		PWY-6922,PWY-5737	UPA00261				
aly1816.6	HIRA-interacting protein 3	GO:0005654,GO:0005634,GO:0005730	n/a												49~77								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1816.7	Unknown		n/a																				
aly1816.8	Cellular tumor antigen p53	GO:0016239,GO:0006919,GO:0009314,GO:0034644,GO:0009411,GO:0000785,GO:0003677,GO:0008219,GO:0007131,GO:0007049,GO:0005737,GO:0043565,GO:0014016,GO:0010212,GO:0045787,GO:0031571,GO:0005634,GO:0010332,GO:0051262,GO:0006357,GO:0003690,GO:2000685,GO:0048477,GO:0042127,GO:0006282,GO:0005515,GO:0030330,GO:0046620,GO:0035234,GO:0008134,GO:0006915,GO:0043066,GO:0006974,GO:0035327,GO:0045893,GO:0009267,GO:0008340,GO:0007405,GO:0006978,GO:0043523,GO:0042771,GO:0044212,GO:0046872,GO:0008630,GO:0003700,GO:0005829,GO:0000122,GO:0042246,GO:0006355,GO:0010165,GO:0046533,GO:0045944,GO:0006351,GO:0005667,GO:0003682,GO:0002039,GO:0003684	CG33336-PB						PF00870		PR00386,PR00386,PR00386		G3DSA:2.60.40.720	SSF49417									
aly1816.9	Peptidyl-tRNA hydrolase 2, mitochondrial	GO:0004045,GO:2000210,GO:0005829,GO:0016020,GO:0010629,GO:0005739,GO:2000811,GO:0003674,GO:0008152	CG1307-PC					TIGR00283	PF01981				G3DSA:3.40.1490.10	SSF102462				PWY-6308					
aly18172.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly182.1	Unknown		n/a																				
aly182.2	RING finger protein nhl-1	GO:0030239,GO:0048747,GO:0006941,GO:0016567,GO:0003674,GO:0008270,GO:0004842,GO:0030018,GO:0046716	CG15105-PC				SM00184		PF01436,PF01436,PF01436,PF01436,PF01436,PF01436	PS51125,PS51125,PS51125,PS51125,PS51125,PS51125,PS51125,PS50089			G3DSA:3.30.40.10,G3DSA:2.120.10.30	SSF57850,SSF101898	125~163,179~199,201~221								
aly18209.1	Origin recognition complex subunit 4	GO:0006270,GO:0017111,GO:0000166,GO:0006260,GO:0005664,GO:0003677,GO:0005524	CG2917-PA			PIRSF007858			PF14629				G3DSA:3.40.50.300										
aly18209.2	Putative ammonium transporter 3	GO:0016021,GO:0016020,GO:0072488,GO:0008519,GO:0015696	CG6499-PB						PF00909,PF00909				G3DSA:1.10.3430.10,G3DSA:1.10.3430.10	SSF111352									
aly18212.1	GTP-binding protein 2	GO:0003924,GO:0043231,GO:0005525	CG2017-PA											SSF50465									
aly18276.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1830.1	Unknown		n/a																				
aly1830.2	MMS19 nucleotide excision repair protein homolog	GO:0005737,GO:0005819,GO:0006281,GO:0005634,GO:0097361,GO:0016226,GO:0006974,GO:0005488,GO:0006259	CG12005-PA						PF12460,PF14500				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371	514~534								
aly1830.3	DNL-type zinc finger protein	GO:0006457,GO:0051087,GO:0005739,GO:0030150,GO:0050821,GO:0008270	CG12379-PB						PF05180	PS51501													
aly1830.4	Docking protein 2	GO:0007394,GO:0000165,GO:0005158,GO:0007476,GO:0031098,GO:0007391,GO:0005622,GO:0005938,GO:0005057,GO:0007169,GO:0007265,GO:0005068,GO:0046529	CG2079-PA				SM00233,SM00310		PF02174,PF00169	PS51064,PS50003			G3DSA:2.30.29.30,G3DSA:2.30.29.30	SSF50729,SSF50729									
aly1830.5	U6 snRNA-associated Sm-like protein LSm1	GO:0044822,GO:0019827,GO:0071044,GO:0000290,GO:0033962,GO:0030532,GO:0003339,GO:0005634,GO:0000932,GO:0000398,GO:0045665,GO:0006396,GO:0008380,GO:0005681,GO:0006397	CG4279-PA				SM00651		PF01423				G3DSA:2.30.30.100	SSF50182									
aly1830.6	Rho GTPase-activating protein 19	GO:0007480,GO:0005096,GO:0005622,GO:0005575,GO:0007165,GO:0005100,GO:0007264	CG6477-PA				SM00324		PF00620	PS50238			G3DSA:1.10.555.10	SSF48350			REACT_11044						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1830.7	Unknown		n/a												12~32								
aly1830.8	Delta-1-pyrroline-5-carboxylate synthase	GO:0019240,GO:0008652,GO:0004349,GO:0006561,GO:0006592,GO:0044822,GO:0005811,GO:0005737,GO:0005739,GO:0005524,GO:0005743,GO:0034641,GO:0004350,GO:0017084,GO:0055129,GO:0006536,GO:0055114,GO:0044281	CG7470-PA																				
aly18312.1	Ubiquitin-conjugating enzyme E2Q-like protein CG4502	GO:0016881,GO:0005575,GO:0016567,GO:0003674,GO:0008150,GO:0016874,GO:0005524	CG4502-PB				SM00212		PF00179	PS50127			G3DSA:3.10.110.10	SSF54495									
aly18312.2	Transport and Golgi organization protein 6 homolog	GO:0005794,GO:0007030,GO:0009306,GO:0005829,GO:0005488,GO:0007095,GO:0016021	CG18398-PA						PF10363				G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371									
aly18312.3	Unknown	GO:0005515	CG16798-PA										G3DSA:2.60.40.10	SSF49265									
aly18312.4	Tetraspanin-7	GO:0003674,GO:0016021,GO:0008150,GO:0016032,GO:0005887	CG9033-PB			PIRSF002419			PF00335		PR00259,PR00259,PR00259			SSF48652									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly18312.5	General transcription factor IIF subunit 2	GO:0001096,GO:0060261,GO:0005674,GO:0008026,GO:0004003,GO:0005634,GO:0003677,GO:0004386,GO:0003824,GO:0045944,GO:0006367,GO:0006366,GO:0032968,GO:0005524	CG6538-PA			PIRSF015849			PF02270				G3DSA:1.10.10.10	SSF50916,SSF46785			REACT_6185,REACT_769,REACT_1788,REACT_1892,REACT_1675,REACT_71						
aly18312.6	TBC1 domain family member 25	GO:0043547,GO:0032313,GO:0031410,GO:0006914,GO:0005096,GO:0005097,GO:0005776,GO:1901096,GO:0008340,GO:0007298	CG8155-PA				SM00164		PF00566	PS50086			G3DSA:1.10.8.270	SSF47923,SSF47923,SSF47923	924~944								
aly18312.7	Growth hormone-inducible transmembrane protein	GO:0005743,GO:0016021,GO:0006915,GO:0070062	CG1287-PA						PF01027														
aly18312.8	Nucleolar complex protein 2 homolog	GO:0022008,GO:0003674,GO:0005730	CG9246-PA						PF03715				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371	512~532								
aly18312.9	Hydrocephalus inducing protein homolog	GO:0042384,GO:0021591,GO:0060438,GO:0005929,GO:0003341,GO:0002064	n/a											SSF49354									
aly1832.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1832.2	Unknown		n/a																				
aly1832.3	Unknown		n/a																				
aly1832.4	Unknown		n/a																				
aly1834.1	Putative inorganic phosphate cotransporter	GO:0015293,GO:0016021,GO:0006814,GO:0015114,GO:0005316,GO:0055085	CG15096-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1834.2	Putative inorganic phosphate cotransporter	GO:0015293,GO:0016021,GO:0006814,GO:0015114,GO:0005316,GO:0055085	CG8791-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly1834.3	Putative inorganic phosphate cotransporter	GO:0015293,GO:0016021,GO:0006814,GO:0015114,GO:0005316,GO:0055085	CG15096-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1834.4	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG42329-PA						PF01757														
aly1834.5	Unknown	GO:0016747	CG13325-PA																				
aly1834.6	Unknown		n/a																				
aly1834.7	Unknown		n/a																				
aly1834.8	Unknown		n/a																				
aly183473.1	Unknown		n/a												23~49								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly18371.1	Neither inactivation nor afterpotential protein G	GO:0005575,GO:0050660,GO:0016614,GO:0008812,GO:0050896,GO:0006810,GO:0007601,GO:0006066,GO:0046154,GO:0005576,GO:0001523,GO:0055114,GO:0016491	CG6728-PA			PIRSF000137			PF05199,PF00732			PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly18371.2	Probable ribosome biogenesis protein RLP24	GO:0003735,GO:0005730,GO:0022625,GO:0006412,GO:0042254	CG6764-PA				SM00746		PF01246			PS01073	G3DSA:2.30.170.20	SSF57716									
aly1838.1	Alcohol dehydrogenase [NADP(+)] A	GO:0004032,GO:0055114,GO:0008106	CG6084-PB			PIRSF000097			PF00248		PR00069,PR00069,PR00069,PR00069,PR00069	PS00062,PS00798,PS00063	G3DSA:3.20.20.100	SSF51430									
aly1838.10	Ribosomal L1 domain-containing protein CG13096	GO:0005575,GO:0003674,GO:0008150,GO:0003723	CG13096-PA						PF00687				G3DSA:3.30.190.20,G3DSA:3.30.190.20,G3DSA:3.40.50.790	SSF56808									
aly1838.11	Unknown		n/a							PS51257													
aly1838.12	Golgi to ER traffic protein 4 homolog	GO:0005737,GO:0006810,GO:0071816,GO:0071818,GO:0005829,GO:0051087,GO:1903071,GO:0005575,GO:0008150,GO:0051220,GO:0003674	CG9853-PC						PF04190														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.13	Nudix hydrolase 8	GO:0016787,GO:0046872,GO:0009611,GO:0051726	CG8128-PA						PF00293	PS51462	PR01356,PR01356,PR01356,PR00502,PR00502	PS00893	G3DSA:3.90.79.10	SSF55811									
aly1838.14	Nudix hydrolase 8	GO:0016787,GO:0046872,GO:0009611,GO:0051726	CG8128-PA						PF00293	PS51462	PR01356,PR01356,PR01356,PR00502,PR00502	PS00893	G3DSA:3.90.79.10	SSF55811									
aly1838.15	Unknown		n/a																				
aly1838.16	Protein dimmed	GO:0005737,GO:0003700,GO:0005634,GO:0002793,GO:0006355,GO:0045944,GO:0006351,GO:0061101,GO:0046887,GO:0046983,GO:0003677,GO:0007275	CG8667-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459									
aly1838.17	Casein kinase I isoform epsilon	GO:0032436,GO:0048148,GO:0030307,GO:0008062,GO:0042306,GO:0046777,GO:0005737,GO:0048511,GO:0005634,GO:0007555,GO:0004674,GO:0043066,GO:0004672,GO:0005524,GO:0006468,GO:0007623,GO:0007622,GO:0042067,GO:0016301,GO:0016310,GO:0042752,GO:0045475,GO:0005886,GO:0007154,GO:0001737,GO:0007446,GO:0016055,GO:0045732,GO:0051781,GO:0005515,GO:0030431	CG2048-PA				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.18	L-xylulose reductase	GO:0042732,GO:0006739,GO:0016614,GO:0070062,GO:0051289,GO:0005997,GO:0005634,GO:0016020,GO:0005902,GO:0005881,GO:0016655,GO:0050038,GO:0005903,GO:0008152,GO:0006006	CG7322-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080	PS00061	G3DSA:3.40.50.720	SSF51735									
aly1838.19	D-erythrulose reductase	GO:0042732,GO:0005737,GO:0016614,GO:0047880,GO:0050038,GO:0008152,GO:0016491	CG7322-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735									
aly1838.2	Unknown		CG17776-PA						PF14880														
aly1838.20	UPF0764 protein C16orf89 homolog	GO:0005829,GO:0016020,GO:0070062,GO:0042803	n/a						PF15882														
aly1838.21	Unknown		CG10311-PA																				
aly1838.22	Unknown		CG34307-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.23	Protein yellow	GO:0060179,GO:0016853,GO:0048067,GO:0005576,GO:0042438,GO:0007275	CG1629-PA						PF03022		PR01366,PR01366,PR01366,PR01366,PR01366,PR01366		G3DSA:2.120.10.30										
aly1838.24	Protein yellow	GO:0060179,GO:0016853,GO:0048067,GO:0005576,GO:0042438,GO:0007275	CG1629-PA						PF03022		PR01366,PR01366,PR01366,PR01366,PR01366		G3DSA:2.120.10.30	SSF63829									
aly1838.25	Unknown		n/a																				
aly1838.26	UPF0764 protein C16orf89 homolog	GO:0005829,GO:0016020,GO:0070062,GO:0042803	n/a						PF15882														
aly1838.27	ATP synthase subunit O, mitochondrial	GO:0015986,GO:0015992,GO:0046933,GO:0005811,GO:0005739,GO:0005743,GO:0005756,GO:0008553	CG4307-PA	MF_01416				TIGR01145	PF00213		PR00125,PR00125,PR00125,PR00125,PR00125		G3DSA:1.10.520.20	SSF47928									
aly1838.28	Protein yellow	GO:0060179,GO:0016853,GO:0048067,GO:0005576,GO:0042438,GO:0007275	CG9891-PA						PF03022		PR01366,PR01366,PR01366,PR01366,PR01366,PR01366		G3DSA:2.120.10.30										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.29	Protein yellow	GO:0060179,GO:0016853,GO:0048067,GO:0005576,GO:0042438,GO:0007275	CG9792-PA						PF03022		PR01366,PR01366,PR01366		G3DSA:2.120.10.30	SSF101898									
aly1838.3	Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial	GO:0003887,GO:0006450,GO:0000002,GO:0070681,GO:0030956,GO:0005739,GO:0005524,GO:0006264,GO:0050567,GO:0005760,GO:0006261,GO:0032543,GO:0007005	CG33084-PB	MF_00122					PF02686				G3DSA:3.40.50.800	SSF52954,SSF141000									
aly1838.30	Unknown		n/a						PF03022														
aly1838.31	Ubiquitin carboxyl-terminal hydrolase 43	GO:0043161,GO:0061136,GO:0004197,GO:0006511,GO:0016579,GO:0004843	CG30421-PA						PF00443	PS50235		PS00973,PS00972		SSF54001,SSF54001									
aly1838.32	ATP-binding cassette sub-family A member 3	GO:0043190,GO:0042626,GO:0006810,GO:0005615,GO:0006869,GO:0097208,GO:0005215,GO:0016021,GO:0016020,GO:0042493,GO:0097233,GO:0005886,GO:0055085,GO:0005524	CG1718-PB				SM00382,SM00382		PF12698,PF12698,PF00005,PF00005	PS50893,PS50893			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540									
aly1838.33	ATP-binding cassette sub-family A member 3	GO:0043190,GO:0042626,GO:0006810,GO:0005615,GO:0006869,GO:0097208,GO:0005215,GO:0016021,GO:0016020,GO:0042493,GO:0097233,GO:0005886,GO:0055085,GO:0005524	CG1718-PB						PF00005				G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.34	ATP-binding cassette sub-family A member 3	GO:0043190,GO:0042626,GO:0005615,GO:0006869,GO:0097208,GO:0005215,GO:0016021,GO:0006810,GO:0097233,GO:0005886,GO:0055085,GO:0005524,GO:0043231	CG1718-PB				SM00382		PF12698,PF12698,PF00005,PF00005	PS50893		PS00211	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									
aly1838.35	28S ribosomal protein S7, mitochondrial	GO:0022627,GO:0006412,GO:0003735,GO:0003723,GO:0005763,GO:0032543	CG5108-PA						PF00177			PS00052	G3DSA:1.10.455.10	SSF47973									
aly1838.36	DNA-directed RNA polymerase I subunit RPA43	GO:0005736,GO:0015630,GO:0005730,GO:0005634,GO:0006360,GO:0006351,GO:0003899	CG13773-PA						PF03876														
aly1838.37	Dual specificity mitogen-activated protein kinase kinase 4	GO:0048666,GO:0007257,GO:0006468,GO:0005829,GO:0048082,GO:0006915,GO:0000165,GO:0007254,GO:0030424,GO:0004674,GO:0046330,GO:0048812,GO:0004713,GO:0071260,GO:0004702,GO:0008545,GO:0005634,GO:0004708,GO:0005524	CG9738-PA				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly1838.38	Transmembrane protein 186	GO:0016021,GO:0005739	CG4627-PA																				
aly1838.39	Transducin beta-like protein 3	GO:0022008,GO:0032040,GO:0006364,GO:0005515,GO:0005730	CG1671-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF08625	PS50082,PS50082,PS50082,PS50082,PS50082,PS50082,PS50082,PS50294	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.4	ER lumen protein-retaining receptor	GO:0006891,GO:0006890,GO:0005783,GO:0030140,GO:0016021,GO:0005046,GO:0006621,GO:0005789,GO:0015031,GO:0046923	CG5183-PA						PF00810		PR00660,PR00660,PR00660,PR00660,PR00660,PR00660,PR00660	PS00952,PS00951											
aly1838.40	Glycine receptor subunit alphaZ1	GO:0045211,GO:0006811,GO:0022824,GO:0034707,GO:0005887,GO:0016935,GO:0016934,GO:0016021,GO:0030054,GO:0016594	CG6927-PA					TIGR00860	PF02931,PF02932		PR00252,PR00252,PR00252,PR00252,PR00253,PR00253,PR00253,PR00253	PS00236	G3DSA:2.70.170.10,G3DSA:1.20.58.390,G3DSA:1.20.58.390	SSF63712,SSF90112									
aly1838.41	Kinesin-like protein KIF19	GO:0060404,GO:0008574,GO:0008017,GO:0007018,GO:0070462,GO:0005524,GO:0008152,GO:0005929,GO:0005871,GO:0005874,GO:0005930,GO:0003777	CG9913-PB				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10	SSF52540	351~378,499~533								
aly1838.42	Mitochondrial dicarboxylate carrier	GO:0015729,GO:0015709,GO:0034641,GO:0044281,GO:0008272,GO:0006094,GO:0005743,GO:0016021,GO:0005740,GO:0005739,GO:0015141,GO:0015140,GO:0035435,GO:0000098,GO:0070221,GO:0005310,GO:0006811,GO:0000096,GO:0005315,GO:0006835,GO:0006839,GO:0055085,GO:0071422,GO:0005975,GO:0015131,GO:0015116,GO:0015117,GO:0022857,GO:0006006,GO:0005634	CG8790-PB						PF00153,PF00153,PF00153	PS50920,PS51257,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly1838.43	Diacylglycerol kinase epsilon	GO:0005737,GO:0016020,GO:0008654,GO:0019992,GO:0016310,GO:0016021,GO:0007596,GO:0007205,GO:0030168,GO:0005886,GO:0003951,GO:0035556,GO:0046872,GO:0004143,GO:0005524	CG8657-PA				SM00045,SM00046		PF00781,PF00609	PS50146,PS50081				SSF111331		00561+2.7.1.107,00564+2.7.1.107	REACT_14797,REACT_604	PWY-7039					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.44	26S proteasome non-ATPase regulatory subunit 10	GO:0032436,GO:0090263,GO:0030307,GO:0000082,GO:0034641,GO:0003674,GO:0044281,GO:0051437,GO:0051436,GO:0042981,GO:0000209,GO:0043409,GO:0005737,GO:0002474,GO:0045111,GO:0005838,GO:0007253,GO:0000122,GO:0005634,GO:0002479,GO:0005654,GO:0010467,GO:0043066,GO:0031398,GO:0070682,G	CG10011-PA				SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796	PS50088,PS50297,PS50088,PS50088,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403									
aly1838.45	Membrane-bound O-acyltransferase domain-containing protein 2	GO:0008654,GO:0016021,GO:0016020,GO:0007009,GO:0007291,GO:0071617,GO:0016746,GO:0030258,GO:0008354	CG18445-PA						PF03062														
aly1838.46	Uncharacterized protein F13E6.1		CG5174-PO						PF04201						153~180								
aly1838.47	Proteasomal ubiquitin receptor ADRM1 homolog	GO:0005737,GO:0010950,GO:0005838,GO:0043161,GO:0005634,GO:0061133,GO:0046331,GO:0043248,GO:0006511,GO:0000502,GO:0008541,GO:0043130	CG13349-PG						PF04683,PF16550														
aly1838.48	Unknown		n/a																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.49	Zinc finger protein 40	GO:0007494,GO:0008586,GO:0007611,GO:0048100,GO:0008270,GO:0003676,GO:0003677,GO:0001745,GO:0008355,GO:0000122,GO:0005634,GO:0007476,GO:0005739,GO:0005654,GO:0046872,GO:0045705,GO:0008285,GO:0048190,GO:0008283,GO:0001105,GO:0045892,GO:0001102,GO:0071837,GO:0007179,GO:0007443,GO:0007398,GO:0003700,GO:0007422,GO:0003705,GO:0007391,GO:0048813,GO:0045944,GO:0006351	CG7734-PF				SM00451,SM00451,SM00451,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly1838.5	Translation factor GUF1 homolog, mitochondrial	GO:0043022,GO:0003924,GO:0005743,GO:0005759,GO:0003746,GO:0045727,GO:0006412,GO:0005525	CG1410-PA	MF_00071				TIGR00231,TIGR01393	PF06421,PF00679,PF00009	PS51722	PR00315,PR00315,PR00315,PR00315		G3DSA:2.40.30.10,G3DSA:3.30.70.870,G3DSA:3.30.70.240,G3DSA:3.40.50.300	SSF52540,SSF54980,SSF54980,SSF50447										
aly1838.50	DNA-directed RNA polymerases I, II, and III subunit RPABC4	GO:0006356,GO:0006363,GO:0008270,GO:0003677,GO:0050434,GO:0034587,GO:0005736,GO:0005634,GO:0040029,GO:0005654,GO:0006360,GO:0010467,GO:0006362,GO:0006367,GO:0006366,GO:0006386,GO:0045814,GO:0006361,GO:0006383,GO:0008380,GO:0006283,GO:0006281,GO:0045087,GO:0006289,GO:0032481,GO:0006368,GO:0035019,GO:0006385,GO:0005829,GO:0000398,GO:0006370,GO:0005665,GO:0006351,GO:0016032,GO:0005666,GO:0003899	CG34186-PA				SM00659		PF03604				G3DSA:2.20.28.30	SSF63393										
aly1838.51	ARL14 effector protein	GO:0005575,GO:0003674,GO:0008150,GO:0005737	CG14464-PC						PF14949														

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.52	Nucleoside diphosphate kinase 7	GO:0006228,GO:0005622,GO:0006241,GO:0004550,GO:0005524,GO:0006165,GO:0046872,GO:0006183	CG8362-PA				SM00676,SM00562,SM00562		PF00334,PF00334	PS51336			G3DSA:3.30.70.141,G3DSA:3.30.70.141	SSF54919,SSF54919		00230+2.7.4.6,00240+2.7.4.6		PWY-7210,PWY-7198,PWY-7176,PWY-7220,PWY-7184,PWY-7187,PWY-7205,PWY-7224,PWY-7197,PWY-7226,PWY-					
aly1838.53	Nucleoside diphosphate kinase 7	GO:0006228,GO:0005622,GO:0006241,GO:0004550,GO:0005524,GO:0006165,GO:0046872,GO:0006183	CG8362-PA				SM00562,SM00676		PF00334	PS51336	PR01243,PR01243,PR01243		G3DSA:3.30.70.141	SSF54919		00230+2.7.4.6,00240+2.7.4.6		PWY-7210,PWY-7198,PWY-7176,PWY-7220,PWY-7184,PWY-7187,PWY-7205,PWY-7224,PWY-7197,PWY-7226,PWY-					
aly1838.54	Nucleoside diphosphate kinase 7	GO:0036064,GO:0007420,GO:0006228,GO:0005813,GO:0007368,GO:0042073,GO:0005622,GO:0060972,GO:0006241,GO:0004550,GO:0005524,GO:0006165,GO:0046872,GO:0003351,GO:0006183,GO:0060830	CG8362-PA				SM00562		PF00334				G3DSA:3.30.70.141	SSF54919		00230+2.7.4.6,00240+2.7.4.6		PWY-7210,PWY-7198,PWY-7176,PWY-7220,PWY-7184,PWY-7187,PWY-7205,PWY-7224,PWY-7197,PWY-7226,PWY-					
aly1838.55	Major facilitator superfamily domain-containing protein 6-B	GO:0016021,GO:0055085	CG31663-PA						PF12832,PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1838.56	Unknown		n/a																				
aly1838.57	Unknown		CG6785-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.58	Enteropeptidase	GO:0004252,GO:0005044,GO:0016021,GO:0016020,GO:0005903,GO:0005515,GO:0006508	CG2105-PB				SM00192,SM00192,SM00192,SM00020		PF00057,PF00057,PF00089	PS50068,PS50068,PS50240,PS50068	PR00261,PR00261,PR00261	PS01209,PS00135,PS01209,PS01209,PS00134	G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.40.10.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.40.10.10	SSF57424,SSF50494,SSF57424,SSF57424										
aly1838.59	Adenylyl cyclase-associated protein 1	GO:0008103,GO:0042052,GO:0007596,GO:0046716,GO:0007163,GO:0007165,GO:0007411,GO:0001667,GO:0005925,GO:0005737,GO:0000902,GO:0002576,GO:0008407,GO:0003779,GO:0048477,GO:0048749,GO:0048190,GO:0072499,GO:0008154,GO:0008360,GO:0030036,GO:0005886,GO:0008179,GO:0030168,GO:0070062,GO:0007015,GO:0006898,GO:0030864,GO:0007190	CG33979-PB				SM00673,SM00673		PF08603,PF01213	PS51329,PS51082		PS01088,PS01089	G3DSA:2.160.20.70	SSF101278,SSF69340	138~158,275~295		REACT_18266						
aly1838.6	WD repeat domain phosphoinositide-interacting protein 3	GO:0005737,GO:0000045,GO:0032266,GO:0005515,GO:0080025	CG11975-PA				SM00320,SM00320			PS50294			G3DSA:2.130.10.10	SSF50978									
aly1838.60	Nicotinate phosphoribosyltransferase	GO:0004514,GO:0004516,GO:0005829,GO:0009435,GO:0019358,GO:0016874,GO:0006979	CG3714-PC			PIRSF000484		TIGR01513	PF04095				G3DSA:3.20.140.10,G3DSA:3.20.140.10	SSF54675,SSF51690,SSF51690		00760+6.3.4.21	REACT_11193	PWY-5381	UPA00253				
aly1838.61	FAST kinase domain-containing protein 3	GO:0044822,GO:0045333,GO:0005739,GO:0004672	n/a				SM00952		PF06743,PF08373	PS51286													

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.62	Solute carrier family 12 member 6	GO:0007638,GO:0010107,GO:0001525,GO:0016021,GO:0071477,GO:0071476,GO:0009612,GO:0015377,GO:0015379,GO:0006813,GO:0006811,GO:0006810,GO:0016323,GO:0019901,GO:0005887,GO:0005886,GO:0055085,GO:0003333,GO:0035826,GO:0035827,GO:0015079,GO:0015171	CG5594-PG					TIGR00930	PF03522,PF03522,PF03522,PF00324,PF00324		PR01081,PR01081,PR01081,PR01081						REACT_15518						
aly1838.63	Trypsin, alkaline B	GO:0004252,GO:0005576,GO:0005615,GO:0006508	CG18681-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1838.64	Trypsin CFT-1	GO:0004252,GO:0005615,GO:0006508	CG9564-PC				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1838.65	Trypsin CFT-1	GO:0004252,GO:0004175,GO:0005615,GO:0006508	CG31954-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1838.66	Trypsin CFT-1	GO:0004252,GO:0005615,GO:0006508	CG16998-PA				SM00020		PF00089				G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.67	Trypsin CFT-1	GO:0004252,GO:0004175,GO:0005615,GO:0006508	CG31954-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1838.68	ABC transporter ced 7	GO:0043190,GO:0042626,GO:0043652,GO:0005215,GO:0016021,GO:0006810,GO:0012501,GO:0005886,GO:0055085,GO:0005524	CG6052-PA																				
aly1838.69	Unknown	GO:0032934,GO:0015918	CG12813-PA						PF02221				G3DSA:2.60.40.770	SSF81296									
aly1838.7	Protein SDA1 homolog	GO:0042273,GO:0005730,GO:0000055,GO:0042254,GO:0030036,GO:0015031,GO:0022008	CG8070-PA						PF05285,PF08158					SSF48371,SSF48371	489~509,257~277								
aly1838.70	TPPP family protein CG45057	GO:0005575,GO:0048812,GO:0003674	CG45057-PE						PF05517					SSF47473									
aly1838.8	Intraflagellar transport protein 140 homolog	GO:0006996,GO:0036064,GO:0030991,GO:0042384,GO:0035058,GO:0007605,GO:0005813,GO:0048705,GO:0061512,GO:0032391,GO:0001750,GO:0031513,GO:0097542,GO:0035845,GO:0003674,GO:0060041,GO:0035721,GO:0072372,GO:1902017,GO:0072001,GO:0005930	CG11838-PB										G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF48452,SSF48452,SSF50978,SSF50978,SSF50978,SSF50978	1229~1256								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1838.9	Nibrin	GO:0000723,GO:0000781,GO:0051321,GO:0008630,GO:0045003,GO:0006281,GO:0016233,GO:0006974,GO:0030870,GO:0005515,GO:0007095,GO:0007093,GO:0042770,GO:0051276	CG6754-PE				SM00240		PF16508,PF00498	PS50006			G3DSA:2.60.200.20,G3DSA:3.40.50.10190	SSF52113,SSF49879										
aly183843.1	Pogo transposable element with KRAB domain	GO:0006355,GO:0005634,GO:0007275,GO:0003676,GO:0003677	n/a						PF03184,PF03221,PF05225	PS51253			G3DSA:3.30.40.10	SSF57903,SSF46689										
aly1841.1	Synaptotagmin like protein 4	GO:0008021,GO:0016331,GO:0005543,GO:0045921,GO:0019898,GO:0010004,GO:0046676,GO:0048489,GO:0007436,GO:0005654,GO:0030667,GO:0005813,GO:0006886,GO:0016020,GO:0005544,GO:0070382,GO:0005509,GO:0071985,GO:0005737,GO:0042043,GO:0016324,GO:0005215,GO:0017178,GO:0030658,GO:0030276,GO:0005886,GO:0007015,GO:0045793,GO:0042249,GO:0050714,GO:0040018,GO:0048791,GO:0005515,GO:0016079,GO:0019905,GO:0005768,GO:0043297,GO:0008270	CG44012-PI				SM00239,SM00239		PF00168,PF00168	PS50004,PS50004	PR00399,PR00399,PR00399,PR00399		G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562										
aly1841.2	Unknown	GO:0046658,GO:0035152,GO:0019991,GO:0005576	CG14430-PA											SSF57302									
aly1841.3	Coronin-2B	GO:0005737,GO:0003779,GO:0072686,GO:0015629,GO:0016020,GO:0030036,GO:0050832,GO:0051015,GO:0005515,GO:0007527	CG9446-PE				SM00320,SM00320,SM00320		PF00400,PF00400,PF16300,PF08953	PS50294,PS50082,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978	557~591									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1841.4	Probable phosphoserine aminotransferase	GO:0004648,GO:0008615,GO:0006564,GO:0030170	CG11899-PA	MF_00160		PIRSF000525			PF00266			PS00595	G3DSA:3.40.640.10,G3DSA:3.40.640.10,G3DSA:3.90.1150.10	SSF53383		00750+2.6.1.52,00260+2.6.1.52,00680+2.6.1.52			UPA00135,UPA00244				
aly1841.5	Fibropellin-1	GO:0035152,GO:0005615,GO:0016324,GO:0030246,GO:0046716,GO:0045746,GO:0016023,GO:0005509,GO:0007155,GO:0005112,GO:0032579	CG9138-PD				SM00042,SM00042,SM00042,SM00231,SM00231,SM00192,SM00034,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179		PF00059,PF00008,PF00008,PF00008,PF00008,PF00008,PF00008,PF00008,PF00008,PF07699,PF07699,PF07699,PF07699,PF07699,PF07699,PF07699,PF00754,PF00754,PF13385,PF12661,PF12661,PF00084,PF00084,PF00084,PF00084,PF02494,PF02494,PF02494,PF07645,PF07645,PF00057,PF00431,PF00431,PF00431	PS50026,PS50026,PS50026,PS50923,PS50022,PS50026,PS50825,PS50026,PS01180,PS50923,PS50026,PS01180,PS50923,PS50026,PS50068,PS50923,PS50923,PS50026,PS01180,PS50026,PS50041,PS50026,PS50026,PS50825,PS50923,PS50026,PS50026,PS50923,PS50825,PS50923,PS50022,PS50026,PS50026,PS50026,PS50026	PS00010,PS00022,PS00022,PS01285,PS01186,PS01186,PS01186,PS01186,PS01186,PS01186,PS01187,PS00022,PS00022,PS01186,PS00010,PS00022,PS00022,PS01186,PS00022,PS00022,PS00022,PS01186,PS00022,PS00022,PS01187,PS00010,PS01186,PS01186,PS00010,PS00010,PS01187,PS00022,PS00010,PS00010,PS00010,PS00022,PS00010,PS01186,PS00010,PS01187,PS00010,PS00022,PS01209,PS00022,PS01187,PS00022,PS00010,PS01187,PS01186	G3DSA:2.10.70.10,G3DSA:2.10.50.10,G3DSA:3.10.100.10,G3DSA:2.60.120.290,G3DSA:2.10.70.10,G3DSA:2.60.120.260,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.290,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:2.60.120.290,G3DSA:2.10.70.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.60.120.260,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57196,SSF57196,SSF57184,SSF57184,SSF49899,SSF56436,SSF57196,SSF57196,SSF57184,SSF57535,SSF57196,SSF57535,SSF57535,SSF57535,SSF49854,SSF57196,SSF49854,SSF49785,SSF57196,SSF57424,SSF57535,SSF57535,SSF57196,SSF49854,SSF49785,SSF57196,SSF57184								
aly1841.6	Cytochrome b5-related protein	GO:0006633,GO:0006629,GO:0020037,GO:0016717,GO:0005811,GO:0005739,GO:0046331,GO:0005506,GO:0046872,GO:0016021,GO:0055114,GO:0016491	CG17928-PA						PF00173,PF00487	PS50255		PS00191	G3DSA:3.10.120.10	SSF55856									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly18452.1	Unknown		n/a																				
aly1846.1	tRNA-specific adenosine deaminase 1	GO:0008033,GO:0004000,GO:0008251,GO:0005575,GO:0003723,GO:0006400,GO:0046872,GO:0006396	CG16889-PA				SM00552		PF02137	PS50141													
aly1846.2	Major facilitator superfamily domain-containing protein 9	GO:0005215,GO:0016021,GO:0048477,GO:0055085,GO:0051119	CG5760-PA						PF07690	PS50850	PR01035,PR01035,PR01035		G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly1846.3	Unknown		n/a																				
aly18462.1	Tetratricopeptide repeat protein 7B	GO:0022008	CG8325-PA																				
aly1847.1	Alpha-2-macroglobulin	GO:0048863,GO:0070062,GO:0072562,GO:0004866,GO:0004867,GO:0001869	n/a						PF01835														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1847.10	Apolipoprotein D	GO:0022626,GO:0005783,GO:0042246,GO:0048678,GO:0030425,GO:0000302,GO:0003674,GO:0051895,GO:0010642,GO:0005615,GO:0014012,GO:0007476,GO:2000405,GO:0048471,GO:0043025,GO:0048662,GO:0006629,GO:0005215,GO:2000098,GO:0042308,GO:0060588,GO:0007420,GO:1900016,GO:0007568,GO:0015485,GO:0042493,GO:0005575,GO:0071638,GO:0006006	CG4139-PA										G3DSA:2.40.128.20	SSF50814									
aly1847.11	Cuticlin-1	GO:0000902,GO:0005214,GO:0016021,GO:0007476,GO:0005886,GO:0060102,GO:0042302	CG9355-PA				SM00241		PF00100	PS51034													
aly1847.12	Cuticlin-1	GO:0007015,GO:0000902,GO:0016324,GO:0016021,GO:0007476,GO:0007160,GO:0005214,GO:0009913,GO:0035017,GO:0003383,GO:0016476,GO:0060102,GO:0042302	CG9369-PA				SM00241		PF00100	PS51034													
aly1847.2	Glutathione S-transferase	GO:0005737,GO:0004364,GO:0006979,GO:0004602,GO:0006749	CG8938-PD						PF02798,PF00043	PS50405,PS50404			G3DSA:3.40.30.10,G3DSA:1.20.1050.10	SSF52833,SSF47616									
aly1847.3	Unknown		n/a						PF00630	PS50194			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF81296,SSF81296	930~957								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1847.4	Vacuolar protein sorting associated protein 72 homolog	GO:0043234,GO:0043486,GO:0005634,GO:0004402,GO:0006355,GO:0010629,GO:0035267,GO:0016573,GO:0003677,GO:0035019,GO:0016568,GO:0006351	CG4621-PA				SM00993		PF08265,PF05764														
aly1847.5	Peripheral plasma membrane protein CASK	GO:0007616,GO:0008582,GO:0007615,GO:0031594,GO:0007163,GO:0007298,GO:0008049,GO:0007274,GO:0048488,GO:0072375,GO:1900244,GO:0004674,GO:0005524,GO:0006468,GO:0042043,GO:2000331,GO:0016081,GO:0016080,GO:0061174,GO:0007628,GO:0008360,GO:0007269,GO:0005886,GO:0007155,GO:0008344,GO:0005954,GO:0040011,GO:0040012,GO:0004683,GO:1900073,GO:0046928,GO:0005515,GO:0046331	CG6703-PH						PF00625			G3DSA:3.40.50.300	SSF52540										
aly1847.6	Peripheral plasma membrane protein CASK	GO:0007616,GO:0008582,GO:0007615,GO:0031594,GO:0007163,GO:0007298,GO:0008049,GO:0007274,GO:0048488,GO:0072375,GO:1900244,GO:0004674,GO:0005524,GO:0006468,GO:0042043,GO:2000331,GO:0016081,GO:0016080,GO:0061174,GO:0007628,GO:0008360,GO:0007269,GO:0005886,GO:0007155,GO:0008344,GO:0005954,GO:0040011,GO:0040012,GO:0004683,GO:1900073,GO:0046928,GO:0005515,GO:0046331	CG6703-PH				SM00072,SM00326,SM00228		PF07653,PF00595,PF00625	PS50106,PS50052,PS50002		PS00856	G3DSA:2.30.30.40,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.30.63.10,G3DSA:2.30.42.10	SSF50044,SSF52540,SSF50156		00230+2.7.4.8		PWY-7221					
aly1847.7	Peripheral plasma membrane protein CASK	GO:0007616,GO:0008582,GO:0007615,GO:0031594,GO:0007163,GO:0007298,GO:0008049,GO:0007274,GO:0048488,GO:0072375,GO:1900244,GO:0004674,GO:0004672,GO:0005524,GO:0006468,GO:0042043,GO:2000331,GO:0016081,GO:0016080,GO:0061174,GO:0007628,GO:0008360,GO:0007269,GO:0005886,GO:0007155,GO:0008344,GO:0005954,GO:0040011,GO:0040012,GO:0004683,GO:1900073,GO:0046928,GO:0005515,GO:0046331	CG6703-PH						PF00069	PS50011			G3DSA:1.10.287.650,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF56112	396~401									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1847.8	Anosmin-1	GO:0009897,GO:0005515,GO:0009986,GO:0005576,GO:0030414,GO:0004867,GO:0007155,GO:0005578	CG6173-PA				SM00060,SM00060,SM00217		PF00095,PF00041	PS50853,PS50853,PS50853,PS51390			G3DSA:2.60.40.10,G3DSA:4.10.75.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF49265,SSF57256										
aly1847.9	Unknown		n/a																				
aly18484.1	Conserved oligomeric Golgi complex subunit 7	GO:0005794,GO:0007030,GO:0007112,GO:0017119,GO:0036063,GO:0005730,GO:0034067,GO:0006886,GO:0000916,GO:0000139,GO:0050821,GO:0006890,GO:0006486,GO:0033365,GO:0043231	CG31040-PA						PF10191						104~124,76~96								
aly18484.2	Unknown	GO:0046872	n/a				SM00355,SM00355,SM00355,SM00355			PS50157		PS00028,PS00028,PS00028,PS00028											
aly18484.3	Unknown		n/a										G3DSA:2.120.10.30	SSF63825									
aly1849.1	Protein lifeguard 4	GO:0005795,GO:0016021,GO:0006915,GO:0000139,GO:0043066,GO:0017146,GO:0050848,GO:0004972	CG3798-PD						PF01027														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1849.10	Unknown		CG31068-PC																				
aly1849.11	Probable phospholipid-transporting ATPase IIB	GO:0000287,GO:0006897,GO:0006812,GO:0016021,GO:0004012,GO:0019829,GO:0006890,GO:0045332,GO:0005886,GO:0015662,GO:0005768,GO:0015914,GO:0005524,GO:0005802	CG31729-PB					TIGR01494,TIGR01652	PF00122,PF16209,PF16212,PF13246		PR00119,PR00119	PS00154	G3DSA:3.40.50.1000,G3DSA:2.70.150.10,G3DSA:2.70.150.10,G3DSA:3.40.1110.10,G3DSA:3.40.1110.10	SSF56784,SSF56784,SSF81660,SSF81660,SSF81660,SSF81665,SSF81665,SSF81665,SSF81653,SSF81653									
aly1849.12	FERM, RhoGEF and pleckstrin domain-containing protein 1	GO:0005089,GO:0035023,GO:0030425,GO:0019898,GO:0030175,GO:0045202,GO:0003677,GO:0007416,GO:0005737,GO:0043547,GO:0016601,GO:0048365,GO:0003779,GO:0030054,GO:0005856,GO:0031234,GO:0030676,GO:0043197,GO:0008092,GO:0005829,GO:0005575,GO:0048813	CG44193-PG				SM00295		PF09379,PF00373,PF09380,PF08736	PS50057	PR00935,PR00935,PR00935,PR00935,PR00661,PR00661,PR00661	PS00660	G3DSA:1.20.80.10,G3DSA:2.30.29.30,G3DSA:3.10.20.90	SSF54236,SSF47031,SSF50729									
aly1849.13	FERM, RhoGEF and pleckstrin domain-containing protein 2	GO:0030676,GO:0005089,GO:0071800,GO:0030316,GO:0043547,GO:0016601,GO:0031532,GO:0005829,GO:0005856,GO:0033623,GO:0016322,GO:0005737,GO:0007155,GO:0007411,GO:0019898,GO:0071526	CG34383-PI				SM00233		PF00169	PS50003			G3DSA:2.30.29.30	SSF50729									
aly1849.14	Adenylate cyclase type 8	GO:0007616,GO:0007268,GO:0004016,GO:0007165,GO:0034199,GO:0035556,GO:0008543,GO:0071377,GO:0010353,GO:0016021,GO:0016020,GO:0007189,GO:0006112,GO:0009190,GO:0044281,GO:0005524,GO:0045087,GO:0031000,GO:0006833,GO:0007173,GO:0005886,GO:0048011,GO:0007611,GO:0055085,GO:0009744,GO:0046872,GO:0007202,GO:0005622,GO:0003091,GO:0007193,GO:0001582,GO:0008294	CG10564-PE				SM00044,SM00044		PF06327,PF00211,PF00211,PF16214	PS50125,PS50125		PS00452,PS00452	G3DSA:3.30.70.1230,G3DSA:3.30.70.1230	SSF55073,SSF55073		00230+4.6.1.1	REACT_14797,REACT_15295,REACT_11061,REACT_1505						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1849.15	Unknown		n/a																				
aly1849.16	Anoctamin-1	GO:0035774,GO:0009897,GO:0050965,GO:0042391,GO:0060438,GO:0034605,GO:0005227,GO:0034707,GO:0006821,GO:0005737,GO:0070062,GO:1902476,GO:0005254,GO:0005229,GO:0016324,GO:0006812,GO:0042803,GO:0005886,GO:1903959,GO:0098655,GO:0007200,GO:0005247,GO:0046982	CG16718-PD						PF04547,PF16178														
aly1849.17	Unknown		n/a																				
aly1849.18	Dolichyl-diphosphoolig osaccharide--protein glycosyltransfe rase subunit STT3A	GO:0016020,GO:0006486,GO:0016021,GO:0043686,GO:0035220,GO:0008250,GO:0022416,GO:0004576,GO:0004579,GO:0018279	CG1518-PA						PF02516										UPA00378				
aly1849.19	Unknown		n/a												20~54								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1849.2	Unknown	GO:0005634,GO:0008270	n/a				SM00868		PF07776					SSF57716									
aly1849.20	Unknown	GO:0008270,GO:0003676	n/a				SM00343,SM00343			PS50158			G3DSA:4.10.60.10	SSF57756									
aly1849.21	Unknown	GO:0005089,GO:0005737,GO:0016601,GO:0008092,GO:0003779,GO:0019898,GO:0005575,GO:0005856,GO:0003677,GO:0035023	CG44193-PG												1447~1474,2514~2534									
aly1849.3	Zinc finger protein 217	GO:0000122,GO:0032504,GO:0008595,GO:0003700,GO:0001078,GO:0005634,GO:0005705,GO:0000118,GO:0006355,GO:0044212,GO:0001077,GO:0045944,GO:0006351,GO:0005654,GO:0003677,GO:0045892,GO:0000978,GO:0046872,GO:0048477	CG17958-PA				SM00868,SM00355,SM00355,SM00355		PF07776	PS50157		PS00028,PS00028,PS00028	G3DSA:3.10.370.10,G3DSA:3.10.370.10	SSF57667,SSF57716										
aly1849.4	Unknown	GO:0003676	n/a				SM00692,SM00980		PF05485	PS50950				SSF57716									
aly1849.5	Periodic tryptophan protein 1 homolog	GO:0005794,GO:0005730,GO:0005634,GO:0030707,GO:0008584,GO:0007281,GO:0031490,GO:0035327,GO:0005515,GO:0036099,GO:0030723,GO:0036098,GO:0010468	CG6751-PA				SM00320,SM00320		PF00400	PS50294,PS50082		PS00678,PS00678	G3DSA:2.130.10.10	SSF50978										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1849.6	Aspartate aminotransferase, cytoplasmic	GO:0008652,GO:0005975,GO:0047801,GO:0006114,GO:0005777,GO:0005829,GO:0006520,GO:0007476,GO:0006536,GO:0080130,GO:0004069,GO:0009058,GO:0006537,GO:0030170,GO:0006103,GO:0005759,GO:0006094,GO:0044281,GO:0006531	CG8430-PB						PF00155		PR00799,PR00799,PR00799,PR00799	PS00105	G3DSA:3.40.640.10	SSF53383		00360+2.6.1.1,00350+2.6.1.1,00400+2.6.1.1,00250+2.6.1.1,00401+2.6.1.1,00950+2.6.1.1,00960+2.6.1.1,00	REACT_13	PWY-5913,PWY-6318,PWY-7383,PWY-6643,PWY-6642,PWY-6638,PWY-7117,PWY-7115					
aly1849.7	Unknown		CG9034-PA																				
aly1849.8	Unknown		CG9034-PA																				
aly1849.9	Replication factor C subunit 1	GO:0006281,GO:0005634,GO:0048813,GO:0003689,GO:0006355,GO:0005663,GO:0046331,GO:0006260,GO:0006351,GO:0003677,GO:0022008,GO:0005875,GO:0005524	CG1119-PB			PIRSF036578	SM00292,SM00382		PF00004,PF00533,PF08519	PS50172			G3DSA:3.40.50.10190,G3DSA:1.20.272.10,G3DSA:3.40.50.300,G3DSA:1.10.8.60	SSF52540,SSF52113,SSF48019	191~211,739~759,1133~1153		REACT_152,REACT_216,REACT_22172,REACT_383,REACT_1538						
aly185.1	Storkhead-box protein 1	GO:0033138,GO:1901858,GO:0010800,GO:0010629,GO:0010628,GO:0003674,GO:0008045,GO:0007067,GO:0061418,GO:0051301,GO:0005737,GO:1904031,GO:0005730,GO:0005813,GO:0005634,GO:0005654,GO:0010468,GO:0006351,GO:0008284,GO:0010971,GO:1902882,GO:0051881,GO:0071500,GO:0005575,GO:0000977,GO:0010821	CG10573-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly185.2	DnaJ homolog subfamily C member 14	GO:0016021,GO:0005789,GO:0050780,GO:0001664,GO:0015031,GO:0009408	CG14650-PA				SM00271		PF14901,PF00226	PS50076	PR00625,PR00625,PR00625		G3DSA:1.10.287.110	SSF46565									
aly185.3	Pre-rRNA-processing protein TSR1 homolog	GO:0022008,GO:0005634,GO:0042255,GO:0042254,GO:0005730	CG7338-PA				SM00785		PF08142,PF04950	PS51714													
aly185.4	Protein transport protein Sec61 subunit alpha isoform 2	GO:0008565,GO:0010507,GO:0005784,GO:0042335,GO:0005791,GO:0008258,GO:0005789,GO:0016021,GO:0007391,GO:0006616,GO:0015031,GO:0048812,GO:0043022,GO:0010942,GO:0098586,GO:0008219,GO:0045169,GO:0034761,GO:0046598	CG9539-PA			PIRSF004557		TIGR00967	PF00344,PF10559			PS00755,PS00756	G3DSA:1.10.3370.10	SSF103491			REACT_15380						
aly185.5	Midnolin-B	GO:0009987,GO:0046331,GO:0005515,GO:0005730	CG32676-PA				SM00213		PF00240	PS50053			G3DSA:3.10.20.90	SSF54236	525~545,231~251								
aly185.6	ATP-binding cassette sub-family D member 3	GO:0006633,GO:0005782,GO:0006635,GO:0016887,GO:0042760,GO:0014070,GO:0042626,GO:0005778,GO:0016021,GO:0016020,GO:0005777,GO:0005524,GO:0042803,GO:0005215,GO:0006810,GO:0005779,GO:0055085,GO:0043190,GO:0007031,GO:0043231,GO:0005829,GO:0042493,GO:0005743	CG12703-PA				SM00382		PF06472,PF00005	PS50929,PS50893		PS00211	G3DSA:3.40.50.300	SSF52540,SSF90123									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly185.7	Heat shock protein 68	GO:0005811,GO:0006457,GO:0031427,GO:0005739,GO:0051082,GO:0042594,GO:0009408,GO:0008340,GO:0022008,GO:0005875,GO:0005524	CG5436-PA						PF00012		PR00301,PR00301		G3DSA:1.20.1270.10,G3DSA:2.60.34.10	SSF100920,SSF100934	153~177								
aly1850.1	Lipase 1	GO:0004806,GO:0006629,GO:0007586,GO:0016788,GO:0016042,GO:0048812,GO:0005576	CG31871-PA			PIRSF000862			PF00561				G3DSA:3.40.50.1820	SSF53474									
aly18514.1	Periodic tryptophan protein 1 homolog	GO:0005794,GO:0005730,GO:0005634,GO:0030707,GO:0008584,GO:0007281,GO:0031490,GO:0035327,GO:0006351,GO:0005515,GO:0036099,GO:0030723,GO:0036098,GO:0010468	CG6751-PA				SM00320			PS50082,PS50294		PS00678	G3DSA:2.130.10.10	SSF50978									
aly18519.1	Ran GTPase-activating protein 1	GO:0044614,GO:0006611,GO:0048678,GO:0030425,GO:0007165,GO:0005737,GO:0072686,GO:0043547,GO:0045132,GO:0000922,GO:0048471,GO:0000777,GO:0005098,GO:0000278,GO:0031965,GO:0005096,GO:0006913,GO:0032853,GO:0022008,GO:0007264,GO:0071375,GO:0005643,GO:0005829,GO:0046826	CG9999-PA										G3DSA:3.80.10.10	SSF52047									
aly18560.1	Pupal cuticle protein Edg-84A	GO:0040003,GO:0005214,GO:0008011,GO:0008010,GO:0031012,GO:0042302	CG1330-PA						PF00379	PS51155	PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1857.1	Ommochrome-binding protein		n/a										G3DSA:2.120.10.30,G3DSA:2.120.10.30	SSF63829,SSF63829									
aly1857.10	Nicotinamide/nicotinic acid mononucleotide adenylyltransferase 1	GO:0097062,GO:0000309,GO:0004515,GO:0005634,GO:0009435,GO:0045494,GO:0005524	CG13645-PA					TIGR00482	PF01467				G3DSA:3.40.50.620	SSF52374,SSF52374		00760+2.7.7.18	REACT_11193	PWY-5381,PWY-5653	UPA00253				
aly1857.11	Methionine--tRNA ligase, mitochondrial	GO:0005759,GO:0004825,GO:0006431,GO:0005739,GO:0005524	CG31322-PA						PF08264,PF09334,PF09334		PR01041,PR01041,PR01041		G3DSA:3.40.50.620,G3DSA:3.40.50.620,G3DSA:1.10.730.10	SSF47323,SSF52374		00450+6.1.1.10,00970+6.1.1.10	REACT_71						
aly1857.12	G protein-coupled receptor kinase 2	GO:0008589,GO:0038032,GO:0003384,GO:0009790,GO:0008277,GO:0007296,GO:0007165,GO:0005737,GO:0007474,GO:0004674,GO:0007186,GO:0005524,GO:0006468,GO:0002805,GO:0043950,GO:0045879,GO:0048601,GO:0050830,GO:0008592,GO:0005886,GO:0007224,GO:0004703	CG17998-PA				SM00315,SM00133		PF00069,PF00615	PS50011,PS50132,PS51285	PR00717,PR00717,PR00717,PR00717,PR00717	PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF48097,SSF48097									
aly1857.2	Ommochrome-binding protein		n/a										G3DSA:2.120.10.30	SSF63829									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1857.3	Unknown		n/a																				
aly1857.4	Putative tyramine receptor 2	GO:0004935,GO:0032795,GO:0008227,GO:0005887,GO:0005886,GO:0004989,GO:0007186,GO:0016021	CG18208-PB						PF00001	PS50262	PR00237,PR00237,PR00237		G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly1857.5	26S protease regulatory subunit 10B	GO:0004175,GO:0036402,GO:0022624,GO:0017025,GO:0090261,GO:0016234,GO:0031595,GO:0031597,GO:0005875,GO:0008540,GO:0005737,GO:0005838,GO:0070062,GO:0043161,GO:0005634,GO:0016020,GO:1901800,GO:0006508,GO:0005524,GO:0017111,GO:0001163,GO:0030163,GO:0030433,GO:0000502,GO:0022008,GO:0045899,GO:1901838	CG3455-PB				SM00382	TIGR01242	PF00004			PS00674	G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540	19~60		REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045							
aly1857.6	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	GO:0005737,GO:0005654,GO:0000185,GO:0001701,GO:0030324,GO:0043406,GO:0019209,GO:0003007,GO:0003824,GO:0043234,GO:0007179	n/a				SM00332		PF00481	PS51746			G3DSA:3.60.40.10	SSF81606,SSF81606									
aly1857.7	Transcription factor BTF3 homolog 4	GO:0007317,GO:0005854,GO:0070201,GO:0060811,GO:0005875	CG3644-PA						PF01849	PS51151													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1857.8	Homeotic protein empty spiracles	GO:0007424,GO:0001700,GO:0007420,GO:0006355,GO:0003700,GO:0035284,GO:0005634,GO:0007383,GO:0014019,GO:0001158,GO:0035288,GO:0007419,GO:0048813,GO:0007389,GO:0007409,GO:0003677,GO:0042305,GO:0035277,GO:0010468,GO:0000980	CG2988-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024,PR00031,PR00031	PS00027	G3DSA:1.10.10.60	SSF46689	251~271								
aly1857.9	Beta-1,4-galactosyltransferase 7	GO:0005794,GO:0006487,GO:0006491,GO:0030206,GO:0048147,GO:0016021,GO:0043206,GO:0030145,GO:0031012,GO:0030166,GO:0015012,GO:0046525,GO:0006029,GO:0008378,GO:0003831,GO:0032580,GO:0046872,GO:0006024	CG11780-PA						PF02709,PF13733	PS51257	PR02050,PR02050,PR02050,PR02050		G3DSA:3.90.550.10	SSF53448					UPA00378				
aly1859.1	Unknown		n/a												420~455								
aly1859.2	Unknown		n/a												86~120,136~156,28~69,173~221,237~271,364~384,274~297,319~349								
aly1859.3	39S ribosomal protein L43, mitochondrial	GO:0003735,GO:0005743,GO:0006412,GO:0005762,GO:0005840	CG5479-PA				SM00916		PF05047				G3DSA:3.40.30.10	SSF52833									
aly1859.4	Zinc finger and BTB domain-containing protein 40	GO:0005634,GO:0006974,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0030282,GO:0006351	CG4707-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12874	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028		SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1859.5	Mannosyl-oligosaccharide glucosidase GCS1	GO:0005783,GO:0010053,GO:0009913,GO:0016021,GO:0009311,GO:0005789,GO:0004573,GO:0004558	CG1597-PC						PF16923,PF03200					SSF48208,SSF48208		00510+3.2.1.106							
aly1859.6	Unknown		n/a																				
aly1863.1	Calcyphosin-like protein	GO:0005737,GO:0022008,GO:0005509	CG10126-PB				SM00054,SM00054,SM00054		PF13202,PF13499	PS50222,PS50222,PS51257,PS50222		PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									
aly1863.10	Lysine-specific demethylase 8	GO:0003682,GO:0000086,GO:0005634,GO:0070544,GO:0051864,GO:0045893,GO:0046872,GO:0006351	CG13902-PB				SM00558		PF13621	PS51184			G3DSA:2.60.120.650	SSF51197									
aly1863.11	Folliculin-interacting protein 1	GO:0005737,GO:0033138,GO:0043547,GO:0000122,GO:0031929,GO:0005085,GO:0001934,GO:0043154,GO:0009267,GO:0032007,GO:0001932,GO:0002904,GO:0002327,GO:2000973	CG3764-PB						PF14636,PF14636,PF14637,PF14638,PF14638														
aly1863.12	Unknown	GO:0016505	CG30116-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1863.13	Uncharacterized WD repeat-containing protein alr3466	GO:0016505,GO:0005515	CG30116-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400	PS50294,PS50082,PS50082,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50998,SSF50978									
aly1863.14	Unknown		n/a												1259~1279								
aly1863.15	Ribosome biogenesis protein TSR3 homolog	GO:0030490	CG4338-PA	MF_01116					PF04034,PF04068														
aly1863.16	Chaoptin (Fragment)	GO:0007155,GO:0050896,GO:0007601,GO:0005886	CG7896-PA				SM00364,SM00364,SM00364,SM00364,SM00364,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13306	PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047,SSF52058,SSF52058	437~457								
aly1863.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1863.3	Unknown		n/a																				
aly1863.4	27 kDa hemolymph protein	GO:0005576	CG9917-PA						PF07165														
aly1863.5	Protein FAM13A		CG6424-PA												190~210								
aly1863.6	Unknown		n/a																				
aly1863.7	G protein pathway suppressor 2	GO:0007254,GO:0017053,GO:0000122,GO:0006325,GO:0003714,GO:0034260,GO:0000188,GO:0005654,GO:0046329,GO:0005095,GO:0007049	CG17002-PB						PF15991						28~115								
aly1863.8	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase	GO:0016779,GO:0000103,GO:0007476,GO:0004020,GO:0004781,GO:0005524	CG8363-PD	MF_00065				TIGR00339,TIGR00455	PF01747,PF14306,PF01583				G3DSA:3.40.50.300,G3DSA:3.40.50.620,G3DSA:3.10.400.10	SSF52374,SSF52540,SSF88697		00230+2.7.7.4,00920+2.7.7.4,00261+2.7.7.4,00920+2.7.1.25,00450+2.7.7.4,00230+2.7.1.25	REACT_13433	PWY-6932,PWY-6683,PWY-5278,PWY-5340	UPA00140				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1863.9	Isovaleryl-CoA dehydrogenase, mitochondrial	GO:0050660,GO:0033539,GO:0051260,GO:0006552,GO:0006551,GO:0005759,GO:0003995,GO:0031966,GO:0055114,GO:0008470	CG6638-PA						PF02770,PF00441,PF02771			PS00072,PS00073	G3DSA:2.40.110.10,G3DSA:1.20.140.10,G3DSA:1.10.540.10	SSF56645,SSF47203										
aly1867.1	Unknown	GO:0042048	CG14509-PC																				
aly18673.1	Unknown		n/a																				
aly1869.1	Unknown		n/a																				
aly1869.2	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase	GO:0030210,GO:0005200,GO:0005783,GO:0008587,GO:0008146,GO:0007166,GO:0007509,GO:0005874,GO:0048488,GO:0007367,GO:0008543,GO:0016021,GO:0007474,GO:0005525,GO:0048312,GO:0016787,GO:0090097,GO:0003924,GO:0006024,GO:0007283,GO:0007507,GO:0006184,GO:0000137,GO:0051258,GO:0007427,GO:0007017,GO:0016055,GO:0007428,GO:0005622,GO:0015012,GO:0006790,GO:0015016,GO:0015014,GO:0045570,GO:0060828,GO:0000139	CG8339-PA						PF00685				G3DSA:3.40.50.300	SSF52540										
aly18698.1	Chloride channel protein 2	GO:0015629,GO:0030554,GO:0016020,GO:0034707,GO:0006821,GO:0005247,GO:0005254,GO:0055085	CG31116-PD						PF00654				G3DSA:1.10.3080.10	SSF81340										
aly18698.2	Chloride channel protein 2	GO:0015629,GO:0030554,GO:0005216,GO:0016020,GO:0034707,GO:0006821,GO:0005247,GO:0005254,GO:0055085	CG31116-PD										G3DSA:1.10.3080.10	SSF54631										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1872.1	Unknown	GO:0005634,GO:0001736,GO:0045879,GO:0035317	CG14821-PE						PF15389														
aly1872.2	Fizzy-related protein homolog	GO:0090344,GO:0010001,GO:0030424,GO:0090302,GO:0007067,GO:0001745,GO:0051301,GO:0005737,GO:0005819,GO:0031572,GO:0016567,GO:0005813,GO:0031536,GO:0005814,GO:0005654,GO:0007088,GO:0008284,GO:0051488,GO:0006281,GO:0031965,GO:0070306,GO:0031145,GO:0008054,GO:0040020,GO:0008347,GO:0010458,GO:0045732,GO:0007455,GO:0005680,GO:0030163	CG3000-PB				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50294,PS50082		PS00678,PS00678	G3DSA:2.130.10.10	SSF50978										
aly1872.3	RNA-binding protein 45	GO:0005737,GO:0007399,GO:0005634,GO:0030154,GO:0000166,GO:0005654,GO:0003723,GO:0003676,GO:0044822,GO:0003729	CG1316-PA				SM00360,SM00360,SM00360,SM00360,SM00360		PF13893,PF00076,PF00076	PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928,SSF54928,SSF54928										
aly1872.4	Histone-lysine N-methyltransferase SMYD3	GO:0005737,GO:0018024,GO:0006325,GO:0005654,GO:0005575,GO:0046872,GO:0006413,GO:0003743	CG13761-PB						PF01753	PS50865		PS01360	G3DSA:2.170.270.10	SSF82199,SSF82199,SSF144232									
aly1872.5	Uncharacterized protein C1orf131 homolog	GO:0044822	CG1738-PA						PF15375						97~117								
aly1872.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1872.7	Unknown		n/a												46~66,124~144								
aly1872.8	Unknown		n/a																				
aly1873.1	FMRFamide receptor	GO:0007218,GO:0004985,GO:0007186,GO:0016021,GO:0004930,GO:0007204,GO:0005829,GO:0002209,GO:0005887,GO:0008188,GO:0001653,GO:0008345,GO:0008344	CG2114-PA						PF10324	PS50262	PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly1873.2	Kallikrein 1-related peptidase b24	GO:0004252,GO:0005634,GO:0006909,GO:0070062,GO:0006508	CG9737-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly1873.3	Putative uncharacterized transposon-derived protein F52C9.6		n/a																				
aly1873.4	Unknown		n/a																				
aly1877.1	Dopamine D2-like receptor	GO:0004930,GO:0007212,GO:0007195,GO:0016021,GO:0007606,GO:0001591,GO:0007194,GO:0004952,GO:0005887,GO:0007268,GO:0007186,GO:0008227	CG33517-PH						PF00001	PS50262	PR00242,PR00242,PR00242,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1877.10	Hepatic leukemia factor	GO:0043565,GO:0048511,GO:0003700,GO:0005634,GO:0006366,GO:0006355,GO:0006351,GO:0003677,GO:0035914,GO:0003690,GO:0007275,GO:0042803	CG7786-PA						PF07716			PS00036	G3DSA:1.20.5.170	SSF57959									
aly1877.11	Protein Smaug	GO:0005737,GO:0000289,GO:0043488,GO:0003723,GO:0030371,GO:0000900,GO:0000932,GO:0017022,GO:0003730,GO:0017148,GO:0051236,GO:0007275,GO:0003729	CG5263-PD				SM00454		PF00536				G3DSA:1.10.150.50,G3DSA:1.25.40.170	SSF47769									
aly1877.12	Zinc finger protein 782	GO:0051726,GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG11247-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776,PF12874,PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57716,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly1877.13	Zinc finger protein 23	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776,PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57716,SSF57667,SSF57667,SSF57667,SSF57667									
aly1877.14	Unknown		CG2556-PA						PF15304						266~289								
aly1877.15	Unknown		n/a																				
aly1877.16	Unknown		n/a																				
aly1877.17	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1877.18	Myb-like protein H	GO:0006355,GO:0005634,GO:0003682,GO:0006351,GO:0003677	n/a																				
aly1877.19	Unknown		n/a																				
aly1877.2	Probable aldehyde oxidase 2	GO:0004031,GO:0050660,GO:0016614,GO:0051537,GO:0009851,GO:0009688,GO:0004854,GO:0005506,GO:0055114,GO:0009055	CG6045-PA				SM01092,SM01008		PF03450,PF01315,PF00941,PF01799,PF02738,PF02738,PF00111	PS51387,PS51085		PS00197	G3DSA:3.30.390.50,G3DSA:3.30.365.10,G3DSA:3.90.1170.50,G3DSA:3.10.20.30,G3DSA:1.10.150.120,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.465.10,G3DSA:3.30.365.10	SSF55447,SSF54665,SSF47741,SSF56176,SSF54292,SSF56003										
aly1877.20	Unknown		n/a																				
aly1877.21	Mitosis initiation protein fs(1)Ya	GO:0005737,GO:0007344,GO:0005652,GO:0006997,GO:0005635,GO:0000280,GO:0006333,GO:0030261,GO:0006260,GO:0005515,GO:0007067,GO:0005654,GO:0051301	CG2707-PA																				
aly1877.3	Indole-3-acetaldehyde oxidase	GO:0004031,GO:0050660,GO:0016614,GO:0008762,GO:0051536,GO:0051537,GO:0050302,GO:0009851,GO:0009688,GO:0004855,GO:0043546,GO:0005506,GO:0005829,GO:0055114,GO:0009055	CG18519-PC				SM01008		PF01315,PF00111,PF03450,PF02738,PF02738,PF01799,PF00941	PS51085,PS51387		PS00197	G3DSA:3.30.465.10,G3DSA:3.30.365.10,G3DSA:3.10.20.30,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.390.50,G3DSA:3.30.365.10,G3DSA:3.90.1170.50,G3DSA:1.10.150.120	SSF47741,SSF55447,SSF56003,SSF56176,SSF54665,SSF54292	869~889									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1877.4	Xanthine dehydrogenase	GO:0050660,GO:0016614,GO:0008762,GO:0005829,GO:0051537,GO:0005777,GO:0016903,GO:0009115,GO:0004855,GO:0004854,GO:0005506,GO:0009055,GO:0043546,GO:0055114,GO:0016491	CG6045-PA				SM01008,SM01092		PF02738,PF02738,PF01799,PF00111,PF03450,PF00941,PF01315	PS51387,PS51085		PS00197	G3DSA:3.30.365.10,G3DSA:3.10.20.30,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.465.10,G3DSA:3.30.365.10,G3DSA:1.10.150.120,G3DSA:3.90.1170.50,G3DSA:3.30.390.50	SSF54292,SSF47741,SSF54665,SSF56003,SSF55447,SSF56176										
aly1877.5	Unknown		n/a																				
aly1877.6	Unknown		n/a																				
aly1877.7	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0005534,GO:0030246	CG16834-PB				SM00034		PF00059	PS50041		PS00615	G3DSA:3.10.100.10	SSF56436									
aly1877.8	40S ribosomal protein S12, mitochondrial	GO:0008049,GO:0007619,GO:0007638,GO:0009612,GO:0032543,GO:0003735,GO:0007605,GO:0005763,GO:0001666,GO:0006412	CG7925-PB					TIGR00981	PF00164		PR01034,PR01034,PR01034,PR01034,PR01034	PS00055	G3DSA:2.40.50.140	SSF50249									
aly1877.9	Hepatic leukemia factor	GO:0006909,GO:0035289,GO:0003677,GO:0007411,GO:0044324,GO:0007275,GO:0007362,GO:0043565,GO:0000122,GO:0007381,GO:0005634,GO:0048511,GO:0006366,GO:0035914,GO:0003690,GO:0010468,GO:0042803,GO:0035271,GO:0008361,GO:0007354,GO:0046982,GO:0040015,GO:0003700,GO:0007431,GO:0003705,GO:0000977,GO:0008293,GO:0000980	CG7952-PB						PF07716	PS50217		PS00036	G3DSA:1.20.5.170	SSF57959									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly188.1	Beta-1,4-N-acetylgalactosaminyltransferase bre-4	GO:0075015,GO:0005794,GO:0005975,GO:0033207,GO:0006486,GO:0009636,GO:0006044,GO:0016021,GO:0009247,GO:0033842,GO:0007528,GO:0045747,GO:0007291,GO:0008376,GO:0046872,GO:0008344	CG8536-PA						PF02709,PF13733		PR02050,PR02050,PR02050,PR02050		G3DSA:3.90.550.10	SSF53448					UPA00378				
aly188.10	Glutathione S-transferase C-terminal domain-containing protein homolog	GO:0005575,GO:0003674,GO:0008150	CG10428-PA						PF13679				G3DSA:3.40.50.150,G3DSA:1.20.1050.10	SSF47616,SSF53335									
aly188.11	1,4-alpha-glucan-branching enzyme	GO:0043169,GO:0005975,GO:0070062,GO:0005977,GO:0005978,GO:0005829,GO:0004553,GO:0044281,GO:0003844,GO:0008340,GO:0006091,GO:0006006	CG33138-PA			PIRSF000463	SM00642		PF02922,PF02806,PF00128				G3DSA:2.60.40.1180,G3DSA:2.60.40.10,G3DSA:3.20.20.80	SSF51011,SSF51445,SSF81296		00500+2.4.1.18	REACT_474	PWY-622,PWY-5067	UPA00164				
aly188.12	39S ribosomal protein L41, mitochondrial	GO:0003735,GO:0006412,GO:0005762,GO:0030529	CG12954-PA						PF09809														
aly188.13	NAD kinase	GO:0019674,GO:0005829,GO:0006741,GO:0008152,GO:0003951,GO:0046872,GO:0005524	CG33156-PE	MF_00361					PF01513				G3DSA:2.60.200.30,G3DSA:3.40.50.10330	SSF111331		00760+2.7.1.23		PWY-5083,PWY-7268,PWY-7269					
aly188.14	6-phosphofructo-2-kinase/fructose 2,6-bisphosphatase	GO:0005975,GO:0016311,GO:0005829,GO:0007476,GO:0044281,GO:0046835,GO:0004331,GO:0003873,GO:0006094,GO:0006000,GO:0006096,GO:0005524,GO:0006003	CG3400-PG				SM00855		PF01591,PF00300		PR00991,PR00991,PR00991,PR00991,PR00991,PR00991		G3DSA:3.40.50.1240,G3DSA:3.40.50.300	SSF52540,SSF53254	270~290	00051+2.7.1.105+3.1.3.46	REACT_474						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly188.15	PI-PLC X domain-containing protein 3	GO:0006650,GO:0008081,GO:0016042,GO:0047396,GO:0004871,GO:0006629	CG10747-PA				SM00148			PS50007			G3DSA:3.20.20.190	SSF51695										
aly188.16	Glyceraldehyde-3-phosphate dehydrogenase	GO:0005737,GO:0004365,GO:0031430,GO:0051287,GO:0005811,GO:0016620,GO:0030018,GO:0006006,GO:0006096,GO:0055114,GO:0050661	CG12055-PA				SM00846		PF02800,PF00044		PR00078,PR00078,PR00078,PR00078,PR00078		G3DSA:3.30.360.10,G3DSA:3.40.50.720	SSF51735,SSF55347			REACT_474						
aly188.17	Glyceraldehyde-3-phosphate dehydrogenase 2	GO:0005737,GO:0004365,GO:0051287,GO:0005811,GO:0016620,GO:0006096,GO:0006006,GO:0005875,GO:0055114,GO:0050661	CG8893-PA			PIRSF000149	SM00846	TIGR01534	PF00044,PF02800		PR00078,PR00078,PR00078,PR00078,PR00078	PS00071	G3DSA:3.40.50.720,G3DSA:3.30.360.10	SSF51735,SSF55347		00010+1.2.1.12,00710+1.2.1.12	REACT_474	PWY-1042,PWY-5484,PWY-7003,PWY-6901	UPA00109				
aly188.18	RalBP1-associated Eps domain-containing protein 2	GO:0005737,GO:0006898,GO:0006461,GO:0007173,GO:0005509,GO:0005515	CG6192-PA				SM00027		PF12763	PS50031,PS50222			G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473,SSF47473	681~708								
aly188.19	Frizzled-4	GO:0061304,GO:0061301,GO:0034446,GO:0001944,GO:0009790,GO:0007163,GO:0007165,GO:0043507,GO:0042701,GO:0005737,GO:0004930,GO:0070062,GO:0016021,GO:0008406,GO:0007186,GO:0010812,GO:0031987,GO:0007605,GO:0009986,GO:0035426,GO:0060070,GO:0030165,GO:0005911,GO:0005886,GO:0042995,GO:0035567,GO:0007223,GO:0001570,GO:0051091,GO:0007420,GO:0030947,GO:0016055,GO:0042813,GO:0004888,GO:0006357,GO:0005515,GO:0017147	CG4626-PB				SM00063		PF01392,PF01534	PS50261,PS50038	PR00489,PR00489,PR00489,PR00489,PR00489,PR00489,PR00489		G3DSA:1.10.2000.10	SSF63501			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly188.2	Vacuolar protein sorting associated protein 11 homolog	GO:0006904,GO:0030139,GO:0003674,GO:0008270,GO:0007040,GO:1901998,GO:0007032,GO:0006886,GO:0005770,GO:0000166,GO:1902115,GO:0031902,GO:1903364,GO:0030897,GO:0035542,GO:1903955,GO:0019905,GO:0005884,GO:0034058,GO:0016197,GO:0030674,GO:0016192,GO:0031647,GO:2000643,GO:0005764,GO:0005765,GO:0033263,GO:0015031,GO:0005768,GO:0005769,GO:0019904	CG32350-PA						PF12451,PF00637	PS50236,PS50089,PS50236			G3DSA:3.30.40.10,G3DSA:2.130.10.10	SSF57850,SSF50978	769~789								
aly188.20	Transcription factor A, mitochondrial	GO:0001077,GO:0042645,GO:0007005,GO:0005813,GO:0005634,GO:0005739,GO:0006264,GO:0010467,GO:0006261,GO:0006366,GO:0005759,GO:0070363,GO:0005694,GO:0033108,GO:0044822,GO:0008301,GO:0045893,GO:0006979,GO:0006996,GO:0006338,GO:0003700,GO:0005829,GO:0006355,GO:0006356,GO:0045944,GO:0006390,GO:0006391,GO:0000978,GO:0003682	CG4217-PB				SM00398,SM00398		PF00505,PF09011	PS50118,PS50118			G3DSA:1.10.30.10,G3DSA:1.10.30.10	SSF47095,SSF47095	123~143								
aly188.21	Transcription factor A, mitochondrial	GO:0001077,GO:0042645,GO:0007005,GO:0005813,GO:0005634,GO:0005739,GO:0006264,GO:0010467,GO:0006261,GO:0006366,GO:0005759,GO:0070363,GO:0005694,GO:0033108,GO:0044822,GO:0008301,GO:0045893,GO:0006979,GO:0006996,GO:0006338,GO:0003700,GO:0005829,GO:0006355,GO:0006356,GO:0045944,GO:0006390,GO:0006391,GO:0000978,GO:0003682	CG4217-PB				SM00398,SM00398		PF00505,PF09011	PS50118,PS50118			G3DSA:1.10.30.10,G3DSA:1.10.30.10	SSF47095,SSF47095	124~144,199~223								
aly188.22	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly188.23	Probable histone-binding protein Caf1	GO:0048666,GO:0042393,GO:0046976,GO:0031491,GO:0042054,GO:0046974,GO:0005700,GO:0031497,GO:0007307,GO:0051567,GO:0016590,GO:0070822,GO:0007346,GO:0042766,GO:0000122,GO:0006342,GO:0005634,GO:0000281,GO:0016571,GO:0016573,GO:0033186,GO:0042826,GO:0042803,GO:0008284,GO:0005667,GO:0006281,GO:0007517,GO:0035035,GO:0016584,GO:0035098,GO:0070734,GO:0016581,GO:0007379,GO:0048813,GO:0006334,GO:0006335,GO:0016589,GO:0035097,GO:0061085,GO:0048812,GO:0006351,G	CG4236-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF12265,PF00400,PF00400,PF00400	PS50294,PS50082,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678	G3DSA:2.130.10.10	SSF50978										
aly188.24	Homogentisate 1,2-dioxygenase	GO:0006570,GO:0006572,GO:0006559,GO:0004411,GO:0046872,GO:0055114	CG4779-PA					TIGR01015	PF04209				G3DSA:2.60.120.10,G3DSA:2.60.120.10	SSF51182		00350+1.13.11.5,00643+1.13.11.5			UPA00139				
aly188.25	Pleckstrin homology domain-containing family M member 2	GO:0005737,GO:0007030,GO:0019894,GO:0032880	CG17360-PA				SM00233			PS50003			G3DSA:2.30.29.30	SSF50729									
aly188.26	Nuclear pore membrane glycoprotein 210-like	GO:0060009,GO:0016021,GO:0007286	n/a												1354~1354								
aly188.27	Unknown	GO:0016021	n/a						PF06140														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly188.28	Protein OSCP1	GO:1903955,GO:0042384,GO:0006810,GO:0009925	CG13178-PA						PF10188														
aly188.29	SET and MYND domain-containing protein 4	GO:0005737,GO:0005634,GO:0010629,GO:0008168,GO:0046872,GO:0042826	CG8378-PA						PF00856	PS50280,PS50865			G3DSA:2.170.270.10,G3DSA:2.170.270.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF82199,SSF82199,SSF144232,SSF48452									
aly188.3	Kinesin-like protein unc-104	GO:0005737,GO:0007528,GO:0040012,GO:0016192,GO:0016188,GO:0005874,GO:0008017,GO:0047496,GO:0008088,GO:0005524,GO:0051963,GO:0045886,GO:0048489,GO:0048490,GO:0005871,GO:0007411,GO:0046847,GO:0008345,GO:0005875,GO:0003777,GO:0048814	CG8566-PD				SM00129,SM00240,SM00233		PF12473,PF16183,PF16183,PF00169,PF12423,PF00498,PF00225	PS50003,PS50067	PR00380,PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10,G3DSA:2.60.200.20,G3DSA:2.30.29.30	SSF50729,SSF52540,SSF49879	430~450,636~685,816~836,376~400								
aly188.30	Protein 5NUC	GO:0016787,GO:0000166,GO:0008253,GO:0008768,GO:0009166,GO:0046872	CG30104-PB						PF02872,PF02872		PR01607,PR01607,PR01607,PR01607,PR01607		G3DSA:3.60.21.10,G3DSA:3.60.21.10,G3DSA:3.90.780.10,G3DSA:3.90.780.10	SSF55816,SSF56300,SSF55816,SSF56300	127~147								
aly188.31	Protein 5NUC	GO:0016787,GO:0000166,GO:0008253,GO:0008768,GO:0009166,GO:0046872	CG30104-PB						PF02872,PF02872,PF00149		PR01607,PR01607,PR01607,PR01607,PR01607,PR01607		G3DSA:3.60.21.10,G3DSA:3.60.21.10,G3DSA:3.90.780.10,G3DSA:3.90.780.10	SSF55816,SSF56300,SSF55816	199~219								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly188.32	Putative uncharacterized transposon-derived protein F52C9.6		n/a																				
aly188.33	Unknown		n/a																				
aly188.4	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0005737,GO:0030728,GO:0007567,GO:0006909,GO:0003824,GO:0004745,GO:0097070,GO:0004022,GO:0007565,GO:0016404,GO:0006693,GO:0007179,GO:0070403,GO:0051287,GO:0004957,GO:0045786,GO:0042572,GO:0042574,GO:0070493,GO:0055114	CG4899-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080	PS00061	G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735,SSF51735									
aly188.5	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0005737,GO:0030728,GO:0070062,GO:0055114,GO:0004022,GO:0016323,GO:0003824,GO:0045786,GO:0007179,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly188.6	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0060206,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0016491,GO:0005737,GO:0030728,GO:0007179,GO:0004022,GO:0003824,GO:0008152,GO:0045786,GO:0055114,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735									
aly188.7	Superoxide dismutase [Mn], mitochondrial	GO:0035206,GO:0019222,GO:0016209,GO:0038001,GO:1903146,GO:0072593,GO:0003007,GO:0019430,GO:0006801,GO:0008340,GO:0005759,GO:0004784,GO:0046872,GO:0055114	CG8905-PA			PIRSF000349			PF00081,PF02777		PR01703,PR01703,PR01703,PR01703,PR01703	PS00088	G3DSA:1.10.287.990	SSF54719,SSF46609	51~71			PWY-6854					
aly188.8	Solute carrier family 25 member 36	GO:0032355,GO:0000002,GO:0015218,GO:0016021,GO:0022857,GO:0005739,GO:0031966,GO:0005743,GO:0005740,GO:0006839,GO:0006864,GO:0007005,GO:0051881	CG18317-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920	PR00784,PR00784,PR00784		G3DSA:1.50.40.10,G3DSA:1.50.40.10	SSF103506,SSF103506									
aly188.9	Tail-anchored protein insertion receptor WRB	GO:0007507,GO:0016021,GO:0071816,GO:0060041,GO:0005789	n/a						PF04420						60~87								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1881.1	Squamous cell carcinoma antigen recognized by T-cells 3	GO:0042393,GO:0000244,GO:0071002,GO:0071001,GO:0003676,GO:0016607,GO:0007417,GO:0005737,GO:0000387,GO:0000902,GO:0030621,GO:0005634,GO:1990381,GO:0030624,GO:0000166,GO:0005654,GO:1903586,GO:0005691,GO:0010468,GO:0017070,GO:0046540,GO:0044822,GO:0048872,GO:0071425,GO:0006334,GO:0000398,GO:0005622,GO:0003723,GO:0015030,GO:0006396,GO:0003729	CG3312-PB						PF00076				G3DSA:3.30.70.330	SSF54928									
aly18826.1	CTL-like protein 2	GO:0005575,GO:0003674,GO:0016021,GO:0008150	CG11880-PA						PF04515								REACT_20679,REACT_15518						
aly18826.10	Protein-serine O-palmitoleoyltransferase porcupine	GO:0006497,GO:0032281,GO:0005783,GO:0009306,GO:0016055,GO:0005789,GO:1990698,GO:0030111,GO:0030176,GO:0016746,GO:0005886,GO:0017147,GO:0045234,GO:0009100	CG6205-PA						PF03062														
aly18826.11	ATP-dependent helicase brm	GO:0035060,GO:0043974,GO:0006909,GO:0008587,GO:0008586,GO:0016887,GO:0003677,GO:0035329,GO:0007517,GO:2000134,GO:0005634,GO:0043044,GO:0003713,GO:0007474,GO:0045742,GO:2000648,GO:0048477,GO:0005524,GO:0048666,GO:0045088,GO:0007480,GO:0035172,GO:0048096,GO:0004386,GO:0045893,GO:0007409,GO:0007406,GO:0022008,GO:0036335,GO:0008094,GO:0070983,GO:0048813,GO:0006357,GO:0006351,GO:0005515	CG5942-PE				SM00592,SM00297,SM00490,SM00573,SM00951,SM00487		PF08880,PF00271,PF07529,PF00439,PF00176,PF14619,PF07533	PS50014,PS51192,PS51666,PS51194,PS51204	PR00503,PR00503,PR00503	PS00633	G3DSA:1.20.920.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF47370,SSF52540,SSF160481	624~660,574~594,688~719,1480~1507								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly18826.12	Zinc finger protein 418	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00692,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00980,SM00868,SM00868		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50950,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57716,SSF57667,SSF57667,SSF57716										
aly18826.13	60S ribosomal protein L5	GO:0008097,GO:0005840,GO:0022625,GO:0005622,GO:0003735,GO:0005515,GO:0006412	CG17489-PA	MF_01337_A					PF00861,PF14204		PR00058,PR00058,PR00058,PR00058,PR00058,PR00058		G3DSA:3.30.420.100	SSF53137,SSF53137									
aly18826.14	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	GO:0006654,GO:0006644,GO:0005783,GO:0008654,GO:0016021,GO:0016020,GO:0001961,GO:0016024,GO:0003841,GO:0019432,GO:0006112,GO:0044281,GO:0046474,GO:0000502,GO:0044255,GO:0005789,GO:0031325,GO:0001819	CG3812-PA				SM00563	TIGR00530	PF01553				G3DSA:3.40.1130.10	SSF69593		00564+2.3.1.51,00561+2.3.1.51	REACT_22258	PWY-7589,PWY-5667,PWY-5981,PWY-7417,PWY-7411,PWY-7587,PWY-6453	UPA00557				
aly18826.15	Protein-associating with the carboxyl-terminal domain of ezrin	GO:0005737,GO:0005794,GO:0030027,GO:0016772,GO:0005488,GO:0004672,GO:0005524	CG1344-PA										G3DSA:1.10.510.10,G3DSA:1.25.10.10,G3DSA:3.20.170.10	SSF48371,SSF56112									
aly18826.16	NADH dehydrogenase [ubiqui] 1 beta subcomplex subunit 8, mitochondrial	GO:0008137,GO:0016021,GO:0005739,GO:0006120,GO:0005747,GO:0003954	CG3192-PA						PF05821														
aly18826.17	Mediator of RNA polymerase II transcription subunit 22	GO:0005634,GO:0001104,GO:0006357,GO:0016592,GO:0007067	CG3034-PA						PF06179						21~48								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly18826.18	Argininosuccinate synthase	GO:0004055,GO:0000050,GO:0000053,GO:0006526,GO:0005524	CG1315-PA	MF_00005				TIGR00032	PF00764			PS00564,PS00565	G3DSA:1.20.5.470,G3DSA:3.40.50.620,G3DSA:3.90.1260.10	SSF69864,SSF52402		00250+6.3.4.5,00330+6.3.4.5		PWY-4984,PWY-5154,PWY-5,PWY-7400,PWY-4983	UPA00068				
aly18826.19	Protein ROP	GO:0005737,GO:0016020,GO:0043195,GO:0007269,GO:0006904,GO:0005829,GO:0016082,GO:0000281,GO:0019898,GO:0007317,GO:0032940,GO:0009416,GO:0006887,GO:0012506,GO:0007268,GO:0015031,GO:0019905,GO:0016192,GO:0000149,GO:0048489	CG15811-PB			PIRSF005715			PF00995				G3DSA:3.90.830.10,G3DSA:3.40.50.2060,G3DSA:3.40.50.1910,G3DSA:3.40.50.1910,G3DSA:1.25.40.60	SSF56815										
aly18826.2	Exosome complex component RRP4	GO:0005737,GO:0034475,GO:0000178,GO:0071051,GO:0071035,GO:0071034,GO:0030037,GO:0005634,GO:0071038,GO:0000176,GO:0000177,GO:0000175,GO:0034427,GO:0003723,GO:0005652,GO:0000467,GO:0005730,GO:0071049,GO:0043928,GO:0010468,GO:0006397	CG3931-PB						PF15985					SSF50249,SSF54791									
aly18826.20	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly18826.3	Mediator of RNA polymerase II transcription subunit 18	GO:0005634,GO:0001104,GO:0006357,GO:0006351,GO:0006366,GO:0016592	CG14802-PA						PF09637														
aly18826.4	HORMA domain-containing protein 1	GO:0005737,GO:0060629,GO:0007126,GO:0042138,GO:0048477,GO:0005634,GO:0001824,GO:0007129,GO:0007283,GO:0051177,GO:0000794,GO:0000795,GO:0051598,GO:0007130,GO:0005694	n/a						PF02301	PS50815			G3DSA:3.30.900.10	SSF56019									
aly18826.5	Unknown		n/a																				
aly18826.6	Ribosomal RNA small subunit methyltransferase NEP1	GO:0032040,GO:0031167,GO:0042274,GO:0005730,GO:0019843,GO:0070037,GO:0042742,GO:0009267,GO:0070475,GO:0008168,GO:0022008,GO:0006364	CG3527-PA						PF03587					SSF75217									
aly18826.7	Autophagy protein 5	GO:0005737,GO:0034045,GO:0006995,GO:0000422,GO:0035071,GO:0006914,GO:0016236,GO:0005776,GO:0000045,GO:0006501,GO:0048102,GO:0044804,GO:0003674,GO:0015031,GO:1902350,GO:0035096,GO:0034274	CG1643-PA						PF04106														
aly18826.8	Torsin-like protein	GO:0040011,GO:0006457,GO:0071426,GO:0048085,GO:0051085,GO:0005635,GO:0005788,GO:0005524,GO:0051082,GO:0016887,GO:0042053,GO:0043104	CG3024-PA				SM00382		PF06309		PR00300,PR00300,PR00300		G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly18826.9	Unknown		n/a																				
aly188320.1	Unknown	GO:0032432,GO:0003779,GO:0016327,GO:0008091,GO:0008092,GO:0016324,GO:0008017,GO:0005543,GO:0030707,GO:0042060,GO:0000281,GO:0010797,GO:0045186,GO:0005912,GO:0005515,GO:0007009,GO:0006897,GO:0032509	CG12008-PE						PF00435				G3DSA:1.20.58.60	SSF46966									
aly1884.1	NADH dehydrogenase [ubiqui] iron-sulfur protein 8, mitochondrial	GO:0051539,GO:0032981,GO:0008137,GO:0005739,GO:0006120,GO:0005747,GO:0006979,GO:0046872,GO:0003954	CG3944-PA	MF_01351				TIGR01971	PF12838	PS51379,PS51379		PS00198,PS00198	G3DSA:1.10.1060.10	SSF54862									
aly1884.2	Unknown		n/a																				
aly1884.3	Unknown		n/a																				
aly18849.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly18850.1	Guanine nucleotide-binding protein-like 1	GO:0005829,GO:0003924,GO:0042254,GO:0006974,GO:0008152,GO:0005634,GO:0005525	CG9320-PA										G3DSA:3.40.50.300	SSF52540									
aly18882.1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1	GO:0000187,GO:0005737,GO:0004435,GO:0045859,GO:0004871,GO:0007264,GO:0007200,GO:0005829,GO:0032835,GO:0005085,GO:0019899,GO:0000139,GO:0008277,GO:0004629,GO:0046578,GO:0005886,GO:0016042	n/a																				
aly18882.2	Cleavage stimulation factor subunit 1	GO:0005737,GO:0044822,GO:0005848,GO:0005654,GO:0005515,GO:0006379,GO:0006397	CG2261-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400	PS50082,PS50082,PS50294,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978									
aly18882.3	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1	GO:0000187,GO:0006651,GO:0005085,GO:0019899,GO:0008277,GO:0007165,GO:0004871,GO:0035556,GO:0005737,GO:0016042,GO:0005509,GO:0006661,GO:0007186,GO:0006629,GO:0046578,GO:0045859,GO:0007629,GO:0017016,GO:0005886,GO:0007265,GO:0004435,GO:0007200,GO:0005829,GO:0000139,GO:0004629	CG4574-PD				SM00149,SM00314,SM00314,SM00148,SM00239		PF00387,PF00788,PF00788,PF00388,PF00168	PS50004,PS50008,PS50200,PS50007,PS50200	PR00390,PR00390,PR00390,PR00390		G3DSA:3.20.20.190,G3DSA:3.20.20.190,G3DSA:3.20.20.190,G3DSA:3.20.20.190,G3DSA:2.60.40.150	SSF49562,SSF54236,SSF51695,SSF51695,SSF51695,SSF54236		00562+3.1.4.11		PWY-6367,PWY-6351,PWY-7039					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly18915.1	Ras-related protein Rab-32	GO:0008152,GO:0055037,GO:0007611,GO:0036461,GO:0007165,GO:0090382,GO:0008355,GO:0030742,GO:0031982,GO:0006886,GO:0016020,GO:0005776,GO:0005739,GO:0035646,GO:0010506,GO:0005525,GO:0006856,GO:0019882,GO:0035651,GO:0003924,GO:0006913,GO:0006727,GO:0048072,GO:0032482,GO:0045335,GO:0008057,GO:0042470,GO:0016192,GO:0030670,GO:0005802,GO:0005764,GO:0010883,GO:0005515,GO:0035650,GO:0015031,GO:1903232,GO:0005769,GO:0045202	CG8024-PB				SM00176,SM00175,SM00174,SM00173	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly18915.2	Mitochondrial folate transporter/carrier	GO:0015884,GO:0016021,GO:0008517,GO:0022857,GO:0005743,GO:0005740,GO:0006839,GO:0055085	CG8026-PD						PF00153,PF00153	PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly1896.1	Unknown		n/a						PF04500														
aly1896.10	Unknown		n/a						PF04500														
aly1896.11	Unknown		n/a						PF04500														
aly1896.12	Unknown		n/a						PF04500														
aly1896.2	Unknown		n/a						PF04500														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1896.3	Unknown		n/a						PF04500														
aly1896.4	Unknown		n/a						PF04500,PF04500														
aly1896.5	Unknown		n/a						PF04500														
aly1896.6	Unknown		n/a																				
aly1896.7	Unknown		n/a						PF04500														
aly1896.8	Unknown		n/a						PF04500														
aly1896.9	Unknown		n/a						PF04500														
aly189642.1	Unknown		n/a																				
aly1898.1	Stress-associated endoplasmic reticulum protein 2	GO:0005783,GO:0016021,GO:0006464,GO:0005789,GO:0015031,GO:0005840	CG32276-PA						PF06624														
aly1898.2	Unknown	GO:0007623,GO:0007444	CG9239-PA																				
aly1898.3	Unknown		n/a						PF13905				G3DSA:3.40.30.10	SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1899.1	Glycoprotein hormone beta-5	GO:0005179,GO:0009755,GO:0002155,GO:0005615,GO:0005576,GO:0001664,GO:0046982	CG40041-PC						PF00007				G3DSA:2.10.90.10	SSF57501									
aly1899.2	Unknown	GO:0007157,GO:0005576,GO:0003674	CG42242-PD				SM00409		PF07686				G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly1899.3	Unknown		n/a																				
aly1899.4	Unknown		n/a																				
aly1899.5	Unknown		n/a																				
aly19.1	Unknown		n/a																				
aly19.2	RILP-like protein homolog	GO:0005575,GO:0048812,GO:0003674	CG11448-PC						PF11461,PF09744					SSF161256	47~123,153~208,263~290								
aly190.1	Down syndrome cell adhesion molecule-like protein 1 homolog	GO:0048704,GO:0007420,GO:0005615,GO:0009986,GO:0016338,GO:0042803,GO:0007162,GO:0005576,GO:0003674,GO:0005515,GO:0005886,GO:0070593,GO:0007157,GO:0007156,GO:0016021,GO:0031225	CG14064-PA				SM00409		PF08205,PF07686	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly190.2	Unknown		n/a																				
aly190.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly19006.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0004252,GO:0004175,GO:0015574,GO:0015771,GO:0016021,GO:0022857,GO:0005886,GO:0006508,GO:0055085	CG6484-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly1901.1	Atrial natriuretic peptide receptor 2	GO:0017046,GO:0060348,GO:0001503,GO:0004872,GO:0007168,GO:0035556,GO:1900194,GO:0016021,GO:0016849,GO:0004672,GO:0009190,GO:0042802,GO:0005525,GO:0004383,GO:0044702,GO:0005886,GO:0042562,GO:0006182,GO:0051447,GO:0016941,GO:0005622,GO:0097011,GO:0005524	CG14501-PA				SM00044		PF00211	PS50125		PS00452	G3DSA:3.30.70.1230	SSF55073									
aly1901.2	Unknown		n/a																				
aly1901.3	Atrial natriuretic peptide receptor 2	GO:0001503,GO:0016941,GO:0004383,GO:0005622,GO:0042802,GO:0004872,GO:0004672,GO:0035556,GO:0006182,GO:0016021,GO:0005524,GO:0005525	CG14501-PA				SM00044		PF00211,PF07701,PF08376	PS50125		PS00452	G3DSA:3.30.70.1230	SSF55073	137~157	00230+4.6.1.2							
aly1901.4	Unknown		n/a																				
aly1901.5	Unknown		n/a												109~143								
aly19013.1	Unknown	GO:0008270,GO:0003676	n/a						PF03564				G3DSA:4.10.60.10										
aly19013.2	Unknown		n/a																				
aly19013.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly19013.4	Unknown		n/a																				
aly1905.1	BRCA1-associated RING domain protein 1	GO:0005200,GO:0006471,GO:0090364,GO:0035220,GO:0008270,GO:0003950,GO:0005737,GO:0043065,GO:0031436,GO:0005730,GO:0005634,GO:0005654,GO:0043066,GO:0070531,GO:0042803,GO:0006281,GO:0022416,GO:0016874,GO:0042325,GO:0007016,GO:0043231,GO:0046826,GO:0085020,GO:0003723,GO:0046982	CG4719-PB				SM00292,SM00292,SM00248,SM00248,SM00248		PF12796,PF13606	PS50297,PS50172,PS50089,PS50172,PS50088,PS50088,PS50088	PR01415,PR01415		G3DSA:3.40.50.10190,G3DSA:3.30.40.10,G3DSA:3.40.50.10190,G3DSA:1.25.40.20	SSF52113,SSF57850,SSF52113,SSF48403										
aly1905.2	Transferrin	GO:0006879,GO:0005615,GO:0006811,GO:0009617,GO:0055072,GO:0008199,GO:0005381,GO:0006826,GO:0046872,GO:0005576	CG3666-PA				SM00094		PF00405,PF00405	PS51408,PS51408	PR00422,PR00422,PR00422,PR00422		G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.190.10	SSF53850,SSF53850										
aly1905.3	Small nuclear ribonucleoprotein Sm D1	GO:0005737,GO:0034715,GO:0000387,GO:0005829,GO:0030532,GO:0071011,GO:0005634,GO:0044822,GO:0000398,GO:0098779,GO:0002230,GO:0005689,GO:0005687,GO:0005685,GO:0034719,GO:0071013,GO:0005681,GO:0034709	CG10753-PA				SM00651		PF01423				G3DSA:2.30.30.100	SSF50182										
aly1905.4	Centrin-1	GO:0005856,GO:0032391,GO:0031683,GO:0008017,GO:0005813,GO:0034605,GO:0005814,GO:0000922,GO:0005509,GO:0007067,GO:0032795,GO:0051301	CG17493-PB				SM00054,SM00054,SM00054		PF13499	PS50222,PS50222,PS50222			G3DSA:1.10.238.10	SSF47473										
aly1905.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1905.6	Phosphatidylethanolamine-binding protein homolog F40A3.3	GO:0005575,GO:0008150,GO:0003674,GO:0008289,GO:0005739	CG6180-PA						PF01161				G3DSA:3.90.280.10	SSF49777									
aly1905.7	Protein translation factor SUI1 homolog	GO:0006417,GO:0071456,GO:0006413,GO:0006412,GO:0003743	CG17737-PA			PIRSF004499		TIGR01160	PF01253	PS50296			G3DSA:3.30.780.10	SSF55159									
aly1905.8	Dynactin subunit 1	GO:0016330,GO:0051383,GO:0042052,GO:0042051,GO:0035371,GO:0007349,GO:0045198,GO:0030286,GO:0031616,GO:0007067,GO:0051028,GO:0005876,GO:0034501,GO:0005737,GO:0005818,GO:0005813,GO:0045502,GO:0001709,GO:0007018,GO:0005739,GO:0051225,GO:0048477,GO:0003774,GO:0003777,GO:0051299,GO:0047497,GO:0035011,GO:0007052,GO:0048491,GO:0005869,GO:0001754,GO:0022008,GO:0001751,GO:0000776,GO:0051642,GO:0008090,GO:0005828,GO:0030496,GO:0051256,GO:0006886	CG9206-PA				SM01052		PF01302	PS50245			G3DSA:2.30.30.190	SSF74924									
aly19073.1	Unknown		n/a																				
aly190867.1	Unknown		n/a																				
aly1911.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1911.2	Lachesin	GO:0004714,GO:0005515,GO:0005886,GO:0007155,GO:0007169,GO:0031225	CG14521-PA				SM00406,SM00408,SM00408,SM00408,SM00408,SM00409,SM00409		PF00047,PF07679,PF07679	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly1913.1	Unknown		n/a																				
aly19141.1	Unknown	GO:0005575,GO:0003674,GO:0008150	CG12970-PC						PF03281														
aly191530.1	Dolichyl-diphosphoolig osaccharide--protein glycosyltransfe rase 48 kDa subunit	GO:0007030,GO:0034389,GO:0034097,GO:0006486,GO:0006487,GO:0016021,GO:0005811,GO:0042110,GO:0005789,GO:0005886,GO:0022008,GO:0004579,GO:0008250,GO:0018279	CG9022-PA						PF03345							00513+2.4.99.18,00510+2.4.99.18			UPA00378				
aly1916.1	Neuroendocrin e convertase 2	GO:0004252,GO:0004175,GO:0030425,GO:0002165,GO:0034231,GO:0008233,GO:0030070,GO:0030133,GO:0035180,GO:0035187,GO:0005615,GO:0016020,GO:0033500,GO:0006508,GO:0030141,GO:0005788,GO:0016485,GO:0016486,GO:0043204,GO:0007399,GO:0016540,GO:0034230,GO:0005576	CG6438-PA						PF16470			PS00136	G3DSA:3.40.50.200,G3DSA:3.30.70.850	SSF54897,SSF52743									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1916.10	Protein doublesex	GO:0048086,GO:0007619,GO:0007485,GO:0035263,GO:0001077,GO:0008270,GO:0003677,GO:0008049,GO:0001078,GO:0007417,GO:0043565,GO:0000122,GO:0005634,GO:0006366,GO:0000987,GO:0007530,GO:0042803,GO:0007486,GO:0035215,GO:0007483,GO:0019101,GO:0019102,GO:0000398,GO:0048071,GO:0007283,GO:0045892,GO:0045893,GO:0046660,GO:0046661,GO:0007548,GO:0046872,GO:0018993,GO:0045433,GO:0003700,GO:0016199,GO:0006355,GO:0045449,GO:0006357,GO:0045944,GO:0005515,GO:0045570,GO:0045496,GO:0045497,GO:0003729	CG11094-PE				SM00301		PF00751	PS50809		PS40000	G3DSA:4.10.1040.10	SSF82927										
aly1916.11	Unknown		n/a																				
aly1916.2	ATP-dependent Clp protease proteolytic subunit, mitochondrial	GO:0004252,GO:0051603,GO:0051260,GO:0005739,GO:0006515,GO:0005759,GO:0006508,GO:0009368	CG5045-PA	MF_00444					PF00574		PR00127,PR00127,PR00127,PR00127,PR00127	PS00382,PS00381	G3DSA:3.90.226.10	SSF52096									
aly1916.3	Unknown		n/a																				
aly1916.4	Unc-112-related protein	GO:0050829,GO:0048738,GO:0050839,GO:0007160,GO:0005737	CG14991-PA				SM00295,SM00233		PF00373	PS50003		PS00661	G3DSA:2.30.29.30,G3DSA:1.20.80.10,G3DSA:1.20.80.10,G3DSA:2.30.29.30	SSF50729,SSF47031,SSF47031,SSF50729										
aly1916.5	Ring canal kelch homolog	GO:0005737,GO:0005856,GO:0006909	CG17754-PC				SM00612,SM00612		PF00651,PF01344				G3DSA:2.120.10.80,G3DSA:3.30.710.10	SSF117281,SSF54695										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1916.6	DNA repair protein RAD51 homolog 1	GO:0008022,GO:0071480,GO:0009994,GO:0000730,GO:0051106,GO:0005739,GO:0007294,GO:1902521,GO:0000228,GO:0007143,GO:0005737,GO:0010569,GO:0070182,GO:0006302,GO:0000724,GO:0009949,GO:0005634,GO:0051260,GO:0000800,GO:0005815,GO:0005654,GO:0031297,GO:0043142,GO:0005759,GO:0045003,GO:0003690,GO:0009636,GO:0048477,GO:0003697,GO:0005524,GO:0072757,GO:0072719,GO:0006281,GO:0042493,GO:0072711,GO:0007126,GO:0016605,GO:0006974,GO:0000793,GO:0000794,GO:0007131,GO:0071479,GO:0048471,GO:0070192,GO:0006310,GO:0008094,GO:0006312,GO:0009951,GO:0000075,GO:0006268,GO:0005730,GO:0000150,GO:0032200,GO:0030717,GO:0010165,GO:0008298,GO:0042802,GO:0005515,GO:1990414,GO:0001932,GO:0003684	CG7948-PA			PIRSF005856	SM00382	TIGR02239	PF14520,PF08423	PS50162,PS50163			G3DSA:1.10.150.20,G3DSA:3.40.50.300	SSF47794,SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1916.7	NAD-dependent protein deacetylase sirtuin-2	GO:0032436,GO:0030426,GO:0010801,GO:0006476,GO:0046970,GO:0061433,GO:0008270,GO:0070933,GO:0070932,GO:0043204,GO:0043209,GO:0004407,GO:0045836,GO:0042903,GO:0033010,GO:0061428,GO:0022011,GO:0005829,GO:0051781,GO:0043130,GO:0033558,GO:0045843,GO:0048487,GO:0034983,GO:0043388,GO:0007067,GO:0043220,GO:1900195,GO:0016575,GO:1900119,GO:0071219,GO:0071456,GO:0048471,GO:0042826,GO:2000378,GO:0071872,GO:0048012,GO:0005720,GO:1900425,GO:0043491,GO:0031641,GO:0048813,GO:0006351,GO:0070446,GO:0042177,GO:0021762,GO:0044242,GO:0005874,GO:0005737,GO:0090042,GO:0051321,GO:0000122,GO:0043161,GO:0005634,GO:1900226,GO:0033270,GO:0008285,GO:0008134,GO:0017136,GO:0035035,GO:0045892,GO:0014065,GO:0051987,GO:0045599,GO:0045598,GO:0097386,GO:0030496,GO:0034979,GO:0045944,GO:2000777,GO:0003682,GO:0051301,GO:0072687,GO:0072686,GO:0005813,GO:0005814,GO:1901026,GO:0005694,GO:0010507,GO:0035729,GO:0006914,GO:0005819,GO:0005886,GO:0008340,GO:0034599,GO:0051726,GO:0043219,GO:0070403,GO:0044224	CG5085-PA						PF02146	PS50305			G3DSA:3.30.1600.10,G3DSA:3.30.1600.10,G3DSA:3.40.50.1220,G3DSA:3.40.50.1220,G3DSA:3.40.50.1220	SSF52467										
aly1916.8	Unknown	GO:0016021,GO:0005272,GO:0006814	CG15555-PA						PF00858				G3DSA:1.10.287.820										
aly1916.9	Unknown	GO:0016021,GO:0016020,GO:0005272,GO:0006814	CG31105-PB						PF00858														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1917.1	Unknown		n/a																				
aly1917.2	Unknown		n/a																				
aly1917.3	Autophagy protein 12-like	GO:0005737,GO:0034045,GO:0006995,GO:0000422,GO:0035071,GO:0019776,GO:0006914,GO:0016236,GO:0000045,GO:0006501,GO:0048102,GO:0044804,GO:0003674,GO:1902350,GO:0035096,GO:0034274,GO:0031386	CG10861-PB						PF04110				G3DSA:3.10.20.90	SSF54236									
aly1917.4	Cilia- and flagella-associated protein 52	GO:0005575,GO:0008150,GO:0042995,GO:0003674,GO:0005737	CG10064-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400	PS50082,PS50294,PS50294,PS50082,PS50082,PS50082		PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978									
aly1917.5	Baculoviral IAP repeat-containing protein 5	GO:0031021,GO:0000086,GO:0015631,GO:0000226,GO:0008270,GO:0045892,GO:0031503,GO:0007067,GO:0051303,GO:0051225,GO:0051301,GO:0005737,GO:0031577,GO:0005634,GO:0031536,GO:0005814,GO:0043066,GO:0005876,GO:0032133,GO:0043027,GO:0042803,GO:0045931,GO:0000910,GO:0006468,GO:0061469,GO:0008017,GO:0005881,GO:0007051,GO:0046331,GO:0048037,GO:0007059,GO:0022008,GO:0061178,GO:0000775,GO:0000777,GO:0007111,GO:0007110,GO:0000915,GO:0005829,GO:0030496,GO:0043154,GO:0006351,GO:0043524	CG12265-PA				SM00238		PF00653	PS50143			G3DSA:1.10.1170.10	SSF57924									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1917.6	Monocarboxylate transporter 12	GO:0005308,GO:0035879,GO:0015129,GO:0008028,GO:0016021,GO:1902598,GO:0015293,GO:0005887,GO:0055085	CG3409-PA						PF07690,PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly192.1	Unknown		n/a																				
aly19213.1	Unknown		n/a																				
aly19213.2	Unknown		n/a																				
aly192267.1	Dymeclin	GO:0005575,GO:0003674,GO:0008150	CG8230-PA						PF09742														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1923.1	Rho-related GTP-binding protein RhoE	GO:0048675,GO:0019897,GO:0007394,GO:0006909,GO:0042052,GO:0016335,GO:0008258,GO:0030032,GO:0032794,GO:0050807,GO:0031941,GO:0030036,GO:0034334,GO:0007419,GO:0007164,GO:0007391,GO:0031175,GO:0007411,GO:0007298,GO:0007413,GO:0071907,GO:0007017,GO:0051963,GO:0007254,GO:0016028,GO:0045216,GO:0048615,GO:0002433,GO:0030707,GO:0051491,GO:0051450,GO:0048814,GO:0005525,GO:0016203,GO:0050975,GO:0008078,GO:0005925,GO:0035212,GO:0008283,GO:0042067,GO:0007424,GO:0003924,GO:0048747,GO:0035011,GO:0035010,GO:0007516,GO:0008045,GO:0007409,GO:0005886,GO:0007520,GO:0007264,GO:0008347,GO:0000902,GO:0035099,GO:0007015,GO:0010593,GO:0007426,GO:0050770,GO:0051726,GO:0070062,GO:0007422,GO:0046664,GO:0030866,GO:0016199,GO:0007390,GO:0006974,GO:0048813,GO:0035320,GO:0007435,GO:0005515,GO:0051017,GO:0045610,GO:0005622,GO:0046843	CG2248-PA				SM00175,SM00174,SM00173	TIGR00231	PF00071	PS51420	PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly1923.10	Fatty-acid amide hydrolase 2	GO:0016787,GO:0016021,GO:0005811,GO:0017064,GO:0016884	CG5112-PA						PF01425				G3DSA:3.90.1300.10	SSF75304		00970+6.3.5.7		PWY-5921					
aly1923.11	S-adenosylmethionine decarboxylase proenzyme	GO:0050829,GO:0006557,GO:0004014,GO:0008295,GO:0006597	CG5029-PA			PIRSF001355		TIGR00535	PF01536			PS01336	G3DSA:3.60.90.10	SSF56276		00270+4.1.1.50,00330+4.1.1.50		PWY-6834	UPA00331				
aly1923.12	Unknown		n/a						PF15503														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1923.13	Activating signal cointegrator 1 complex subunit 2	GO:0006307,GO:0006281,GO:0005654,GO:0006355,GO:0006351,GO:0005515	CG2701-PA				SM00546		PF02845	PS51140				SSF46934									
aly1923.2	Lysozyme 2	GO:0019835,GO:0005615,GO:0032504,GO:0003796,GO:0005576,GO:0042742	CG6426-PA						PF05497														
aly1923.3	Zinc finger with UFM1-specific peptidase domain protein	GO:0005575,GO:0046872,GO:0008150,GO:0016790	CG30157-PA				SM00355,SM00355,SM00355,SM00355		PF07910	PS50157		PS00028											
aly1923.4	Sialin	GO:0006865,GO:0006820,GO:0015136,GO:0030054,GO:0005737,GO:0044267,GO:0015992,GO:0006488,GO:0016021,GO:0016020,GO:0043687,GO:0018279,GO:0015739,GO:0005351,GO:0006811,GO:0006817,GO:0005887,GO:0005886,GO:0055085,GO:0030672,GO:0005436,GO:0005764,GO:0005765	CG3036-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly1923.5	Protein bicaudal C	GO:0005515,GO:0030036,GO:0000226,GO:0003723,GO:0005887,GO:0007067,GO:0003729,GO:0048477,GO:0007275,GO:0007319,GO:0007297	CG4824-PB				SM00322,SM00322,SM00454		PF00013,PF00013,PF00536	PS50105,PS50084,PS50084			G3DSA:1.10.150.50,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10	SSF47769,SSF54791,SSF54791									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1923.6	Cytochrome c oxidase copper chaperone	GO:0016531,GO:0005758,GO:0008535,GO:0005507,GO:0006825	CG9065-PA						PF05051				G3DSA:1.10.810.10	SSF47072									
aly1923.7	Sodium-coupled neutral amino acid transporter 9 homolog	GO:0016021,GO:0006865	n/a						PF01490														
aly1923.8	Phosphoglucomutase	GO:0005975,GO:0005978,GO:0005829,GO:0000287,GO:0060361,GO:0005992,GO:0046331,GO:0004614,GO:0004619,GO:0019388,GO:0006006	CG5165-PA						PF02879,PF02880,PF02878,PF00408		PR00509,PR00509,PR00509,PR00509	PS00710	G3DSA:3.40.120.10,G3DSA:3.40.120.10,G3DSA:3.30.310.50,G3DSA:3.40.120.10	SSF53738,SSF55957,SSF53738,SSF53738		00520+5.4.2.10		PWY-6749						
aly1923.9	Fatty-acid amide hydrolase 2	GO:0016787,GO:0016021,GO:0005811,GO:0017064,GO:0016884	CG5112-PA						PF01425				G3DSA:3.90.1300.10	SSF75304		00970+6.3.5.7		PWY-5921					
aly192871.1	Unknown		n/a						PF10512														
aly193.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly193.2	Enhancer of split mbeta protein	GO:0048749,GO:0043565,GO:0007219,GO:0007399,GO:0000122,GO:0003700,GO:0005634,GO:0030154,GO:0006355,GO:0045892,GO:0006351,GO:0003677,GO:0046983	CG14548-PA				SM00511,SM00353		PF00010,PF07527	PS51054,PS50888			G3DSA:4.10.280.10	SSF158457,SSF47459									
aly193.3	Enhancer of split mgamma protein	GO:0048749,GO:0043565,GO:0007219,GO:0048190,GO:0007399,GO:0000122,GO:0003700,GO:0005634,GO:0002052,GO:0045892,GO:0006351,GO:0003677,GO:0046983,GO:0008134	CG8333-PA				SM00511,SM00353		PF07527,PF00010	PS51054,PS50888			G3DSA:4.10.280.10	SSF158457,SSF47459									
aly193.4	Unknown		n/a				SM00233			PS50003				SSF50729,SSF50729									
aly1931.1	Unknown		n/a																				
aly1931.10	Unknown	GO:0006623	CG2093-PA																				
aly1931.11	Short neuropeptide F	GO:0007218,GO:0005576,GO:0005184,GO:0040014,GO:0032095	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1931.12	DNA-directed RNA polymerase II subunit RPB1	GO:0007498,GO:0006366,GO:0046331,GO:0005665,GO:0003677,GO:0003899,GO:0046872	CG43897-PM				SM00735		PF15936														
aly1931.13	Probable E3 ubiquitin-protein ligase HERC4	GO:0005737,GO:0016874,GO:0005634,GO:0030154,GO:0016567,GO:0007283,GO:0042787,GO:0061630,GO:0004842,GO:0005829	CG9153-PC				SM00119		PF00415,PF00415,PF00415,PF00415,PF00415,PF00632	PS50237,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012	PR00633,PR00633,PR00633,PR00633,PR00633	PS00626,PS00626,PS00626,PS00626	G3DSA:3.30.2160.10,G3DSA:2.130.10.30	SSF50985,SSF50985,SSF56204					UPA00143				
aly1931.14	Zinc finger SWIM domain containing protein 8	GO:0008270	CG34401-PB						PF04434	PS50966					868~888								
aly1931.15	Unknown		n/a																				
aly1931.16	Alanine--glyoxylate aminotransferase 2-like	GO:0008453,GO:0035094,GO:0005739,GO:0003824,GO:0019544,GO:0004587,GO:0030170	CG8745-PA						PF00202			PS00600	G3DSA:3.40.640.10,G3DSA:3.90.1150.10	SSF53383									
aly1931.17	Nucleic-acid-binding protein from transposon X-element	GO:0006313,GO:0019013,GO:0008270,GO:0003676	n/a										G3DSA:4.10.60.10										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1931.18	Retinol dehydrogenase 11	GO:0016614,GO:0016062,GO:0004745,GO:0016021,GO:0052650,GO:0005789,GO:0001917,GO:0008152,GO:0042572,GO:0005622,GO:0042574,GO:0016491	CG7675-PB						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly1931.19	Unknown		n/a																				
aly1931.2	Unknown		n/a																				
aly1931.20	Unknown		n/a																				
aly1931.21	Unknown		n/a																				
aly1931.3	Unknown		n/a																				
aly1931.4	Unknown		CG31191-PD												70~90								
aly1931.5	Wiskott-Aldrich syndrome protein family member 1	GO:0005856,GO:0005737,GO:0005739,GO:0008104,GO:0043195,GO:0016601,GO:0042734,GO:0030027,GO:2000601,GO:0030036,GO:0005741,GO:0031209,GO:0005515,GO:0072673,GO:0032403,GO:0007411,GO:0030054,GO:0045202	CG31043-PA																				
aly1931.6	U1 small nuclear ribonucleoprotein C	GO:0000387,GO:0000243,GO:0000381,GO:0030619,GO:0030532,GO:0005634,GO:0000398,GO:0005692,GO:0007052,GO:0000395,GO:0008270,GO:0003676,GO:0071004,GO:0022008,GO:0005685,GO:0003729	CG5454-PA	MF_03153		PIRSF037969	SM00451		PF06220	PS50171				SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1931.7	CTP synthase	GO:0005737,GO:0006221,GO:0044210,GO:0006541,GO:0006241,GO:0003883,GO:0097268,GO:0022008,GO:0005524	CG45070-PA					TIGR00337	PF06418,PF00117	PS51273			G3DSA:3.40.50.880,G3DSA:3.40.50.300	SSF52540,SSF52317		00240+6.3.4.2	REACT_1698	PWY-7185,PWY-7176,PWY-7177	UPA00159				
aly1931.8	Vacuolar protein sorting associated protein 13C	GO:0070062,GO:0006623,GO:0045053,GO:0005623,GO:0019898,GO:0005622	CG2093-PA						PF12624,PF16908,PF16910,PF16910						101~136,223~243,1656~1656								
aly1931.9	Vacuolar protein sorting associated protein 13C	GO:0070062,GO:0006623,GO:0045053,GO:0005623,GO:0019898,GO:0005622	CG2093-PA						PF06650,PF16909						1405~1410								
aly193168.1	Trypsin CFT-1	GO:0004252,GO:0004175,GO:0005615,GO:0006508	CG6483-PA						PF00089			PS00134	G3DSA:2.40.10.10	SSF50494									
aly19343.1	Unknown		n/a																				
aly1935.1	Neuropeptides capa receptor	GO:0004930,GO:0051928,GO:0007186,GO:0016021,GO:0007589,GO:0007218,GO:0016323,GO:0071465,GO:0005887,GO:0008188,GO:0001607	CG14575-PB						PF00001	PS50262	PR01565,PR01565,PR01565,PR01565,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1935.10	Glucosamine-6-phosphate isomerase	GO:0005737,GO:0016787,GO:0005975,GO:0006043,GO:0006044,GO:0004342,GO:0005575,GO:0006091	CG6957-PA	MF_01241				TIGR00502	PF01182			PS01161	G3DSA:3.40.50.1360	SSF100950		00520+3.5.99.6		PWY-5514,PWY-6906,PWY-6855	UPA00629				
aly1935.11	Replication factor C subunit 2	GO:0000819,GO:0000076,GO:0007067,GO:0006281,GO:0004003,GO:0006271,GO:0016321,GO:0005663,GO:0046331,GO:0006260,GO:0006261,GO:0003677,GO:0007076,GO:0000077,GO:0022008,GO:0005634,GO:0005875,GO:0005524	CG14999-PA				SM00382		PF00004,PF08542				G3DSA:1.10.8.60,G3DSA:1.20.272.10,G3DSA:3.40.50.300	SSF48019,SSF52540			REACT_152,REACT_216,REACT_22172,REACT_383,REACT_1538						
aly1935.12	Charged multivesicular body protein 2a	GO:0016197,GO:0007034,GO:0000815,GO:0043162,GO:0042059,GO:0031902,GO:0045746,GO:0005771,GO:0003674,GO:0008593,GO:0015031,GO:0005769	CG14542-PA						PF03357						15~42								
aly1935.13	Unknown		n/a																				
aly1935.2	Host cell factor 1	GO:0019046,GO:0045927,GO:0004402,GO:0030425,GO:0030424,GO:0050821,GO:0010628,GO:0051568,GO:0043254,GO:0007049,GO:0005737,GO:0045787,GO:0000123,GO:0000122,GO:0006325,GO:0006355,GO:0005634,GO:0016020,GO:0003713,GO:0005739,GO:0005654,GO:0007005,GO:0016573,GO:0070688,GO:0043025,G	CG1710-PB						PF13415,PF13415,PF01344				G3DSA:2.120.10.80,G3DSA:2.120.10.80	SSF117281									
aly1935.3	Prothoracicostatic peptide	GO:0005179,GO:0007218,GO:0005184,GO:0005615,GO:0016085,GO:0016087,GO:0001664,GO:0007186,GO:0002168	CG6456-PA																				

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1935.4	Prolyl 3-hydroxylase sudestada1	GO:0005737,GO:0031418,GO:0016706,GO:0005634,GO:0019511,GO:0005575,GO:0018126,GO:0006417,GO:0005506,GO:0031543,GO:0055114	CG44254-PA				SM00702		PF10637,PF13640														
aly1935.5	tRNA:m(4)X modification enzyme TRM13 homolog	GO:0008168,GO:0008175,GO:0046872,GO:0008033,GO:0030488	CG18048-PA						PF11722,PF05206,PF05253									PWY-6829					
aly1935.6	Probable ADP-ribosylation factor GTPase-activating protein AGD8	GO:0005737,GO:0046872,GO:0032312,GO:0005829,GO:0005096,GO:0046331,GO:0008060,GO:0008270,GO:0001745,GO:0005912	CG6838-PH																				
aly1935.7	ADP-ribosylation factor GTPase-activating protein 3	GO:0005737,GO:0046872,GO:0016192,GO:0032312,GO:0005096,GO:0000139,GO:0046331,GO:0008060,GO:0008270,GO:0015031,GO:0001745,GO:0005912	CG6838-PH				SM00105		PF01412	PS50115	PR00405,PR00405,PR00405			SSF57863									
aly1935.8	E3 ubiquitin-protein ligase TRIM33	GO:0008270,GO:0003677,GO:0007411,GO:0000122,GO:0006325,GO:0004842,GO:0005634,GO:0003713,GO:0005654,GO:0010467,GO:0070412,GO:0070410,GO:0048666,GO:0006367,GO:0017015,GO:0045892,GO:0030514,GO:0016874,GO:0007179,GO:0043231,GO:0007422,GO:0005622,GO:0016567,GO:0048813,GO:0006351,GO:0003682	CG5206-PC				SM00336,SM00336,SM00184,SM00502		PF00643,PF00643	PS50119,PS50119,PS50089			G3DSA:3.30.40.10,G3DSA:4.10.45.10	SSF57850,SSF57845									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1935.9	Transcription intermediary factor 1-alpha	GO:0010628,GO:0008270,GO:0007411,GO:0042981,GO:0046777,GO:0005737,GO:0043565,GO:0005719,GO:0006325,GO:0016922,GO:0005634,GO:0003713,GO:0005654,GO:0070577,GO:0004672,GO:1901796,GO:0048666,GO:0008285,GO:0006468,GO:0071391,GO:0034056,GO:0045892,GO:0045893,GO:0016874,GO:0005726,GO:0007422,GO:0004842,GO:0031647,GO:0030163,GO:0016567,GO:0048813,GO:0070562,GO:0006351,GO:0005515,GO:0061630,GO:0003682,GO:0002039,GO:0055074	CG5206-PC				SM00249,SM00297		PF00628,PF00439	PS50014,PS50016	PR00503,PR00503	PS01359	G3DSA:3.30.40.10,G3DSA:1.20.920.10,G3DSA:1.20.920.10	SSF57903,SSF47370									
aly1937.1	Unknown		n/a																				
aly1937.10	60 kDa SS-A/Ro ribonucleoprotein	GO:0005737,GO:0030030,GO:0034336,GO:0030529,GO:0003723,GO:0046872	n/a						PF05731	PS50988				SSF53300,SSF140864									
aly1937.11	Coiled-coil domain-containing protein 28A		CG10874-PD						PF13270														
aly1937.12	GTPase-activating Rap/Ran-GAP domain-like protein 3	GO:0051056,GO:0005099,GO:0060293,GO:0005096,GO:0032861,GO:0046582,GO:0007265,GO:0002121	CG44086-PH						PF02145,PF00780	PS50085,PS50219				SSF111347									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1937.13	Unknown		n/a																				
aly1937.14	39S ribosomal protein L30, mitochondrial	GO:0070126,GO:0006996,GO:0070124,GO:0070125,GO:0005840,GO:0032543,GO:0003735,GO:0005743,GO:0005762,GO:0006412	CG7038-PA						PF00327				G3DSA:3.30.1390.20	SSF55129									
aly1937.15	Unknown	GO:0005575,GO:0003674,GO:0008150	CG33228-PB																				
aly1937.16	Cyclic AMP-dependent transcription factor ATF-6 beta	GO:0005794,GO:0006351,GO:1990440,GO:0032993,GO:0043565,GO:0003700,GO:0005634,GO:0036500,GO:0005789,GO:0006355,GO:0044212,GO:0030176,GO:0007165,GO:0035497,GO:0005622,GO:0042803	CG3136-PC				SM00338		PF00170	PS50217			G3DSA:1.20.5.170	SSF57959	771~771,337~371								
aly1937.17	Probable E3 ubiquitin-protein ligase HERC2	GO:0005737,GO:0020037,GO:0016874,GO:0005634,GO:0005085,GO:0005814,GO:0016567,GO:0042787,GO:0046872,GO:0004842	CG11734-PC				SM00119		PF00173,PF06701,PF00632,PF00415,PF00415,PF00415,PF00415,PF00415,PF00415,PF00415,PF00415,PF00415,PF0041	PS50012,PS50237,PS50012,PS51416,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012	PR00633,PR00633,PR00633,PR00633,PR00633,PR00633		G3DSA:3.30.2160.10,G3DSA:2.130.10.30,G3DSA:2.130.10.30,G3DSA:2.130.10.30,G3DSA:3.10.120.10	SSF56204,SSF50985,SSF55856,SSF50985,SSF159034,SSF50985,SSF50985	1655~1675,3760~3760				UPA00143				
aly1937.18	Leucine-rich repeat-containing protein 20	GO:0005575,GO:0003012,GO:0003674,GO:0005515	CG2471-PC						PF13855				G3DSA:3.80.10.10	SSF52075									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1937.19	PDZ domain-containing protein 8	GO:0022604,GO:0007010,GO:0019992,GO:0016020,GO:0005622,GO:0016032,GO:0035556,GO:0046872	CG10362-PA				SM00109			PS50081		PS00479	G3DSA:3.30.60.20,G3DSA:2.30.42.10	SSF57889,SSF50156									
aly1937.2	Unknown		n/a																				
aly1937.20	Phosphoglycerate kinase	GO:0005737,GO:0031430,GO:0016310,GO:0046716,GO:0007525,GO:0005524,GO:0007268,GO:0007520,GO:0004618,GO:0006096,GO:0030018	CG3127-PE	MF_00145		PIRSF000724			PF00162		PR00477,PR00477,PR00477,PR00477,PR00477,PR00477,PR00477,PR00477	PS00111	G3DSA:3.40.50.1260,G3DSA:3.40.50.1270	SSF53748		00710+2.7.2.3,00010+2.7.2.3		PWY-1042,PWY-6886,PWY-5484,PWY-7003,PWY-6901	UPA00109				
aly1937.21	Protein will die slowly	GO:0048188,GO:0016573,GO:0006338,GO:0044545,GO:0004402,GO:0005875,GO:0005671,GO:0005515,GO:0051568,GO:0007095,GO:0022008,GO:0044666,GO:0005634,GO:0044665	CG17437-PA			PIRSF002394	SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50294,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678,PS00678	G3DSA:2.130.10.10	SSF50978									
aly1937.22	Unknown		n/a																				
aly1937.23	Voltage-dependent calcium channel type A subunit alpha-1	GO:0007632,GO:0006887,GO:0007619,GO:0008331,GO:0008332,GO:0005886,GO:0045887,GO:0005891,GO:0050908,GO:0007275,GO:0086010,GO:0048786,GO:0002027,GO:0005509,GO:0010524,GO:0042045,GO:0016324,GO:0006816,GO:0007602,GO:0034220,GO:0046928,GO:0007269,GO:0007268,GO:0016323,GO:0008344,G	CG43368-PN				SM01062		PF00520,PF00520,PF00520,PF16905,PF08763	PS50222	PR00167,PR00167,PR00167,PR00167,PR00167,PR00167,PR00167		G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350	SSF81324,SSF81324,SSF81324,SSF81324,SSF47473,SSF81324,SSF81324	364~384,1668~1674,1654~1654,713~751									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1937.24	Unknown		n/a																				
aly1937.25	Small RNA 2'-O-methyltransferase	GO:0034587,GO:0035194,GO:0030422,GO:0008173,GO:0008171,GO:0003723,GO:0001510,GO:0046872	CG12367-PA										G3DSA:3.40.50.150	SSF53335									
aly1937.26	Probable chitinase 3	GO:0005737,GO:0040003,GO:0005615,GO:0010716,GO:0000272,GO:0005576,GO:0008061,GO:0004568,GO:0006030,GO:0006032,GO:0016490	CG17052-PA				SM00494,SM00494,SM00494		PF01607,PF01607,PF01607	PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625,SSF57625									
aly1937.27	Chondroitin proteoglycan 2	GO:0040003,GO:0005615,GO:0010716,GO:0000281,GO:0009790,GO:0005576,GO:0008061,GO:0006030,GO:0016490	CG17052-PA				SM00494,SM00494,SM00494		PF01607,PF01607,PF01607	PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625,SSF57625									
aly1937.28	Peritrophin-1	GO:0005615,GO:0032504,GO:0005576,GO:0008061,GO:0006030,GO:0016490	CG17058-PA				SM00494,SM00494,SM00494		PF01607,PF01607,PF01607	PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625,SSF57625									
aly1937.29	Peritrophin-44	GO:0006030,GO:0005576,GO:0008061,GO:0016490	CG4778-PA				SM00494,SM00494,SM00494,SM00494,SM00494		PF01607,PF01607,PF01607,PF01607,PF01607	PS50940,PS50940,PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1937.3	Unknown		n/a																				
aly1937.30	Chondroitin proteoglycan-2	GO:0030703,GO:0000281,GO:0009790,GO:0005576,GO:0008061,GO:0032465,GO:0006030,GO:0016490	CG4778-PA				SM00494,SM00494		PF01607,PF01607	PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625									
aly1937.31	Unknown	GO:0006030,GO:0005576,GO:0008061,GO:0016490	CG10287-PA				SM00494,SM00494,SM00494		PF01607,PF01607,PF01607	PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625,SSF57625									
aly1937.32	Unknown	GO:0006030,GO:0005576,GO:0008061	CG13675-PD				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly1937.33	Unknown		n/a																				
aly1937.34	ZZ-type zinc finger-containing protein 3	GO:0000123,GO:0043966,GO:0006338,GO:0043967,GO:0031965,GO:0005634,GO:0005730,GO:0004402,GO:0006355,GO:0005671,GO:0006351,GO:0016573,GO:0003677,GO:0003682,GO:0008270	CG9200-PA				SM00717		PF00249	PS51294				SSF46689	37~57								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1937.35	Unknown		n/a																				
aly1937.36	E3 ubiquitin-protein ligase HERC2	GO:0005085,GO:0008270,GO:0005737,GO:0044267,GO:0043547,GO:0016567,GO:0004842,GO:0005634,GO:0016020,GO:0005814,GO:0005654,GO:0042787,GO:0046872,GO:0020037,GO:0006281,GO:0043687,GO:0006974,GO:0007283,GO:0016925,GO:0016874,GO:0031625,GO:0032183,GO:0005743,GO:0006886	CG11734-PC						PF11515				G3DSA:2.30.30.30	SSF63748					UPA00143				
aly1937.37	Unknown		n/a																				
aly1937.4	Probable Ras GTPase-activating protein	GO:0005737,GO:0005099,GO:0043547,GO:0005096,GO:0007476,GO:0007165,GO:0045179,GO:0007265,GO:0031235,GO:0002121,GO:0046580	CG42684-PI				SM00239,SM00323		PF12004,PF00168	PS50018,PS50003			G3DSA:2.30.29.30,G3DSA:1.10.510.10,G3DSA:2.60.40.150,G3DSA:1.10.506.10,G3DSA:1.10.494.10	SSF48350,SSF48350,SSF50729,SSF49562	1320~1347,1466~1466,1369~1389,551~578								
aly1937.5	Unknown		CG13127-PA						PF15995					SSF101447,SSF101447	24~44								
aly1937.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1937.7	Hormone receptor 4	GO:0048638,GO:0035073,GO:0040007,GO:0043565,GO:0005634,GO:0007552,GO:0003707,GO:0006355,GO:0008270,GO:0043401,GO:0071456,GO:0030518,GO:0004879,GO:0006351	CG43934-PI				SM00430,SM00399		PF00104,PF00105	PS51030	PR00047,PR00047,PR00047,PR00047	PS00031	G3DSA:3.30.50.10,G3DSA:1.10.565.10,G3DSA:1.10.565.10	SSF48508,SSF57716			REACT_71							
aly1937.8	Eukaryotic translation initiation factor 3 subunit I	GO:0006446,GO:0005852,GO:0016282,GO:0005829,GO:0006412,GO:0005515,GO:0033290,GO:0001731,GO:0006413,GO:0005875,GO:0003743	CG8882-PA	MF_03008			SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400	PS50082,PS50082,PS50294,PS50294,PS50082,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978									
aly1937.9	Serine/threonine-protein phosphatase 6 catalytic subunit	GO:0005737,GO:0016787,GO:0000278,GO:0006470,GO:0005829,GO:0000082,GO:0004722,GO:0046872,GO:0007049	CG12217-PD				SM00156		PF00149		PR00114,PR00114,PR00114,PR00114,PR00114,PR00114,PR00114	PS00125	G3DSA:3.60.21.10	SSF56300									
aly194264.1	4-hydroxybutyrate coenzyme A transferase	GO:0008411,GO:0006084,GO:0022008,GO:0005811,GO:0016740	CG7920-PA										G3DSA:3.40.1080.10										
aly19461.1	Unknown	GO:0003677	CG8359-PA				SM00595		PF02944,PF10545	PS51031,PS51029													
aly19461.2	Unknown		n/a												579~599								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly19461.3	Unknown		n/a																				
aly19461.4	Unknown		n/a												2~22								
aly19461.5	Unknown		n/a												354~385,305~325								
aly19461.6	Solute carrier family 22 member 13	GO:0090416,GO:0070062,GO:0016324,GO:0005215,GO:0016021,GO:0008513,GO:0022857,GO:2001142,GO:0015747,GO:0055085	CG42269-PE						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly19477.1	Unknown		n/a																				
aly1949.1	Neuropeptide Y receptor type 2	GO:0003151,GO:0004930,GO:0001601,GO:0036400,GO:0040018,GO:0016021,GO:0005886,GO:0007218,GO:0031513,GO:0004983,GO:0003214,GO:0005887,GO:0008188,GO:0007193,GO:0070374,GO:0007186,GO:2000253	CG7395-PA						PF00001	PS50262	PR01012,PR01012,PR01012,PR01012,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1952.1	Unknown		n/a																				
aly1952.2	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG14205-PA				SM00703		PF01757														
aly1952.3	Insulinoma-associated protein 1a	GO:0043565,GO:0003310,GO:0003309,GO:0003676,GO:0017053,GO:0000122,GO:0003700,GO:0043697,GO:0005634,GO:0010564,GO:0060290,GO:0070654,GO:0031490,GO:0045892,GO:0060221,GO:0001047,GO:0042670,GO:0046872,GO:0006351	CG12809-PB				SM00355,SM00355,SM00355		PF12874	PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly19531.1	Unknown		n/a																				
aly19531.2	Unknown		n/a																				
aly19531.3	Unknown		CG13698-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly19531.4	Unknown		n/a						PF02244				G3DSA:3.30.70.340	SSF54897									
aly19531.5	Unknown		n/a										G3DSA:3.40.630.10										
aly195340.1	Unknown		n/a																				
aly1957.1	Irregular chiasm C-roughest protein	GO:0048749,GO:0016202,GO:0045177,GO:0001745,GO:0046667,GO:0016021,GO:0030165,GO:0046331,GO:0005913,GO:0007409,GO:0005886,GO:0007520,GO:0046666,GO:0007156,GO:0042802	CG4125-PA				SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408		PF07679,PF07679,PF13927,PF13927,PF08205	PS50835,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF48726									
aly19594.1	Unknown		n/a																				
aly19602.1	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0016020,GO:0030672,GO:0006629,GO:0005215,GO:0016021,GO:0006810,GO:0022857,GO:0001669,GO:0005886,GO:0006836,GO:0016298,GO:0055085,GO:0030054	CG31272-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly19602.10	Cadherin-87A	GO:0016339,GO:0016020,GO:0005509,GO:0005887,GO:0005886,GO:0044331,GO:0007156,GO:0016021	CG6977-PA				SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112		PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028	PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00232,PS00232,PS00232,PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313									
aly19602.11	Plasma kallikrein	GO:0004252,GO:0042730,GO:0005615,GO:0097421,GO:0007596,GO:0031639,GO:0006954,GO:0006508,GO:0051919,GO:0070062	CG14892-PA				SM00020		PF00089,PF00089	PS50240	PR00722,PR00722	PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494,SSF50494	253~273								
aly19602.12	Scavenger receptor class B member 1	GO:0034375,GO:0006869,GO:0015914,GO:0043691,GO:0005901,GO:0051000,GO:0070328,GO:0032497,GO:0010867,GO:0005737,GO:0050764,GO:0070062,GO:0010886,GO:0016020,GO:0043654,GO:0035461,GO:0010899,GO:0001786,GO:0042803,GO:0005319,GO:0006702,GO:0008035,GO:0006707,GO:0015920,GO:0009986,GO:0006910,GO:0006952,GO:0043534,GO:0005887,GO:0005886,GO:0007155,GO:0042632,GO:0001530,GO:0030169,GO:0031528,GO:0005044,GO:0006898,GO:0044406,GO:0034384,GO:0005765,GO:0033344,GO:0006694,GO:0034383,GO:0001875,GO:0070506,GO:0001935	CG10345-PA						PF01130		PR01609,PR01609,PR01609												
aly19602.2	Organic cation/carnitine transporter 5	GO:0071472,GO:0016021,GO:0008513,GO:0070417,GO:0022857,GO:0006811,GO:0042631,GO:0009705,GO:0055085,GO:0005524	CG15221-PB										G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly19602.3	Organic cation/carnitine transporter 7	GO:0090416,GO:0090417,GO:0016021,GO:0008513,GO:0022857,GO:2001142,GO:2001143,GO:0005886,GO:0055085,GO:0005524	CG15221-PB						PF07690	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly19602.4	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0030672,GO:0005215,GO:0016021,GO:0007268,GO:0022857,GO:0001669,GO:0006836,GO:0055085,GO:0030054	CG31106-PB						PF07690	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly19602.5	THAP domain containing protein 2	GO:0005730,GO:0003700,GO:0005634,GO:0048813,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG10431-PA				SM00692,SM00980		PF05485	PS50950				SSF57716									
aly19602.6	Protein atonal	GO:0000187,GO:0016330,GO:0045465,GO:0045464,GO:0001748,GO:0003677,GO:0001746,GO:0001745,GO:0007455,GO:0005634,GO:0007438,GO:0048800,GO:0048801,GO:0016360,GO:0000981,GO:0048666,GO:0007605,GO:0008038,GO:0007173,GO:0007423,GO:0045165,GO:0007420,GO:0007399,GO:0007224,GO:0003700,GO:0007460,GO:0045433,GO:0006355,GO:0048813,GO:0045944,GO:0006351,GO:0046983,GO:0046982,GO:0007422	CG7508-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459									
aly19602.7	Unknown		n/a																				
aly19602.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly19602.9	Unknown		n/a							PS51257													
aly1963.1	Unknown		n/a																				
aly1968.1	Tyrosine-protein kinase Dnt	GO:0016203,GO:0006468,GO:0007435,GO:0016204,GO:0016021,GO:0018108,GO:0004714,GO:0046331,GO:0007165,GO:0005886,GO:0007411,GO:0005524,GO:0004713	CG17559-PA				SM00469		PF02019	PS50814			G3DSA:3.30.200.20		239~259								
aly1968.10	Unknown	GO:0006030,GO:0016810,GO:0005576,GO:0005975,GO:0008061	CG31973-PB				SM00494		PF01522,PF01607	PS50940			G3DSA:2.170.140.10,G3DSA:3.20.20.370	SSF57625,SSF88713									
aly1968.11	Glutamate receptor ionotropic, kainate 3	GO:0042391,GO:0007216,GO:0030425,GO:0050907,GO:0001640,GO:0035249,GO:0030054,GO:0032983,GO:0016021,GO:0016020,GO:0015277,GO:0015276,GO:0007215,GO:0004970,GO:0035235,GO:0005234,GO:0045211,GO:0005887,GO:0005886,GO:0042734,GO:0034220,GO:0007196	CG2657-PB						PF00060				G3DSA:3.40.190.10,G3DSA:1.10.287.70	SSF53850,SSF53850									
aly1968.12	Myocyte-specific enhancer factor 2	GO:0007496,GO:0007498,GO:0052576,GO:0001077,GO:0003677,GO:0032968,GO:0007517,GO:0019730,GO:0005634,GO:0007519,GO:0030707,GO:0006366,GO:0010468,GO:0016202,GO:0019915,GO:0048747,GO:0045475,GO:0007520,GO:0007507,GO:0003700,GO:0006355,GO:0046983	CG1429-PH				SM00432		PF12347,PF00319	PS50066	PR00404,PR00404,PR00404	PS00350		SSF55455			REACT_21303						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1968.13	Unknown		n/a																				
aly1968.14	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly1968.15	Peptidylglycine alpha-hydroxylating monooxygenase	GO:0004504,GO:0005615,GO:0032504,GO:0016020,GO:0007613,GO:0055114,GO:0006518,GO:0005507,GO:0001519	CG3832-PB						PF03712,PF01082		PR00790,PR00790,PR00790	PS00085	G3DSA:2.60.120.310,G3DSA:2.60.120.230	SSF49742,SSF49742									
aly1968.16	Unknown		n/a												360~370								
aly1968.17	Unknown		n/a												399~453								
aly1968.18	E3 ubiquitin-protein ligase CCNB1IP1	GO:0061630,GO:0001825,GO:0000795,GO:0016567,GO:0051026,GO:0008270,GO:0007286,GO:0007131,GO:0016874	n/a						PF14634				G3DSA:3.30.40.10		127~182								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1968.19	Unknown		n/a																				
aly1968.2	Glycogenin-1	GO:0005575,GO:0005978,GO:0046872,GO:0008466,GO:0005536	CG44244-PE						PF01501				G3DSA:3.90.550.10	SSF53448									
aly1968.20	Unknown		n/a																				
aly1968.3	Guanine nucleotide exchange factor DBS	GO:0005089,GO:0043065,GO:0005615,GO:0051056,GO:0030027,GO:0097190,GO:0005829,GO:0005886,GO:0005085,GO:0005545,GO:0005575,GO:0035025,GO:0045944,GO:0035023,GO:0048011,GO:0007266,GO:0007264	CG30440-PA				SM00325,SM00516,SM00326,SM00233		PF13716,PF00018,PF00621	PS50002,PS50010,PS50191,PS50003		PS00741	G3DSA:1.20.58.60,G3DSA:2.30.29.30,G3DSA:3.40.525.10,G3DSA:2.30.30.40,G3DSA:1.20.900.10	SSF48065,SSF50729,SSF46966,SSF50044,SSF52087	270~290		REACT_14797,REACT_11044,REACT_11061							
aly1968.4	RNA exonuclease 4	GO:0004527,GO:0000027,GO:0006364,GO:0003676,GO:0005730	CG6833-PA				SM00479		PF00929				G3DSA:3.30.420.10	SSF53098									
aly1968.5	Adenylate kinase	GO:0006172,GO:0046034,GO:0005829,GO:0005811,GO:0005739,GO:0005743,GO:0004017,GO:0005758,GO:0022008,GO:0046033,GO:0005524	CG3140-PA	MF_00235,MF_03168				TIGR01351	PF05191,PF00406		PR00094,PR00094,PR00094,PR00094,PR00094	PS00113	G3DSA:3.40.50.300	SSF52540		00230+2.7.4.3		PWY-7219	UPA00588				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1968.6	Nucleoporin NUP188 homolog	GO:0017056,GO:0005643,GO:0044611,GO:0006999,GO:0015031,GO:0051028	CG8771-PC						PF10487						1852~1852								
aly1968.7	Double-stranded RNA-binding protein Staufen homolog 2	GO:0055059,GO:0008104,GO:0005783,GO:0007616,GO:0005874,GO:0005875,GO:0005737,GO:0045177,GO:0010606,GO:0016020,GO:0045179,GO:0008298,GO:0003730,GO:0007318,GO:0009925,GO:0006403,GO:0048477,GO:0044822,GO:0006810,GO:0046012,GO:0046011,GO:0016324,GO:0008017,GO:0019094,GO:0007317,GO:0007316,GO:0007315,GO:0045180,GO:0005938,GO:0045450,GO:0007400,GO:0045167,GO:0007017,GO:0008595,GO:0005730,GO:0000932,GO:0003725,GO:0045451,GO:0003729	CG5753-PA				SM00358,SM00358,SM00358		PF00035,PF16482	PS50137,PS50137,PS50137,PS50137			G3DSA:3.30.160.20,G3DSA:3.30.160.20,G3DSA:3.30.160.20,G3DSA:3.30.160.20	SSF54768,SSF54768,SSF54768,SSF54768									
aly1968.8	Prolyl endopeptidase	GO:0005737,GO:0004252,GO:0019538,GO:0005634,GO:0016020,GO:0052689,GO:0006508,GO:0070008	CG5355-PA						PF02897,PF00326		PR00862,PR00862,PR00862,PR00862,PR00862,PR00862	PS00708	G3DSA:3.40.50.1820,G3DSA:2.130.10.120	SSF53474,SSF50993									
aly1968.9	PAS domain-containing serine/threonine-protein kinase	GO:0005737,GO:0005794,GO:0006468,GO:0035091,GO:0005634,GO:2000505,GO:0043576,GO:0045719,GO:0004674,GO:0070092,GO:0007165,GO:0004871,GO:0004672,GO:0045727,GO:0046777,GO:0005524	CG3105-PA				SM00220		PF13188,PF00069	PS50112,PS50011		PS00108,PS00107	G3DSA:3.30.450.20,G3DSA:1.10.510.10,G3DSA:3.30.450.20,G3DSA:3.30.200.20	SSF56112,SSF55785,SSF55785									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly196910.1	Protein diaphanous	GO:0008104,GO:0030589,GO:0090303,GO:0017048,GO:0007349,GO:0007279,GO:0005488,GO:0003383,GO:0005912,GO:0051225,GO:0005737,GO:0045177,GO:0045010,GO:0030838,GO:0000281,GO:0005546,GO:0003779,GO:0009306,GO:0016476,GO:0043234,GO:0032507,GO:0030029,GO:0007424,GO:0007605,GO:0032154,GO:0035011,GO:0007283,GO:0051489,GO:0005938,GO:0012506,GO:0022008,GO:0005826,GO:0007111,GO:0007110,GO:0007015,GO:0000915,GO:0005856,GO:0031532,GO:0097320,GO:0005515,GO:0000910,GO:0005884,GO:0045448	CG1768-PD						PF06371					SSF48371										
aly1970.1	Unknown		n/a						PF08828														
aly1970.2	Protein UXT homolog	GO:0006457,GO:0001106,GO:0016272,GO:0051082	CG15266-PA						PF02996		PR01502,PR01502,PR01502,PR01502		G3DSA:1.10.287.370	SSF46579	18~45								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1970.3	Homeobox protein prospero	GO:0055059,GO:0008104,GO:0006909,GO:0007619,GO:0070314,GO:0007419,GO:0010629,GO:0010628,GO:0010001,GO:0003677,GO:0007411,GO:0008049,GO:0001078,GO:0005875,GO:0007416,GO:0007417,GO:0050909,GO:0060385,GO:0000122,GO:0008356,GO:0005634,GO:0045179,GO:0045178,GO:0045664,GO:0008285,GO:0042676,GO:0055060,GO:0045180,GO:0005938,GO:0007409,GO:0005886,GO:0001754,GO:0007405,GO:0042673,GO:0007402,GO:0007400,GO:0190180,GO:0045165,GO:0050771,GO:0007420,GO:0007423,GO:0007422,GO:0003700,GO:0070983,GO:0007465,GO:0045676,GO:0006355,GO:0048813,GO:0006351,GO:0007399,GO:0001708,GO:0007406	CG17228-PI						PF05044				G3DSA:1.10.10.500	SSF46689	277~311,378~401								
aly1970.4	Unknown		n/a																				
aly1970.5	Unknown		n/a																				
aly1975.1	Glycogen [starch] synthase	GO:0004373,GO:0005978,GO:1902350,GO:0045819,GO:0045772,GO:0005776,GO:0031410	CG6904-PA						PF05693				G3DSA:3.40.50.2000	SSF53756,SSF53756		00500+2.4.1.11	REACT_474	PWY-5067	UPA00164				
aly1975.2	Unknown		n/a						PF09104				G3DSA:2.40.50.140,G3DSA:2.40.50.140	SSF50249,SSF50249									
aly1975.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1975.4	Unknown		n/a																				
aly1975.5	Unknown		n/a																				
aly1975.6	Unknown		n/a												33~53								
aly1975.7	Unknown		n/a												96~116								
aly19758.1	Unknown		n/a																				
aly19776.1	Craniofacial development protein 2	GO:0005737,GO:0005634	n/a						PF00078				G3DSA:3.60.10.10	SSF56219									
aly19776.2	Unknown		n/a																				
aly1979.1	Mitochondrial coenzyme A transporter SLC25A42	GO:0005347,GO:0045089,GO:0015228,GO:0015866,GO:0015867,GO:0016021,GO:0080121,GO:0005740,GO:0005739,GO:0080122,GO:0005743,GO:0022857,GO:0043262,GO:0008152,GO:0050829,GO:0035349,GO:0055085,GO:0015217	CG4241-PA						PF00153	PS50920	PR00926,PR00926		G3DSA:1.50.40.10	SSF103506									
aly1979.2	Thioredoxin domain-containing protein 9	GO:0045454,GO:0005623,GO:0005524	CG4511-PA						PF00085				G3DSA:3.40.30.10	SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1979.3	E3 ubiquitin-protein ligase RFWD3	GO:0005737,GO:0016605,GO:0010212,GO:0006281,GO:0097371,GO:0005634,GO:0031571,GO:0016567,GO:0004842,GO:0008270,GO:0005515,GO:0035861,GO:0002039,GO:0016874,GO:1903146,GO:2000001	CG13025-PA				SM00184		PF13639	PS50089			G3DSA:3.30.40.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF57850	224~251								
aly1979.4	BTB/POZ domain-containing protein 7	GO:0005634,GO:0007275,GO:0005515,GO:0060693	CG16952-PA							PS50097			G3DSA:3.30.710.10	SSF54695									
aly1979.5	Unknown		CG6156-PA																				
aly198.1	Unknown	GO:0000723,GO:0003678,GO:0006281	n/a						PF05970														
aly198.2	Netrin receptor UNC5C	GO:0007432,GO:0016021,GO:0006915,GO:0005043,GO:0005042,GO:0007165,GO:0008045,GO:0007411,GO:0007275,GO:0008347	CG8166-PA				SM00218,SM00005,SM00408,SM00209,SM00209,SM00409		PF07679,PF00791,PF00531	PS51145,PS50017,PS50835,PS50092,PS50092			G3DSA:2.60.40.10,G3DSA:1.10.533.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10	SSF48726,SSF82895,SSF82895,SSF47986	1035~1035								
aly198.3	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0006979,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0004601,GO:0055114	CG3477-PA						PF03098,PF03098	PS50292			G3DSA:1.10.640.10,G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									
aly198.4	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098,PF03098	PS50292,PS50292	PR00457,PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10,G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113,SSF48113									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly198.5	Netrin receptor unc-5	GO:0007432,GO:0016021,GO:0005043,GO:0005042,GO:0007165,GO:0008045,GO:0050919,GO:0007411,GO:0008347	CG8166-PA				SM00408,SM00209,SM00209,SM00409,SM00409		PF07679	PS50092,PS50092,PS50835			G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF82895										
aly198.6	PR domain zinc finger protein 8	GO:0003682,GO:0003700,GO:0005634,GO:0003714,GO:0021540,GO:0046974,GO:0006351,GO:0003676,GO:0003677,GO:0045892,GO:0021957,GO:0046872	CG13287-PB				SM00355,SM00355			PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667									
aly198.7	Unknown		n/a																				
aly198003.1	Unknown		n/a																				
aly1981.1	Probable galactose-1-phosphate uridylyltransferase	GO:0006012,GO:0033501,GO:0008108,GO:0005575,GO:0003824,GO:0008270,GO:0008344	CG9232-PA					TIGR00209	PF02744				G3DSA:3.30.428.10	SSF54197		00520+2.7.7.12,00052+2.7.7.12		PWY-6317,PWY-6527	UPA00214				
aly1981.2	Zinc finger protein 27	GO:0005737,GO:0005819,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0046872,GO:0005876,GO:0006351	CG8474-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly19838.1	Spectrin beta chain, non-erythrocytic 5	GO:0032432,GO:0019894,GO:0032029,GO:0030036,GO:0000281,GO:0007009,GO:0007041,GO:0007411,GO:0030507,GO:0005737,GO:0016020,GO:0045505,GO:0005543,GO:0051260,GO:0030707,GO:0003779,GO:0051693,GO:0034452,GO:0032391,GO:0032509,GO:0016324,GO:0008017,GO:0016327,GO:0042060,GO:0010797,GO:0045186,GO:0005912,GO:0006897,GO:0043621,GO:0070062,GO:0097381,GO:0007030,GO:0008091,GO:0008092,GO:0005829,GO:0005515	CG12008-PE						PF00435				G3DSA:1.20.58.60	SSF46966									
aly1984.1	Unknown		n/a																				
aly1984.2	Probable G-protein coupled receptor Mth-like 1	GO:0004930,GO:0007369,GO:0042594,GO:0007472,GO:0016021,GO:0016020,GO:0007476,GO:0006950,GO:0007509,GO:0004888,GO:0007166,GO:0005886,GO:0008340,GO:0070252,GO:0007186	CG4521-PA						PF00002	PS50261													
aly1984.3	Protein-tyrosine sulfotransferase	GO:0006478,GO:0005794,GO:0009306,GO:0016021,GO:0000139,GO:0008476	CG15758-PB						PF13469				G3DSA:3.40.50.300	SSF52540,SSF52540									
aly1984.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1984.5	Helicase domino	GO:0035207,GO:0035222,GO:0002165,GO:0035267,GO:0003677,GO:0007049,GO:0000381,GO:0000123,GO:0006325,GO:0043486,GO:0005634,GO:0045747,GO:0016458,GO:0016573,GO:0048477,GO:0005524,GO:0008283,GO:0004386,GO:0035019,GO:0022008,GO:0036098,GO:0008094,GO:0070983,GO:0010629,GO:0006355,GO:0048813,GO:0006351,GO:0005515,GO:0030097,GO:2000637	CG9696-PG				SM00490,SM00573,SM00487		PF00271,PF00176,PF07529	PS51192,PS51204,PS51194			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	260~280,190~210								
aly1984.6	Unknown		n/a																				
aly1984.7	Helicase domino	GO:0035207,GO:0035222,GO:0002165,GO:0035267,GO:0003677,GO:0007049,GO:0000381,GO:0000123,GO:0006325,GO:0043486,GO:0005634,GO:0045747,GO:0016458,GO:0016573,GO:0048477,GO:0005524,GO:0008283,GO:0004386,GO:0035019,GO:0022008,GO:0036098,GO:0008094,GO:0070983,GO:0010629,GO:0006355,GO:0048813,GO:0006351,GO:0005515,GO:0030097,GO:2000637	CG9696-PG																				
aly19841.1	Membrane-associated transporter protein	GO:0050896,GO:0007601,GO:0048066,GO:0033162,GO:0042438,GO:0016021	CG40467-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1987.1	Unconventional myosin-XVIIIa	GO:0031032,GO:0030017,GO:0003677,GO:0042641,GO:0000146,GO:0042623,GO:0090164,GO:0016020,GO:0090161,GO:0016459,GO:0016477,GO:0003774,GO:0005524,GO:0048194,GO:0005793,GO:0044822,GO:0043066,GO:0030898,GO:0008150,GO:0051015,GO:0043531,GO:0007030,GO:0050714,GO:0005802,GO:0000139,GO:0006259	CG31045-PB				SM00242,SM00228		PF00063	PS50106,PS51456	PR00193,PR00193		G3DSA:2.30.42.10,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF50156,SSF50156	1351~1353,105~125								
aly1987.2	Fatty acid-binding protein	GO:0005737,GO:0007616,GO:0005215,GO:0006810,GO:0008289,GO:0005504,GO:0005875	CG6783-PC						PF00061		PR00178,PR00178,PR00178	PS00214	G3DSA:2.40.128.20	SSF50814									
aly1987.3	Unknown		n/a																				
aly1987.4	Transcription factor Adf-1	GO:0040011,GO:0006366,GO:0050773,GO:0007616,GO:0005634,GO:0005705,GO:0007613,GO:0007611,GO:0005575,GO:0048813,GO:0046331,GO:0003674,GO:0045893,GO:0005667,GO:0003677,GO:0001077,GO:0045944,GO:0008345,GO:0003712,GO:0007416,GO:0008355	CG8765-PA				SM00595		PF10545	PS51029,PS50090			G3DSA:1.10.10.60	SSF46689									
aly19870.1	Unknown		n/a																				
aly19878.1	Dual specificity protein phosphatase 13 isoform B	GO:0007126,GO:0008138,GO:0006470,GO:0004725,GO:0005575,GO:0007283	CG7378-PC				SM00195		PF00782	PS50056,PS50054		PS00383	G3DSA:3.90.190.10	SSF52799									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly198914.1	Unknown	GO:0043190,GO:0042626,GO:0005215,GO:0006810,GO:0005886,GO:0005524	CG9990-PA																				
aly1992.1	Unknown		n/a																				
aly1992.2	Unknown		n/a																				
aly199236.1	Histone acetyltransferase KAT7	GO:0009996,GO:0003713,GO:0043982,GO:0008270,GO:0010485,GO:0000123,GO:0005634,GO:0004402,GO:0005654,GO:0016458,GO:0006260,GO:0016747,GO:0016360,GO:0046529,GO:0048666,GO:0048190,GO:0043966,GO:0008134,GO:0022416,GO:0045892,GO:0003700,GO:0043983,GO:0043981,GO:0006355,GO:0048813,GO:0045944,GO:0006351	CG5229-PA						PF01853	PS51726			G3DSA:3.40.630.30	SSF55729									
aly1993.1	Turripeptide Lol9.1	GO:0005615,GO:0032504,GO:0005576,GO:0005515,GO:0004867,GO:0004857,GO:0043086	CG42474-PA				SM00280		PF07648	PS51465		PS00282	G3DSA:3.30.60.30	SSF100895									
aly1993.2	Pancreatic secretory trypsin inhibitor	GO:0090281,GO:0070062,GO:0050732,GO:0060046,GO:0010751,GO:0005515,GO:0004867,GO:2001256,GO:1900004,GO:0005615	CG45011-PA				SM00280		PF00050	PS51465		PS00282	G3DSA:3.30.60.30	SSF100895									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly1993.3	Unknown		n/a				SM00280		PF07648	PS51465		PS00282	G3DSA:3.30.60.30	SSF100895									
aly1993.4	Unknown		n/a				SM00280		PF07648	PS51465		PS00282	G3DSA:3.30.60.30	SSF100895									
aly199740.1	Succinate dehydrogenase [ubiqui] flavoprotein subunit A, mitochondrial	GO:0050660,GO:0005739,GO:0006105,GO:0005743,GO:0006099,GO:0022900,GO:0008177,GO:0022904,GO:0004776,GO:0005749	CG17246-PB										G3DSA:3.50.50.60										
aly2.1	Filamin-A	GO:0008104,GO:0035204,GO:0015629,GO:0048149,GO:0035324,GO:0007611,GO:0007301,GO:0007303,GO:0008045,GO:0007067,GO:0008355,GO:0035183,GO:0035182,GO:0030708,GO:0030725,GO:0005634,GO:0045179,GO:0003779,GO:0005886,GO:0048471,GO:0005884,GO:0008302,GO:0008340,GO:0005829,GO:0051495	CG3937-PM				SM00557,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557,SM00557		PF00630,PF00630,PF00630,PF00630,PF00630,PF00630,PF00630,PF00630	PS50194,PS50194,PS50194,PS50194,PS50194,PS50194,PS50194,PS50194			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF81296,SSF81296,SSF81296,SSF81296,SSF81296,SSF81296,SSF81296,SSF81296									
aly2.2	Zinc finger protein rotund	GO:0048749,GO:0000122,GO:0003700,GO:0005634,GO:0007480,GO:0003705,GO:0006355,GO:0022416,GO:0045892,GO:0006351,GO:0003676,GO:0046872,GO:0001708	CG32466-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2.3	Unknown		n/a																				
aly200.1	Kynureninase	GO:0005737,GO:0030429,GO:0034354,GO:0097053,GO:0019805,GO:0030170,GO:0043420,GO:0006569	n/a	MF_01970		PIRSF038800		TIGR01814	PF00266				G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383		00380+3.7.1.3		PWY-5651,PWY-6309	UPA00334,UPA00253				
aly200.2	Cytochrome b-c1 complex subunit 2, mitochondrial	GO:0004222,GO:0070062,GO:0005750,GO:0043209,GO:0005811,GO:0008121,GO:0006122,GO:0005739,GO:0005743,GO:0003824,GO:0009060,GO:0044237,GO:0022904,GO:0046872,GO:0044281,GO:0005875,GO:0006119	CG4169-PA						PF00675,PF08213				G3DSA:3.30.830.10,G3DSA:3.30.830.10	SSF63411,SSF63411									
aly200.3	Cytochrome P450 6k1	GO:0004497,GO:0016020,GO:0043231,GO:0020037,GO:0016705,GO:0005789,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG8859-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly20048.1	Deoxycytidylate deaminase	GO:0004132,GO:0003824,GO:0009165,GO:0008270,GO:0006220	CG6951-PB						PF00383	PS51747			G3DSA:3.40.140.10	SSF53927									
aly2007.1	Unknown	GO:0003674,GO:0005576,GO:0008150	CG13532-PA										G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2007.2	Cytochrome P450 6a2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0046680,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly2007.3	Unknown	GO:0003674,GO:0005576,GO:0008150,GO:0005515	CG13532-PA										G3DSA:2.60.40.10	SSF48726									
aly2007.4	Unknown	GO:0006030,GO:0005576,GO:0008061	CG32036-PC				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly2007.5	Unknown		n/a																				
aly2007.6	Unknown		n/a																				
aly2007.7	Unknown		n/a																				
aly200885.1	Unknown		n/a																				
aly200934.1	PHD finger-like domain-containing protein 5A	GO:0016607,GO:0071011,GO:0071013,GO:0000398,GO:0003700,GO:0045893,GO:0005689,GO:0003677,GO:0005686,GO:0016363,GO:0044822,GO:0006351	CG9548-PA						PF03660														
aly2011.1	Phospholipase A2 isozymes PA3A/PA3B/PA5	GO:0004623,GO:0006644,GO:0005576,GO:0005509,GO:0016042	CG42237-PA						PF05826			PS00118	G3DSA:1.20.90.10	SSF48619		00564+3.1.1.4,00590+3.1.1.4,00592+3.1.1.4,00591+3.1.1.4,00565+3.1.1.4		PWY-7409,PWY-7417,PWY-6803,PWY-7416					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2011.10	WD repeat-containing protein 24	GO:0007031,GO:0035859,GO:0005053	CG7609-PC				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400	PS50082,PS50082,PS50294,PS50082		PS00678,PS00678,PS00678	G3DSA:2.130.10.10	SSF50978									
aly2011.11	Ubiquitin carboxyl-terminal hydrolase 30 homolog	GO:1901562,GO:0044313,GO:0016021,GO:0005741,GO:0035871,GO:0006511,GO:0016579,GO:0004843	CG3016-PA											SSF54001									
aly2011.12	Ubiquitin carboxyl-terminal hydrolase 30 homolog	GO:1901562,GO:0044313,GO:0016021,GO:0035871,GO:0004843,GO:0005741,GO:0006511,GO:0016579,GO:0036459	CG3016-PA						PF00443	PS50235		PS00973		SSF54001,SSF54001									
aly2011.13	Eukaryotic translation initiation factor 6	GO:0005737,GO:0042273,GO:0005730,GO:0005829,GO:0000054,GO:0042256,GO:0043023,GO:0043022,GO:0006413,GO:0006412,GO:0003743	CG17611-PA	MF_00032		PIRSF006413	SM00654	TIGR00323	PF01912				G3DSA:3.75.10.10	SSF55909									
aly2011.14	E3 ubiquitin-protein ligase MARCH3	GO:0006897,GO:0016567,GO:0016874,GO:0016021,GO:0005764,GO:0030659,GO:0008270,GO:0005768,GO:0031901	CG13442-PA				SM00744		PF12906	PS51292			G3DSA:3.30.40.10	SSF57850					UPA00143				
aly2011.15	Smoothelin-like protein 1	GO:0005856,GO:0005737,GO:0005200,GO:0045907,GO:0007498,GO:0005634,GO:0045908,GO:0031674,GO:0003779,GO:0031430,GO:0005515,GO:0043292,GO:0005875	CG34417-PT				SM00033		PF00307,PF12510,PF12510	PS50021			G3DSA:1.10.418.10	SSF47576	3777~3780,2357~2377								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2011.16	Unknown	GO:0016772	CG9259-PA				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly2011.17	Unknown	GO:0016772	CG9259-PA				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly2011.18	Unknown	GO:0005737,GO:0005634,GO:0070883,GO:0003725,GO:0000785,GO:0005515,GO:0003682	CG17686-PD				SM00358			PS50137			G3DSA:3.30.160.20	SSF54768									
aly2011.19	Unknown	GO:0005634,GO:0003725,GO:0035197	CG12493-PA				SM00358		PF00035	PS50137			G3DSA:3.30.160.20	SSF54768									
aly2011.2	Rab GTPase-binding effector protein 1	GO:0005737,GO:0006897,GO:0043231,GO:0055037,GO:0006915,GO:0005096,GO:0017137,GO:0030139,GO:0016192,GO:0008270,GO:0015031,GO:0005768,GO:0005769,GO:0042803	CG4030-PA				SM00064		PF09311,PF09311,PF01363,PF03528	PS50178,PS50089			G3DSA:3.30.40.10,G3DSA:1.20.5.730	SSF57903	55~96,30~50,377~397,223~257,440~505,174~201,111~138								
aly2011.20	Tip elongation aberrant protein 1	GO:0031500,GO:0003700,GO:0005634,GO:0051285,GO:0010570,GO:0051286,GO:0015630,GO:0071963,GO:0005515,GO:0035839,GO:0035838,GO:0005874,GO:0032153,GO:0034613,GO:2000771	CG3711-PD						PF13418,PF13418,PF01344				G3DSA:2.120.10.80,G3DSA:2.120.10.80	SSF117281,SSF117281									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2011.21	Ras-related protein M-Ras	GO:0030742,GO:0070062,GO:0016020,GO:0003924,GO:0005622,GO:0005575,GO:0019003,GO:0005515,GO:0005886,GO:0006184,GO:0007265,GO:0007264,GO:0005525	CG1167-PA				SM00173,SM00175,SM00174	TIGR00231	PF00071	PS51421	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly2011.22	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0045455,GO:0055114,GO:0016491	CG9512-PA			PIRSF000137			PF05199,PF00732			PS00623	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly2011.23	Calcitonin receptor	GO:0008036,GO:0004930,GO:0016021,GO:0016020,GO:0005887,GO:0008188,GO:0005886,GO:0007186,GO:0004948	CG32843-PC				SM00008		PF02793,PF00002	PS50227,PS50261	PR00249,PR00249,PR00249	PS00649		SSF111418									
aly2011.24	Unknown		n/a																				
aly2011.25	Unknown	GO:0005856,GO:0003779,GO:0005200,GO:0005875,GO:0007498	CG34417-PT												566~586								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2011.3	Structural maintenance of chromosomes protein 1B	GO:0016319,GO:0000794,GO:0010629,GO:0003677,GO:0007064,GO:0008278,GO:0007062,GO:0005737,GO:0007126,GO:0005634,GO:0000800,GO:0005654,GO:0005694,GO:0005524,GO:0030893,GO:0016322,GO:0035327,GO:0034991,GO:0000795,GO:0000775,GO:0046982,GO:0005700,GO:0048813,GO:0003682	CG6057-PA				SM00968		PF02463,PF06470				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF75553	195~229,238~293,727~747,958~985,305~356,923~950,367~412,832~859,679~703,430~464								
aly2011.4	Transmembrane protein 222	GO:0016021	CG8372-PB						PF05608,PF05608														
aly2011.5	Unknown	GO:0005575,GO:0003674,GO:0008150	CG15891-PA							PS51497													
aly2011.6	Histone deacetylase 4	GO:0005737,GO:0016575,GO:0032041,GO:0007399,GO:0030183,GO:0006325,GO:0004407,GO:0005634,GO:0008134,GO:0042113,GO:0000118,GO:0006355,GO:0045892,GO:0006351,GO:0006954,GO:0046872,GO:0045843,GO:0016568	CG1770-PG						PF00850		PR01270,PR01270,PR01270		G3DSA:3.40.800.20,G3DSA:3.40.800.20	SSF52768									
aly2011.7	WD repeat-containing protein mio-B	GO:0043234,GO:0040020,GO:0006302,GO:0051082,GO:0030716,GO:0007294,GO:0006457,GO:0035859	CG7074-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2011.8	WD repeat-containing protein mio	GO:0043234,GO:0045793,GO:0040020,GO:0006302,GO:0009994,GO:0007294,GO:0032008,GO:0051082,GO:0030716,GO:0005515,GO:0034198,GO:0006457,GO:0001674,GO:0035859,GO:0007275	CG7074-PA										G3DSA:2.130.10.10	SSF50978									
aly2011.9	Ras-related protein Ral-a	GO:0022604,GO:0008152,GO:0045087,GO:0005886,GO:0003924,GO:0007464,GO:0007391,GO:0005622,GO:0046329,GO:0030165,GO:0045824,GO:0005515,GO:0008593,GO:0050829,GO:0006184,GO:0007265,GO:0007298,GO:0005525	CG2849-PA				SM00175,SM00173,SM00174	TIGR00231	PF00071	PS51421	PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly2012.1	Protein jim lovell	GO:0031987,GO:0030536,GO:0042332,GO:0048060,GO:0005634,GO:0007418,GO:0003677,GO:0008049,GO:0048477,GO:0008346	CG16778-PE				SM00225		PF05225,PF00651	PS50097,PS50960			G3DSA:3.30.710.10	SSF46689,SSF54695									
aly2012.10	Unknown	GO:0005575,GO:0003674,GO:0008150	CG5080-PB												244~264,192~216,152~172								
aly2012.11	UPF0047 protein YjbQ	GO:0005575,GO:0008150,GO:0003674	CG31688-PF					TIGR00149	PF01894			PS01314	G3DSA:2.60.120.460	SSF111038									
aly2012.12	Transmembrane inner ear expressed protein	GO:0007605,GO:0016021,GO:0042472	CG15130-PB						PF16038														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.13	Actin-related protein 2/3 complex subunit 2	GO:0003779,GO:0008360,GO:0005200,GO:0000902,GO:0030031,GO:0045179,GO:0030866,GO:0008064,GO:0046331,GO:0005885,GO:0034314	CG10954-PA						PF04045				G3DSA:3.30.1460.20,G3DSA:3.30.1460.20	SSF69645,SSF69645									
aly2012.14	Target of rapamycin	GO:0051124,GO:0016310,GO:0008144,GO:0009594,GO:0032645,GO:0007411,GO:0005622,GO:0007049,GO:0040007,GO:0042331,GO:0008406,GO:0004672,GO:0046622,GO:0005524,GO:0006468,GO:2000331,GO:0007584,GO:0016301,GO:0030307,GO:2000377,GO:0006974,GO:0001558,GO:0007520,GO:0008340,GO:2001023,GO:0007525,GO:0043621,GO:0045793,GO:0016773,GO:0040018,GO:0090070,GO:0000724,GO:0016242,GO:0048813,GO:0032456,GO:0046983,GO:0001934	CG5092-PB				SM00146		PF00454,PF08771,PF11865,PF02259,PF02260	PS51190,PS50290,PS51189		PS00915,PS00916	G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.40.10,G3DSA:3.30.1010.10,G3DSA:1.10.1070.11,G3DSA:1.10.1070.11,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.20.120.150	SSF47212,SSF56112,SSF56112,SSF48371,SSF48371,SSF48371,SSF48371	1374~1394								
aly2012.15	Cytidine deaminase	GO:0003824,GO:0004126,GO:0008270,GO:0009972	CG8360-PA					TIGR01354	PF00383	PS51747		PS00903	G3DSA:3.40.140.10	SSF53927		00240+3.5.4.5,00983+3.5.4.5		PWY-7193,PWY-7199,PWY-7181,PWY-6556					
aly2012.16	Target of rapamycin	GO:0051124,GO:0016310,GO:0008144,GO:0009594,GO:0032645,GO:0007411,GO:0005622,GO:0007049,GO:0040007,GO:0042331,GO:0008406,GO:0004672,GO:0046622,GO:0005524,GO:0006468,GO:0032456,GO:2000331,GO:0007584,GO:0016301,GO:0030307,GO:2000377,GO:0006974,GO:0001558,GO:0007520,GO:0008340,GO:2001023,GO:0007525,GO:0043621,GO:0045793,GO:0016773,GO:0040018,GO:0090070,GO:0000724,GO:0016242,GO:0048813,GO:0005515,GO:0046983,GO:0001934	CG5092-PB				SM00146		PF02260,PF02259,PF08771,PF11865,PF00454	PS51190,PS50290,PS51189		PS00916,PS00915	G3DSA:3.30.1010.10,G3DSA:1.25.40.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.10.1070.11,G3DSA:1.10.1070.11,G3DSA:1.10.1070.11,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48371,SSF48371,SSF56112,SSF56112,SSF47212,SSF48371,SSF48371	48~68								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.17	Ubiquitin conjugation factor E4 B	GO:0005737,GO:0008626,GO:0034450,GO:0006457,GO:0009411,GO:0016874,GO:0005634,GO:0000151,GO:0019899,GO:0016567,GO:0006511,GO:0042787,GO:0051082,GO:0043161,GO:0004842	CG9934-PA				SM00504		PF04564,PF10408	PS51698			G3DSA:3.30.40.10	SSF57850					UPA00143				
aly2012.18	UbiA prenyltransferase domain-containing protein 1 homolog	GO:0004659,GO:0016021,GO:0016020,GO:0005739,GO:0031966,GO:0012505,GO:0009234	CG5876-PA			PIRSF005355		TIGR00751	PF01040														
aly2012.19	Sedoheptulokinase	GO:0005737,GO:0005975,GO:0016773,GO:0016310,GO:0071353,GO:0050727,GO:0046835,GO:0035963,GO:0050277,GO:0009052,GO:0071222,GO:0043030,GO:0005524	n/a						PF00370				G3DSA:3.30.420.40	SSF53067,SSF53067,SSF53067									
aly2012.2	Tat-binding homolog 7	GO:0008104,GO:0008103,GO:0005783,GO:0043523,GO:0000226,GO:0043525,GO:0016887,GO:0032436,GO:0005875,GO:0046598,GO:0042052,GO:0005737,GO:0007029,GO:0005811,GO:0006200,GO:0006508,GO:0005524,GO:0098586,GO:0016320,GO:0017111,GO:0007317,GO:0030433,GO:0000502,GO:0045451,GO:0007030,GO:0031445,GO:0045169,GO:0048813,GO:0006511,GO:0006351,GO:0005515	CG2331-PC				SM00382,SM00297		PF00439,PF00004	PS50014	PR00503,PR00503,PR00503,PR00503	PS00674,PS00633	G3DSA:3.40.50.300,G3DSA:1.10.8.60,G3DSA:1.20.920.10	SSF52540,SSF47370	216~243								
aly2012.20	Unknown		n/a												164~198								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.21	Zinc finger CCHC domain containing protein 9	GO:0044822,GO:0010923,GO:0008270,GO:0003676	n/a				SM00343,SM00343,SM00343,SM00343		PF00098,PF00098	PS50158,PS50158			G3DSA:4.10.60.10,G3DSA:4.10.60.10,G3DSA:4.10.60.10	SSF57756,SSF57756	28~48,294~314								
aly2012.22	Protein msta, isoform A	GO:0008168,GO:0010629,GO:0042826	CG43129-PD						PF00856				G3DSA:2.170.270.10,G3DSA:2.170.270.10	SSF82199,SSF82199									
aly2012.23	Voltage-dependent anion-selective channel	GO:0030382,GO:0006811,GO:0005811,GO:0005739,GO:0055085,GO:0007291,GO:0006839,GO:0006820,GO:0005741,GO:0005875,GO:0015288,GO:0016006,GO:0007602,GO:0046930,GO:0044070,GO:1903959,GO:0008308,GO:0007005	CG6647-PA						PF01459		PR00185,PR00185,PR00185,PR00185		G3DSA:2.40.160.10										
aly2012.24	COP9 signalosome complex subunit 4	GO:0044212,GO:0070062,GO:0019781,GO:0032435,GO:0000338,GO:0010388,GO:0005634,GO:0005654,GO:0008021,GO:0050821,GO:0046331,GO:0005515,GO:0007095,GO:0001751,GO:0030054,GO:0008180	CG8725-PA				SM00088		PF01399				G3DSA:1.10.10.10	SSF46785									
aly2012.25	Protein lin-54	GO:0000794,GO:0000122,GO:0031523,GO:0007307,GO:0001046,GO:0005700,GO:0070176,GO:0006357,GO:0000785,GO:0006351,GO:0005515,GO:0003677,GO:0030849,GO:0008340,GO:0005634,GO:0048477,GO:0030317,GO:0007049	CG6061-PB						PF03638,PF03638	PS51634													
aly2012.26	Protein msta, isoform A	GO:0008168,GO:0010629,GO:0042826	CG9642-PA						PF00856	PS50280			G3DSA:2.170.270.10,G3DSA:2.170.270.10	SSF82199,SSF82199									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.27	Erlin-2-B	GO:0016021,GO:0005789,GO:0008203	n/a				SM00244		PF01145														
aly2012.28	Elongation factor 1-beta'	GO:0003747,GO:0005853,GO:0005829,GO:0005811,GO:0005085,GO:0003746,GO:0006414	CG6341-PB				SM00888		PF10587,PF00736			PS00824,PS00825	G3DSA:1.20.1050.10,G3DSA:3.30.70.60	SSF47616,SSF54984			REACT_17015,REACT_71						
aly2012.29	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	GO:0008637,GO:0046872,GO:0051539,GO:0008137,GO:0051536,GO:0051537,GO:0005739,GO:0042773,GO:0045333,GO:0005747,GO:0009055,GO:0003954,GO:0055114,GO:0016491	CG2286-PA				SM00929	TIGR01973	PF13510,PF09326,PF10588,PF00384	PS51085,PS51669		PS00643,PS00642,PS00641	G3DSA:3.40.50.740,G3DSA:3.40.50.740,G3DSA:3.40.50.740,G3DSA:3.10.20.30	SSF54292,SSF54862,SSF53706										
aly2012.3	Uncharacterized protein C17orf59 homolog		CG17180-PA						PF10157						229~249,155~175								
aly2012.30	Reversion-inducing cysteine-rich protein with Kazal motifs	GO:0045747,GO:0001955,GO:0005886,GO:0035115,GO:0030198,GO:0004866,GO:0004867,GO:0010951,GO:0007566,GO:0031225	CG5392-PA																				
aly2012.31	Brefeldin A-inhibited guanine nucleotide-exchange protein 3	GO:0005802,GO:0016192,GO:0016021,GO:0010923,GO:0005086,GO:0032012,GO:0043547	CG5937-PC				SM00222		PF16213,PF09324				G3DSA:1.10.1000.11	SSF48425,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371	162~182								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.32	NADH dehydrogenase [ubiqui] 1 beta subcomplex subunit 5, mitochondrial	GO:0008137,GO:0016021,GO:0000302,GO:0005743,GO:0005747,GO:0008340,GO:0070469,GO:0006120,GO:0003954,GO:0055114	CG9762-PA						PF09781						133~153								
aly2012.33	Reticulocyte-binding protein 2 homolog a	GO:0016337,GO:0016021,GO:0016020,GO:0008270,GO:0005886,GO:0008201	CG8910-PA						PF13920	PS50089			G3DSA:3.30.40.10	SSF57850	42~62,384~456								
aly2012.34	Unknown		n/a						PF03372				G3DSA:3.60.10.10	SSF56219									
aly2012.35	Unknown		n/a												94~142								
aly2012.36	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.37	Glutamate receptor ionotropic, kainate 3	GO:0042391,GO:0015277,GO:0060025,GO:0030425,GO:0030424,GO:0008066,GO:0004872,GO:0001640,GO:0035249,GO:0004970,GO:0032983,GO:0016020,GO:0007216,GO:0007215,GO:0007268,GO:0030054,GO:0005216,GO:0032839,GO:0035235,GO:0006811,GO:0005234,GO:0034220,GO:0005887,GO:0005886,GO:0043204,GO:0043195,GO:0042734,GO:0045211,GO:0051967,GO:0007196	CG5621-PC				SM00079,SM00918		PF00060,PF10613,PF01094		PR00177,PR00177		G3DSA:3.40.50.2300,G3DSA:1.10.287.70,G3DSA:3.40.190.10,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300	SSF53822,SSF53850,SSF53850									
aly2012.38	Glutamate receptor ionotropic, kainate 3	GO:0042391,GO:0015277,GO:0060025,GO:0030425,GO:0030424,GO:0008066,GO:0004872,GO:0001640,GO:0035249,GO:0004970,GO:0032983,GO:0016020,GO:0007216,GO:0007215,GO:0007268,GO:0030054,GO:0005216,GO:0032839,GO:0035235,GO:0006811,GO:0005234,GO:0034220,GO:0005887,GO:0005886,GO:0043204,GO:0043195,GO:0042734,GO:0045211,GO:0051967,GO:0007196	CG5621-PC				SM00918,SM00079		PF10613,PF01094,PF00060		PR00177,PR00177,PR00177		G3DSA:3.40.190.10,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:1.10.287.70	SSF53850,SSF53850,SSF53822									
aly2012.39	Unknown		n/a																				
aly2012.4	Putative nuclease HARBI1	GO:0005737,GO:0005813,GO:0005634,GO:0046872,GO:0004518	CG7492-PA						PF13359														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.40	Glutamate receptor ionotropic, kainate 2	GO:0060025,GO:0019228,GO:0050806,GO:0030425,GO:0050804,GO:0043524,GO:0043525,GO:0060080,GO:0046328,GO:0048169,GO:0035249,GO:0030054,GO:0001662,GO:0032983,GO:0006886,GO:0016020,GO:0015277,GO:0007215,GO:0007268,GO:0004970,GO:0032839,GO:0035235,GO:0006874,GO:0006811,GO:0006810,GO:0005234,GO:0034220,GO:0051402,GO:0014069,GO:0005887,GO:0005886,GO:0060079,GO:0043204,GO:0043195,GO:0042734,GO:0045211,GO:0051967,GO:0048172,GO:0043113	CG3822-PA				SM00079,SM00918		PF10613,PF00060,PF01094		PR00177,PR00177,PR00177,PR00177		G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:1.10.287.70,G3DSA:3.40.50.2300,G3DSA:3.40.190.10	SSF53850,SSF53850,SSF81324,SSF53822										
aly2012.41	Glutamate receptor ionotropic, kainate 2	GO:0042391,GO:0032839,GO:0060025,GO:0019228,GO:0050806,GO:0030425,GO:0050804,GO:0043524,GO:0043525,GO:0060080,GO:0046328,GO:0048169,GO:0035249,GO:0004970,GO:0001662,GO:0032983,GO:0006886,GO:0016020,GO:0015277,GO:0030054,GO:0043025,GO:0008328,GO:0035235,GO:0006874,GO:0006811,GO:0005234,GO:0034220,GO:0051402,GO:0014069,GO:0007268,GO:0005886,GO:0060079,GO:0043204,GO:0043195,GO:0042734,GO:0045211,GO:0051967,GO:0048172,GO:0043113,GO:0045202	CG8681-PB				SM00918,SM00079		PF10613,PF01094,PF00060		PR00177,PR00177,PR00177		G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:1.10.287.70,G3DSA:3.40.190.10	SSF53822,SSF81324,SSF53850,SSF53850										
aly2012.42	Glutamate receptor ionotropic, kainate 2	GO:0060025,GO:0019228,GO:0050806,GO:0030425,GO:0050804,GO:0043524,GO:0043525,GO:0060080,GO:0046328,GO:0048169,GO:0035249,GO:0030054,GO:0001662,GO:0032983,GO:0006886,GO:0015277,GO:0007215,GO:0007268,GO:0032839,GO:0035235,GO:0006874,GO:0006811,GO:0006810,GO:0005234,GO:0034220,GO:0051402,GO:0014069,GO:0005887,GO:0005886,GO:0060079,GO:0043204,GO:0043195,GO:0042734,GO:0045211,GO:0051967,GO:0048172,GO:0043113	CG3822-PA				SM00918,SM00079		PF00060,PF01094,PF10613		PR00177,PR00177,PR00177		G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.190.10,G3DSA:1.10.287.70,G3DSA:3.40.50.2300	SSF81324,SSF53850,SSF53850,SSF53822										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.43	Glutamate receptor ionotropic, kainate 3	GO:0042391,GO:0060025,GO:0030425,GO:0030424,GO:0008066,GO:0007165,GO:0035249,GO:0030054,GO:0032983,GO:0016020,GO:0015277,GO:0004970,GO:0005886,GO:0032839,GO:0035235,GO:0006811,GO:0005234,GO:0045211,GO:0007268,GO:0043204,GO:0043195,GO:0042734,GO:0034220,GO:0051967	CG3822-PA				SM00079,SM00918		PF10613,PF01094,PF00060				G3DSA:3.40.190.10,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:1.10.287.70,G3DSA:3.40.50.2300	SSF53850,SSF53850,SSF53822,SSF81324										
aly2012.44	Unknown	GO:0006629,GO:0008081	CG5895-PA										G3DSA:3.20.20.190,G3DSA:3.20.20.190	SSF51695									
aly2012.45	Palmitoleoyl-protein carboxylesterase notum1a	GO:0090090,GO:0019213,GO:0048190,GO:0005615,GO:0048076,GO:0016055,GO:1990697,GO:0006029,GO:0021532,GO:0006507,GO:1990699,GO:0005576,GO:0030178,GO:0009952	CG13076-PA						PF03283				G3DSA:3.40.50.1820										
aly2012.46	Protein unc-13 homolog D	GO:0008021,GO:0002432,GO:0006909,GO:0005515,GO:0002467,GO:1900026,GO:0043304,GO:0055037,GO:0016082,GO:0033093,GO:0017137,GO:0045921,GO:0070382,GO:0005770,GO:0043320,GO:0003674,GO:0005764,GO:0007269,GO:1903307,GO:0016020,GO:0051607	CG34349-PC				SM00239,SM00239		PF00168,PF00168	PS51259,PS51258,PS50004,PS50004	PR00360,PR00360,PR00360		G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562,SSF49562									
aly2012.47	Succinate-semialdehyde dehydrogenase, mitochondrial	GO:0007417,GO:0004029,GO:0051287,GO:0031406,GO:0016620,GO:0005739,GO:0006105,GO:0009013,GO:0008152,GO:0009450,GO:0004777,GO:0055114,GO:0016491	CG4685-PE						PF00171			PS00687,PS00070	G3DSA:3.40.309.10,G3DSA:3.40.605.10	SSF53720									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.48	Unknown		n/a																				
aly2012.49	Unknown		CG14569-PA																				
aly2012.5	Monocyte to macrophage differentiation factor 2	GO:0019835,GO:0006468,GO:0006909,GO:0016021,GO:0046579,GO:0000139,GO:0045666,GO:0004672,GO:0048471,GO:0045860,GO:0022008,GO:0032880	CG4615-PA					TIGR01065	PF03006														
aly2012.50	Ribonuclease H2 subunit A	GO:0016070,GO:0090502,GO:0006298,GO:0004523,GO:0032299,GO:0043137,GO:0003723,GO:0046872	CG13690-PA					TIGR00729	PF01351				G3DSA:3.30.420.10,G3DSA:1.10.10.460	SSF53098									
aly2012.51	Zinc finger and BTB domain-containing protein 17	GO:0001702,GO:0006351,GO:0007398,GO:0003700,GO:0005634,GO:1903955,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:1903146,GO:0045893	CG17328-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF13912,PF13894	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly2012.52	Protein FRA10AC1 homolog	GO:0005634	CG16890-PA						PF09725														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.53	Cytosolic purine 5'-nucleotidase	GO:0005737,GO:0006139,GO:0016311,GO:0005829,GO:0008253,GO:0000166,GO:0046040,GO:0046872,GO:0046085,GO:0042802	CG32549-PG					TIGR02244	PF05761				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF56784									
aly2012.54	Unknown		n/a																				
aly2012.55	BRCA1-A complex subunit Abraxas	GO:0031572,GO:0006302,GO:0005634,GO:0031593,GO:0070531,GO:0010212,GO:0045739,GO:0016568	n/a								PR02051,PR02051,PR02051,PR02051				222~256								
aly2012.56	Hermansky-Pudlak syndrome 1 protein homolog	GO:0060967,GO:0003674,GO:0031085,GO:0006909	CG12855-PA												289~309								
aly2012.57	Dihydroorotate dehydrogenase (qui), mitochondrial	GO:0005737,GO:0006222,GO:0006207,GO:0016021,GO:0016020,GO:0004158,GO:0005743,GO:0044205,GO:0005758,GO:0004152,GO:0055114	CG9741-PA					TIGR01036	PF01180			PS00911,PS00912	G3DSA:3.20.20.70	SSF51395		00240+1.3.5.2		PWY-5686	UPA00070				
aly2012.58	ATP synthase subunit s, mitochondrial	GO:0045263,GO:0046872,GO:0015992,GO:0000276,GO:0005739,GO:0005743,GO:0008553,GO:0006754	CG10731-PB										G3DSA:3.80.10.10	SSF52047									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.59	Ras-related protein Rab-4B	GO:0055037,GO:0006897,GO:0031982,GO:0048471,GO:0030100,GO:0006886,GO:0016020,GO:0003924,GO:0005739,GO:0032482,GO:0046323,GO:0016192,GO:0007165,GO:0008152,GO:0005886,GO:0045202,GO:0032593,GO:0043025,GO:0015031,GO:0005525	CG4921-PB				SM00173,SM00174,SM00175		PF00071	PS51419	PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly2012.6	Arginine--tRNA ligase, cytoplasmic	GO:0005737,GO:0034618,GO:0017101,GO:0004812,GO:0004814,GO:0006420,GO:0016020,GO:0005739,GO:0000166,GO:0005654,GO:0000049,GO:0006418,GO:0005524,GO:0070062	CG9020-PA				SM01016,SM00836	TIGR00456	PF03485,PF05746,PF00750		PR01038,PR01038,PR01038,PR01038	PS00178	G3DSA:1.10.730.10,G3DSA:3.30.1360.70,G3DSA:3.40.50.620,G3DSA:1.10.730.10	SSF47323,SSF52374,SSF55190	6~33	00970+6.1.1.19	REACT_71						
aly2012.60	Hexokinase type 2	GO:0005975,GO:0016773,GO:0060361,GO:0005829,GO:0004396,GO:0004340,GO:0019158,GO:0046835,GO:0019318,GO:0051156,GO:0001678,GO:0008865,GO:0006096,GO:0005524	CG3001-PA						PF00349,PF03727	PS51748	PR00475,PR00475,PR00475,PR00475,PR00475,PR00475	PS00378	G3DSA:3.30.420.40,G3DSA:3.40.367.20	SSF53067,SSF53067		00010+2.7.1.1,00051+2.7.1.1,00520+2.7.1.1,00524+2.7.1.1,00521+2.7.1.1,00052+2.7.1.1,00500+2.7.1.1	REACT_474,REACT_15518	PWY-2722,PWY-621,PWY-5661						
aly2012.61	Unknown		n/a																				
aly2012.62	Protein sevenless	GO:0006468,GO:0007601,GO:0005515,GO:0008595,GO:0042067,GO:0008288,GO:0007465,GO:0018108,GO:0005524,GO:0045467,GO:0045466,GO:0004714,GO:0045464,GO:0046534,GO:0004713,GO:0005887,GO:0005886,GO:0008293,GO:0007169,GO:0045678	CG18085-PA				SM00135,SM00219,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060		PF07714,PF00041,PF00041,PF00041,PF00041,PF00041	PS50853,PS50853,PS50853,PS50853,PS50011,PS50853,PS50853,PS50853,PS50853	PR00109,PR00109,PR00109,PR00109,PR00109,PR00109	PS00239,PS00109,PS00107	G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.30.200.20,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:1.10.510.10,G3DSA:2.60.40.10	SSF49265,SSF49265,SSF63825,SSF49265,SSF49265,SSF63825,SSF63825,SSF49265,SSF49265,SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.63	Smad nuclear interacting protein 1	GO:0005634,GO:0004864,GO:0035196,GO:0005515	CG17168-PA				SM00240		PF00498	PS50006			G3DSA:2.60.200.20	SSF49879									
aly2012.64	Threonine aspartase 1	GO:0016787,GO:0004175,GO:0004298,GO:0005575,GO:0016485,GO:0007283,GO:0045893,GO:0050829,GO:0006508,GO:0004067	CG5241-PA						PF01112,PF01112					SSF56235									
aly2012.65	Protein Daple	GO:0005737,GO:0007015,GO:0045793,GO:0031648,GO:0005829,GO:0016055,GO:0051260,GO:0031098,GO:0005575,GO:0030165,GO:0003674,GO:0001932,GO:0043621	CG12734-PA						PF05622					SSF116907	235~279,1052~1079,779~813,884~935,290~365,376~396,828~855,943~977,467~522,537~585,617~658,445~465									
aly2012.66	Coiled-coil domain-containing protein 149		CG14868-PA						PF09789						318~338,149~176,88~122								
aly2012.67	UPF0668 protein C10orf76 homolog	GO:0016021	CG8379-PB						PF04588,PF08427	PS51503													
aly2012.68	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.69	Unknown		n/a																				
aly2012.7	Uncharacterized protein KIAA0556	GO:0005654,GO:0005634,GO:0005615,GO:0005886	n/a						PF14652,PF14652,PF14652														
aly2012.70	Pancreatic lipase-related protein 2	GO:0009395,GO:0047714,GO:0004806,GO:0005615,GO:0016042,GO:0005575,GO:0005509,GO:0019376,GO:0004620,GO:0016298,GO:0047372	CG6472-PB						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly2012.71	Probable malate dehydrogenase, glyoxysomal	GO:0044262,GO:0016615,GO:0006919,GO:0035070,GO:0031998,GO:0035209,GO:0080093,GO:0005811,GO:0005777,GO:0006099,GO:0005739,GO:0006108,GO:0043067,GO:0030060,GO:0005759,GO:0009514,GO:0006097,GO:0043068,GO:0009507	CG7998-PA						PF00056				G3DSA:3.40.50.720,G3DSA:3.90.110.10	SSF51735,SSF56327									
aly2012.72	Proto-oncogene tyrosine-protein kinase ROS	GO:0030154,GO:0018108,GO:0045467,GO:0045466,GO:0010629,GO:0045464,GO:0007169,GO:0010966,GO:0023014,GO:0016049,GO:0038083,GO:0016021,GO:0016020,GO:0004714,GO:0004713,GO:0048471,GO:0002066,GO:0005524,GO:0006468,GO:0008283,GO:0042067,GO:0009986,GO:0008288,GO:0008595,GO:0019903,GO:0005887,GO:0005886,GO:0007465,GO:0007283,GO:0046534,GO:0005515,GO:0008293,GO:0032006,GO:0070372,GO:0045678	CG18085-PA										G3DSA:2.60.40.10	SSF49265									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2012.8	DNA-directed RNA polymerase, mitochondrial	GO:0006996,GO:0044822,GO:0005739,GO:0006390,GO:0010467,GO:0006391,GO:0006351,GO:0003677,GO:0005759,GO:0003899,GO:0042645,GO:0007005	CG4644-PB						PF14700,PF00940,PF00940	PS51375		PS00900	G3DSA:1.10.287.260,G3DSA:1.10.150.20,G3DSA:3.30.70.370,G3DSA:3.30.70.370,G3DSA:3.30.70.370,G3DSA:1.10.287.280	SSF56672	315~345,573~593	00240+2.7.7.6,00230+2.7.7.6							
aly2012.9	Zinc finger protein 229	GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG14711-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57716,SSF57667										
aly2016.1	Transcriptional repressor scratch 1	GO:0000122,GO:0003700,GO:0005634,GO:0006355,GO:0048813,GO:0006351,GO:0003676,GO:0003677,GO:2001222,GO:0046872	CG1130-PA				SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										
aly2016.2	Transcriptional repressor scratch 1	GO:0000122,GO:0003700,GO:0005634,GO:0006355,GO:0048813,GO:0006351,GO:0003676,GO:0003677,GO:2001222,GO:0046872	CG1130-PA				SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF00096,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly2016.3	JNK-interacting protein 3	GO:0019894,GO:0016192,GO:0030140,GO:0009967,GO:0016021,GO:0016020,GO:0008088,GO:0000139,GO:0005078,GO:0005515,GO:0046328	CG8110-PA						PF16471,PF09744				G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:1.20.5.1000	SSF50998,SSF50998	351~399,122~170,427~447,69~117									
aly2016.4	DnaJ homolog subfamily C member 22	GO:0007424,GO:0006897,GO:0035159,GO:0016021,GO:0051087,GO:0031410,GO:0051082,GO:0035002,GO:0030198,GO:0042026,GO:0005886,GO:0005769	CG9089-PA				SM00271		PF00226,PF05154	PS50076	PR00625,PR00625,PR00625		G3DSA:1.10.287.110	SSF46565										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2016.5	Epidermal growth factor receptor	GO:2001234,GO:0000086,GO:0008586,GO:0045466,GO:0003015,GO:0007169,GO:0007298,GO:0001745,GO:0001742,GO:0045468,GO:2000134,GO:0007367,GO:0007455,GO:0016021,GO:0007369,GO:0004713,GO:0016203,GO:0008071,GO:0007173,GO:0019904,GO:0035277,GO:0001751,GO:0001752,GO:0007443,GO:0007447,GO:0007444,GO:0046845,GO:0042694,GO:0046843,GO:0048749,GO:0035160,GO:0008314,GO:0008313,GO:0000578,GO:0035310,GO:0007346,GO:0007431,GO:0008406,GO:0005886,GO:0048477,GO:0005524,GO:0009880,GO:0035309,GO:0007458,GO:0007350,GO:0048865,GO:0007424,GO:0045165,GO:0007421,GO:0007420,GO:0007422,GO:0005006,GO:0016318,GO:0048149,GO:0035225,GO:0048140,GO:0046673,GO:0009790,GO:0009792,GO:0030381,GO:0001709,GO:0008284,GO:0007482,GO:0048139,GO:0001654,GO:0009953,GO:0009952,GO:0030718,GO:0009950,GO:0005515,GO:0045610,GO:0048546,GO:0016333,GO:0035202,GO:0016330,GO:0016337,GO:0030031,GO:0018108,GO:0090303,GO:0007309,GO:0008355,GO:0002009,GO:0007479,GO:0007472,GO:0007473,GO:0007476,GO:0007477,GO:0007474,GO:0043066,GO:0061331,GO:0006468,GO:0035088,GO:0042676,GO:0007314,GO:0005887,GO:0007310,GO:0008340,GO:0022008,GO:0007469,GO:0007391,GO:0007390,GO:0004888	CG10079-PB				SM00261,SM00261,SM00261,SM00261,SM00261		PF00757,PF01030,PF01030,PF14843				G3DSA:3.80.20.20,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:3.80.20.20,G3DSA:3.80.20.20	SSF57184,SSF52058,SSF52058,SSF57184,SSF57184									
aly2016.6	Unknown	GO:0016772	CG2004-PA				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly2016.7	Epidermal growth factor receptor	GO:2001234,GO:0000086,GO:0008586,GO:0045466,GO:0003015,GO:0007169,GO:0007298,GO:0001745,GO:0001742,GO:0045468,GO:2000134,GO:0007367,GO:0007455,GO:0016021,GO:0007369,GO:0004714,GO:0004713,GO:0016203,GO:0008071,GO:0007173,GO:0019904,GO:0035277,GO:0001751,GO:0001752,GO:0007443,G	CG10079-PB				SM00261						G3DSA:2.10.220.10	SSF57184									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2026.1	Dipeptidyl peptidase 8	GO:0005737,GO:0004177,GO:0016020,GO:0008239,GO:0006508,GO:0005654,GO:0008236	CG3744-PD						PF00930,PF00326,PF00326				G3DSA:2.140.10.30,G3DSA:2.140.10.30,G3DSA:3.40.50.1820	SSF53474,SSF82171,SSF82171										
aly2026.2	Mediator of RNA polymerase II transcription subunit 28	GO:0005634,GO:0001104,GO:0006355,GO:0006357,GO:0006351,GO:0016592,GO:0022008	CG5121-PA						PF11594						126~146								
aly2026.3	Probable lysine-specific demethylase 4B	GO:0005634,GO:0070544,GO:0016577,GO:0051864,GO:0032454,GO:0006351,GO:0033169,GO:0045892,GO:0046872	CG33182-PE				SM00545,SM00558		PF02373,PF02375	PS51184,PS51183				SSF51197										
aly2026.4	Putative U5 small nuclear ribonucleoprotein 200 kDa helicase	GO:0000381,GO:0030532,GO:0071011,GO:0005634,GO:0004004,GO:0008380,GO:0003724,GO:0000398,GO:0003676,GO:0005681,GO:0007067,GO:0071013,GO:0005682,GO:0005524	CG5931-PA				SM00973,SM00487,SM00611,SM00490		PF00270,PF00270,PF00271,PF02889	PS51192,PS51194			G3DSA:1.10.3380.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF81296,SSF158702,SSF46785,SSF52540,SSF52540										
aly2027.1	Unknown	GO:0005575,GO:0003674,GO:0008150	CG12970-PC						PF03281						418~438								
aly2027.2	ADP-ribosylation factor-like protein 8B-A	GO:0005819,GO:0000819,GO:0005764,GO:0005765,GO:0007059,GO:0007067,GO:0007264,GO:0031902,GO:0051301,GO:0005525	CG7891-PA				SM00177,SM00178,SM00175	TIGR00231	PF00025	PS51417	PR00328,PR00328,PR00328		G3DSA:3.40.50.300	SSF52540										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2027.3	Hairy/enhancer-of-split related with YRPW motif protein 2	GO:0060347,GO:2001212,GO:0032922,GO:0001570,GO:0042826,GO:0003184,GO:0060977,GO:0060633,GO:0055015,GO:0060716,GO:0010667,GO:0060045,GO:0010629,GO:0003677,GO:0003171,GO:0036304,GO:0003222,GO:0045165,GO:0005737,GO:0003150,GO:0007219,GO:0090102,GO:0000122,GO:0009948,GO:0005634,GO:0005654,GO:0003300,GO:0003208,GO:0045746,GO:0035939,GO:0045607,GO:0010460,GO:0000988,GO:0035910,GO:0010468,GO:0035912,GO:0061314,GO:0003151,GO:0003195,GO:0017053,GO:0003199,GO:0008134,GO:0065004,GO:0007389,GO:0042752,GO:0060317,GO:0045892,GO:0060948,GO:0001102,GO:2000820,GO:0060411,GO:0061156,GO:0014031,GO:0003214,GO:0003215,GO:0016580,GO:0014898,GO:0003700,GO:0000983,GO:0043565,GO:0003186,GO:0006355,GO:0048813,GO:0006357,GO:0045944,GO:0006351,GO:0005667,GO:0060413,GO:0060412,GO:0046983,GO:0060840,GO:0001568,GO:0060842,GO:2000678	CG17100-PA				SM00511,SM00353		PF07527,PF00010	PS51054,PS50888			G3DSA:4.10.280.10	SSF47459,SSF158457	100~120								
aly2027.4	Unknown	GO:0032922,GO:0000122,GO:0003700,GO:0005634,GO:0042752,GO:0006355,GO:0048813,GO:0003677,GO:0046983	CG17100-PA																				
aly2027.5	Unknown		n/a						PF13873,PF13873														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2027.6	Unknown		n/a																				
aly2027.7	Unknown		n/a																				
aly203.1	Unknown	GO:0007157,GO:0005576,GO:0003674,GO:0031225	CG14064-PA							PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726									
aly203.10	Unknown		CG7031-PA																				
aly203.11	Protein yellow	GO:0060179,GO:0016853,GO:0048067,GO:0005576,GO:0042438,GO:0007275	CG4182-PA						PF03022				G3DSA:2.120.10.30,G3DSA:2.120.10.30										
aly203.12	Protein yellow	GO:0060179,GO:0016853,GO:0048067,GO:0005576,GO:0042438,GO:0007275	CG4182-PA						PF03022				G3DSA:2.120.10.30										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly203.13	Lambda-crystallin homolog	GO:0005794,GO:0006631,GO:0070062,GO:0005730,GO:0005829,GO:0050104,GO:0070403,GO:0005886,GO:0003857,GO:0055114,GO:0016491	CG9914-PA						PF00725,PF02737		PR00411,PR00411	PS00067	G3DSA:3.40.50.720,G3DSA:1.10.1040.10	SSF48179,SSF51735		00623+1.1.1.35,00650+5.1.2.3+4.2.1.17+1.1.1.35,00903+4.2.1.17,00592+4.2.1.17,00281+4.2.1.17+1.1.1.3		PWY-6435,PWY-6944,PWY-7046,PWY-7216,PWY-1361,PWY-735,PWY-7606,PWY-5177,PWY-6583,PWY-5109,PWY-	UPA00659				
aly203.14	Serine/threonine-protein kinase STK11	GO:0055059,GO:0016020,GO:0007409,GO:0030308,GO:0001894,GO:0050852,GO:0042593,GO:0030111,GO:0007163,GO:0044281,GO:0045201,GO:0051291,GO:0046328,GO:0060770,GO:0032147,GO:0046777,GO:0072332,GO:0005737,GO:0030709,GO:0010212,GO:0070062,GO:0033993,GO:0005634,GO:0000287,GO:0001944,GO:0005739,GO:0051896,GO:0043065,GO:0004674,GO:0006112,GO:0004672,GO:0005524,GO:0048814,GO:0008285,GO:0006468,GO:0030010,GO:0042304,GO:0071493,GO:0016325,GO:0006914,GO:0033762,GO:0008286,GO:0036399,GO:0036398,GO:0007050,GO:0060070,GO:0007052,GO:0045059,GO:0043276,GO:0007286,GO:0008340,GO:0097484,GO:0051645,GO:0030295,GO:0030511,GO:0045451,GO:0006974,GO:1900182,GO:0050772,GO:0050731,GO:0005829,GO:0007391,GO:0001558,GO:0045722,GO:0045860,GO:0002039	CG9374-PE				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112										
aly203.15	Unknown	GO:0006030,GO:0005576,GO:0008061	CG13643-PD						PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly203.16	Elongation of very long chain fatty acids protein AAEL008004	GO:0006633,GO:0005575,GO:0016021,GO:0030497,GO:0003843,GO:0016740,GO:0030176,GO:0009922	CG2781-PA						PF01151						268~288	00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					
aly203.17	Elongation of very long chain fatty acids protein AAEL008004	GO:0006633,GO:0005575,GO:0016021,GO:0030497,GO:0009922,GO:0016740,GO:0030176,GO:0000038	CG31523-PC						PF01151							00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					
aly203.18	Putative uncharacterized transposon-derived protein F52C9.6		n/a																				
aly203.19	Unknown		n/a																				
aly203.2	GTPase Era, mitochondrial	GO:0043024,GO:0019843,GO:0000028,GO:0005743,GO:0005759,GO:0005875,GO:0005525	CG7488-PA					TIGR00231	PF01926	PS51713	PR00326,PR00326		G3DSA:3.40.50.300,G3DSA:3.30.300.20	SSF52540									
aly203.20	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly203.21	Unknown		n/a																				
aly203.3	Atherin	GO:0005737,GO:0005576,GO:0008270	CG2662-PA				SM00384,SM00384,SM00249,SM00249			PS50016,PS50016			G3DSA:1.10.150.50,G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57903,SSF47769,SSF57903										
aly203.4	Mpv17-like protein 2	GO:0003674,GO:0016021,GO:0008150,GO:0005743	CG32262-PA						PF04117														
aly203.5	Unknown	GO:0006856,GO:0032483,GO:0017137,GO:0006727,GO:0060967,GO:0010883,GO:0017112,GO:0008057,GO:0010506	CG31037-PA						PF13540			PS00626	G3DSA:2.130.10.30,G3DSA:2.130.10.10	SSF50985,SSF50978									
aly203.6	Unknown		n/a										G3DSA:2.130.10.30										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly203.7	Dihydrolipoyl dehydrogenase	GO:0005737,GO:0005960,GO:0005947,GO:0006546,GO:0005811,GO:0006748,GO:0006099,GO:0050660,GO:0004148,GO:0045454,GO:0006096	CG7430-PB			PIRSF000350		TIGR01350	PF02852,PF07992		PR00368,PR00368,PR00368,PR00368,PR00368,PR00411,PR00411,PR00411,PR00411,PR00411,PR00411,PR00411,PR00411,PR00411	PS00076	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.30.390.30	SSF51905,SSF55424		00280+1.8.1.4,00620+1.8.1.4,00020+1.8.1.4,00010+1.8.1.4,00260+1.8.1.4		PWY-5046,PWY-5084					
aly203.8	Protein FAM107B		CG9328-PA						PF06625						174~174								
aly203.9	Unknown		n/a																				
aly2030.1	Unknown		n/a																				
aly204.1	Voltage-dependent calcium channel subunit alpha-2/delta-4	GO:0051924,GO:0070588,GO:0005891,GO:0005246,GO:0050908,GO:0046872,GO:0005245	CG42817-PA				SM00327		PF13768,PF08399,PF02743	PS50234			G3DSA:3.30.450.20,G3DSA:3.30.450.20,G3DSA:3.40.50.410,G3DSA:3.30.450.20,G3DSA:3.30.450.20	SSF53300									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly204.10	6-pyruvoyl tetrahydrobiopterin synthase	GO:0006729,GO:0006728,GO:0046209,GO:0005829,GO:0006520,GO:0050999,GO:0005739,GO:0005737,GO:0042802,GO:0046872,GO:0044281,GO:0003874,GO:0007417	CG16784-PC					TIGR00039	PF01242			PS00988,PS00987	G3DSA:3.30.479.10	SSF55620		00790+4.2.3.12		PWY-5664,PWY-5663,PWY-7442,PWY-6983	UPA00849				
aly204.11	Alkaline ceramidase	GO:0005783,GO:0017040,GO:0019216,GO:0016021,GO:0016811,GO:0006665,GO:0046514,GO:0006672,GO:0007420	CG13969-PB						PF05875								REACT_22258						
aly204.12	Proteasomal ATPase-associated factor 1	GO:0048188,GO:0016573,GO:0006338,GO:0000502,GO:0044545,GO:0004402,GO:0005875,GO:0005671,GO:0005515,GO:0051568,GO:0007095,GO:0022008,GO:0044666,GO:0005634,GO:0044665	CG17437-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400	PS50082,PS50294,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978									
aly204.13	Sorting nexin-17	GO:0030659,GO:0035091,GO:0005829,GO:0016023,GO:0007165,GO:0015031,GO:0005769	CG5734-PA				SM00312		PF00787	PS50195			G3DSA:3.30.1520.10	SSF64268									
aly204.14	Cytochrome b-c1 complex subunit 7	GO:0008121,GO:0006122,GO:0000302,GO:0005750,GO:0034551,GO:0008340	CG17856-PA			PIRSF000022			PF02271				G3DSA:1.10.1090.10	SSF81524	94~108								
aly204.15	Lipoyltransferase 1, mitochondrial	GO:0005575,GO:0016746,GO:0009249,GO:0017118,GO:0005739	CG44243-PA							PS51733			G3DSA:3.90.1550.10	SSF55681		00785+2.3.1.181		PWY-6987,PWY-7381					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly204.2	Unknown		n/a																				
aly204.3	Voltage-dependent calcium channel subunit alpha-2/delta-4	GO:0051924,GO:0070588,GO:0048786,GO:0005891,GO:0031629,GO:0007528,GO:0045886,GO:0045202,GO:0019233,GO:0005246,GO:0005245,GO:0046872,GO:0007274,GO:0050908,GO:0048488	CG12295-PC				SM00327		PF02743,PF08399,PF00092	PS50234			G3DSA:3.30.450.20,G3DSA:3.40.50.410,G3DSA:3.30.450.20,G3DSA:3.30.450.20	SSF53300										
aly204.4	Peptide chain release factor 1-like, mitochondrial	GO:0006415,GO:0016149,GO:0005739	CG5705-PA				SM00937		PF03462,PF00472			PS00745	G3DSA:3.30.160.20	SSF75620	47~67								
aly204.5	Fork head domain-containing protein FD4	GO:0043565,GO:0051090,GO:0000122,GO:0003700,GO:0005634,GO:0030154,GO:0009888,GO:0003705,GO:0009790,GO:0048813,GO:0006357,GO:0048806,GO:0007389,GO:0005667,GO:0007275,GO:0008301,GO:0003690,GO:0009653,GO:0008134,GO:0000981,GO:0006351	CG11921-PA				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00657,PS00658	G3DSA:1.10.10.10	SSF46785									
aly204.6	Fork head domain-containing protein FD4	GO:0030154,GO:0009790,GO:0009653,GO:0007275,GO:0043565,GO:0000122,GO:0005634,GO:0048806,GO:0003690,GO:0000981,GO:0007389,GO:0008134,GO:0009888,GO:0008301,GO:0051090,GO:0003700,GO:0003705,GO:0006355,GO:0048813,GO:0006357,GO:0006351,GO:0005667	CG11921-PA				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00657,PS00658	G3DSA:1.10.10.10	SSF46785									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly204.7	Unknown		n/a																				
aly204.8	Fork head domain-containing protein FD4	GO:0030154,GO:0009790,GO:0009653,GO:0007275,GO:0043565,GO:0000122,GO:0005634,GO:0048806,GO:0003690,GO:0000981,GO:0007389,GO:0008134,GO:0009888,GO:0008301,GO:0051090,GO:0003700,GO:0003705,GO:0006355,GO:0048813,GO:0006357,GO:0006351,GO:0005667	CG11921-PA				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00657,PS00658	G3DSA:1.10.10.10	SSF46785										
aly204.9	Electron transfer flavoprotein subunit alpha, mitochondrial	GO:0007443,GO:0007424,GO:0050660,GO:0048567,GO:0008258,GO:0017133,GO:0005811,GO:0009055,GO:0005759,GO:0006119,GO:0055114,GO:0002009	CG8996-PB			PIRSF000089	SM00893		PF00766,PF01012			PS00696	G3DSA:3.40.50.1220,G3DSA:3.40.50.620	SSF52402,SSF52467			REACT_6305							
aly2041.1	Unknown		n/a																				
aly2041.10	Vacuolar-sorting protein SNF8	GO:0036258,GO:0008283,GO:0000814,GO:0043162,GO:0042059,GO:0003674,GO:0043328,GO:0008593,GO:0042981,GO:0045450	CG6637-PA			PIRSF017215			PF04157				G3DSA:1.10.10.10,G3DSA:1.10.10.10	SSF46785,SSF46785	32~52,119~139								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2041.11	Unknown		n/a												57~84,244~264,6~26,397~417,277~297,118~201,436~456,461~488								
aly2041.12	Histone deacetylase 11	GO:0000118,GO:0032041,GO:0070062,GO:0004407,GO:0005634,GO:0016575,GO:0006355,GO:0006351,GO:0005886,GO:0014003,GO:0008134,GO:0016568	CG31119-PA						PF00850				G3DSA:3.40.800.20,G3DSA:3.40.800.20	SSF52768									
aly2041.13	RIB43A-like with coiled-coils protein 2	GO:0005634	CG7264-PA						PF05914						44~71,287~307,215~252,165~192								
aly2041.14	tRNA 2-thiocytidine biosynthesis protein TtcA	GO:0005737,GO:0008033,GO:0005524	n/a						PF01171				G3DSA:3.40.640.10,G3DSA:3.40.50.620,G3DSA:3.90.1150.10,G3DSA:3.90.1150.10	SSF52402,SSF53383,SSF53383	870~885								
aly2041.15	Unknown		n/a																				
aly2041.16	Protein mesh	GO:0016328,GO:0016021,GO:0090528,GO:0007160,GO:0003674,GO:0005920,GO:0005918	CG31004-PD				SM00539,SM00723,SM00032,SM00216		PF06119,PF03782,PF00094,PF00084	PS51233,PS50856,PS50923,PS51220			G3DSA:2.60.40.10,G3DSA:2.10.70.10	SSF57535,SSF81296									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2041.17	Glycosyltransferase-like protein LARGE2	GO:0005794,GO:0035269,GO:0006486,GO:0008532,GO:0016021,GO:0042285,GO:0000139,GO:0015020,GO:0046872	CG3253-PA						PF01501,PF13896				G3DSA:3.90.550.10	SSF53448,SSF53448,SSF53448									
aly2041.18	Intraflagellar transport protein 57 homolog	GO:0030992,GO:0042384,GO:0060271,GO:0005794,GO:0005813,GO:0006919,GO:0042073,GO:0003674,GO:0005929,GO:0036064,GO:0042981,GO:0006915	CG8853-PA						PF10498						340~360								
aly2041.19	Myosin light chain kinase, smooth muscle	GO:0005737,GO:0007015,GO:0006468,GO:0004687,GO:0046872,GO:0030027,GO:0006914,GO:0032008,GO:0032154,GO:0005575,GO:0004674,GO:0008360,GO:0004672,GO:0005856,GO:0046777,GO:0005524	CG42347-PC				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly2041.2	Unknown	GO:0005576	n/a						PF05849														
aly2041.20	40S ribosomal protein S16	GO:0022627,GO:0003735,GO:0007052,GO:0000022,GO:0006412,GO:0005840	CG4046-PB						PF00380			PS00360	G3DSA:3.30.230.10	SSF54211									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2041.21	Unknown	GO:0008105,GO:0008104,GO:0055059,GO:0005488,GO:0050829,GO:0008356,GO:0061382,GO:0005737,GO:0045177,GO:0045176,GO:0045179,GO:0006403,GO:0045175,GO:0040001,GO:0009786,GO:0005938,GO:0007525,GO:0007400,GO:0045167,GO:0007010,GO:0008093,GO:0007423,GO:0007422,GO:0051960,GO:0005515	CG11312-PA										G3DSA:1.25.10.10	SSF48371									
aly2041.22	MIT domain-containing protein 1	GO:0032091,GO:0043231,GO:0035091,GO:0006810,GO:0030496,GO:0000920,GO:0019898,GO:0000281,GO:0042803,GO:0031902,GO:0019904,GO:0070062	CG14985-PB				SM00745		PF04212,PF16565				G3DSA:1.20.58.280	SSF116846									
aly2041.23	DNA-directed RNA polymerase III subunit RPC3	GO:0045089,GO:0051607,GO:0045087,GO:0003677,GO:0006351,GO:0032728,GO:0005666,GO:0003899,GO:0006383,GO:0005634	CG12267-PA						PF05645,PF08221														
aly2041.24	DNA-directed RNA polymerase III subunit RPC3	GO:0045089,GO:0051607,GO:0045087,GO:0003677,GO:0006351,GO:0032728,GO:0005666,GO:0003899,GO:0006383,GO:0005634	CG12267-PA												116~136								
aly2041.25	Ubiquitin-like protein 3	GO:0070062,GO:0005622,GO:0005575,GO:0008150,GO:0005886,GO:0003674	CG9038-PA						PF13881				G3DSA:3.10.20.90	SSF54236									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2041.26	Protein mesh	GO:0016328,GO:0016021,GO:0090528,GO:0007160,GO:0003674,GO:0005920,GO:0005918	CG31004-PD																				
aly2041.3	Unknown		n/a																				
aly2041.4	Unknown		n/a																				
aly2041.5	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	GO:0004174,GO:0005811,GO:0006635,GO:0031305,GO:0005875,GO:0016491,GO:0016020,GO:0005739,GO:0022900,GO:0046872,GO:0006119,GO:0017133,GO:0031966,GO:0043783,GO:0048039,GO:0048038,GO:0006979,GO:0055114,GO:0009055,GO:0051539,GO:0033539,GO:0005743	CG12140-PB						PF05187,PF07992	PS51379	PR00411,PR00411		G3DSA:3.50.50.60	SSF54862,SSF51905,SSF51905									
aly2041.6	Malignant T-cell-amplified sequence 1 homolog	GO:0005737,GO:0045948,GO:0003723,GO:0002188	CG5941-PA			PIRSF005067	SM00359	TIGR00451	PF01472	PS50890			G3DSA:2.30.130.10	SSF88697									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2041.7	Adiponectin receptor protein	GO:0009755,GO:0032024,GO:0070328,GO:0097003,GO:0016021,GO:0033211,GO:0042593,GO:0005886,GO:0019395,GO:0036099,GO:0046872,GO:0007186,GO:0042562	CG5315-PC						PF03006						28~48								
aly2041.8	WD repeat-containing protein 18	GO:0005737,GO:0005654,GO:0007275	CG14805-PA				SM00320,SM00320,SM00320,SM00320		PF01693,PF00400,PF00400	PS50082,PS50294,PS50082			G3DSA:1.25.40.20,G3DSA:3.40.970.10,G3DSA:2.130.10.10	SSF50978,SSF48403	345~365,394~414								
aly2041.9	Unknown		n/a						PF16045	PS50896					347~367,304~338								
aly20447.1	C-mannosyltransferase dpy-19	GO:0005737,GO:0007399,GO:0016021,GO:0030154,GO:0005789,GO:0008152,GO:0048471,GO:0018406,GO:0000030	CG6659-PA						PF10034														
aly2045.1	Feline leukemia virus subgroup C receptor-related protein 1	GO:0042733,GO:0001701,GO:0015232,GO:0048704,GO:0046620,GO:0001618,GO:0016021,GO:0097037,GO:0005739,GO:0048536,GO:0060323,GO:0043249,GO:0035264,GO:0005886,GO:0006839,GO:0055085,GO:0001568	CG1358-PC										G3DSA:1.20.1250.20	SSF103473									
aly2045.2	Uncharacterized MFS-type transporter C09D4.1	GO:0016021,GO:0055085	CG1358-PC										G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2045.3	Proteasome subunit beta type-2	GO:0004175,GO:0090263,GO:0000082,GO:0010499,GO:0034641,GO:0051439,GO:0044281,GO:0051437,GO:0051436,GO:0042981,GO:0000209,GO:0014070,GO:0005737,GO:0002474,GO:0005839,GO:0043161,GO:0005634,GO:0016020,GO:0002479,GO:0005654,GO:0010467,GO:0043066,GO:0002223,GO:0090090,GO:0006915,GO:0000278,GO:0032504,GO:0045087,GO:0009987,GO:0031145,GO:0006974,GO:0012501,GO:0006977,GO:0010243,GO:0000502,GO:0070062,GO:0051603,GO:0005829,GO:0042590,GO:0004298,GO:0016032,GO:0006521	CG17331-PB						PF00227			G3DSA:3.60.20.10	SSF56235			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045							
aly20541.1	Monocarboxylate transporter 9	GO:0015718,GO:0015293,GO:0008028,GO:0016021,GO:0034220,GO:0005886,GO:0055085,GO:0046415	CG3409-PA							PS50850			G3DSA:1.20.1250.20	SSF103473									
aly20557.1	Pleckstrin homology domain-containing family G member 1	GO:0005089,GO:0017160,GO:0007480,GO:0005085,GO:0007474,GO:0005575,GO:0032489	CG30115-PE							PS50003			G3DSA:2.30.29.30	SSF50729									
aly2058.1	Protein eva-1 homolog C	GO:0016021,GO:0030246	CG42402-PE						PF02140,PF02140	PS50228,PS50228													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly20599.1	Transcription elongation regulator 1	GO:0005730,GO:0015629,GO:0006355,GO:0071011,GO:0003713,GO:0005634,GO:0000122,GO:0044822,GO:0006366,GO:0000398,GO:0006354,GO:0003700,GO:0001106,GO:0001103,GO:0071013	CG42724-PC				SM00441,SM00441,SM00441		PF01846,PF01846,PF01846	PS51676,PS51676,PS51676			G3DSA:2.20.70.10,G3DSA:1.10.10.440,G3DSA:1.10.10.440,G3DSA:1.10.10.440	SSF81698,SSF81698,SSF51045,SSF81698	180~211								
aly20599.2	Unknown	GO:0005515	n/a				SM00320,SM00320,SM00320			PS50294			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978									
aly20599.3	Galectin-9	GO:0005737,GO:0005829,GO:0030246,GO:0008039,GO:0005576,GO:0015143,GO:0016936,GO:0007157	CG11372-PA				SM00908,SM00276		PF00337	PS51304			G3DSA:2.60.120.200	SSF49899									
aly20599.4	Unknown		n/a																				
aly207.1	Protein phosphatase 1 regulatory subunit 36	GO:0010923,GO:0019902,GO:0004864	CG31391-PA						PF14895														
aly207.10	Ribose-5-phosphate isomerase	GO:0009052,GO:0001315,GO:0004751,GO:0043231,GO:0048029	CG30410-PC					TIGR00021	PF06026				G3DSA:3.40.50.1360,G3DSA:3.30.70.260	SSF100950,SSF75445		00051+5.3.1.6,00030+5.3.1.6,00710+5.3.1.6		PWY-5723,PWY-1861	UPA00115				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly207.11	Unknown		n/a																				
aly207.12	Unknown	GO:0019069	n/a						PF05929						90~131								
aly207.13	Carbonic anhydrase-related protein 10	GO:0004089,GO:0008270,GO:0005576	CG32698-PA				SM01057		PF00194	PS51144			G3DSA:3.10.200.10	SSF51069									
aly207.2	Probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase	GO:0006487,GO:0016021,GO:0006490,GO:0042283,GO:0005789,GO:0097502,GO:0016758,GO:0000033	CG4542-PA						PF03155								REACT_17015		UPA00378				
aly207.3	Immunoglobulin superfamily member 10	GO:0001503,GO:0005576	n/a				SM00409		PF00047	PS50835			G3DSA:2.60.40.10	SSF48726									
aly207.4	Anaphase-promoting complex subunit 4	GO:0019903,GO:0000278,GO:0070979,GO:0005829,GO:0005634,GO:0031145,GO:0005654,GO:0051437,GO:0051439,GO:0007094,GO:0007067,GO:0051436,GO:0004842,GO:0030071,GO:0051301,GO:0005680	CG32707-PA						PF12894,PF12896				G3DSA:2.130.10.10	SSF50969					UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly207.5	COP9 signalosome complex subunit 3	GO:0005737,GO:0051726,GO:0050821,GO:0046331,GO:0005515,GO:0006511,GO:0007095,GO:0010388,GO:0008180	CG18332-PA				SM00088		PF01399				G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.10.10.10	SSF46785										
aly207.6	Uroporphyrinogen decarboxylase	GO:0005737,GO:0006783,GO:0006782,GO:0005829,GO:0006779,GO:0004853	CG1818-PA	MF_00218				TIGR01464	PF01208			PS00906,PS00907	G3DSA:3.20.20.210	SSF51726		00860+4.1.1.37		PWY-5531,PWY-7159	UPA00251				
aly207.7	Protein bric-a-brac 1	GO:0008104,GO:0048086,GO:0008258,GO:0045197,GO:0035149,GO:0061024,GO:0003677,GO:0007417,GO:0007478,GO:0007435,GO:0007431,GO:0007455,GO:0005634,GO:0008406,GO:0016477,GO:0048092,GO:0007442,GO:0007548,GO:0048071,GO:0048070,GO:0008360,GO:0035297,GO:0046660,GO:0007443,GO:0007424,GO:0007427,GO:0007426,GO:0007010,GO:0003700,GO:0007428,GO:0007391,GO:0006355,GO:0006351,GO:0003680	CG7230-PC				SM00225		PF00651,PF05225	PS50097,PS50960			G3DSA:3.30.710.10	SSF46689,SSF54695										
aly207.8	Sterol regulatory element-binding protein 1	GO:0006633,GO:0006909,GO:0005789,GO:0001077,GO:0003677,GO:0010867,GO:0005737,GO:0000902,GO:0005634,GO:0016020,GO:0008610,GO:0032933,GO:0031965,GO:0055089,GO:0045893,GO:0012507,GO:0042304,GO:0008203,GO:0003700,GO:0000139,GO:0006355,GO:0006351,GO:0046983,GO:0016021	CG8522-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly207.9	Centrin-1	GO:0005856,GO:0032391,GO:0034605,GO:0005814,GO:0000922,GO:0005509,GO:0007067,GO:0051301	CG17493-PB				SM00054,SM00054,SM00054,SM00054		PF13499,PF13833	PS50222,PS50222,PS50222,PS50222		PS00039,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly2074.1	Homeobox protein not2	GO:0043565,GO:0003700,GO:0014028,GO:0005634,GO:0006355,GO:0045892,GO:0006351,GO:0003677	CG18599-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly2074.2	Serine hydrolase-like protein	GO:0007586,GO:0005575,GO:0016787,GO:0009636,GO:0017171	CG3943-PA						PF00561				G3DSA:3.40.50.1820	SSF53474									
aly2074.3	Serine hydrolase-like protein	GO:0016787	CG11309-PA						PF00561				G3DSA:3.40.50.1820	SSF53474									
aly2074.4	Serine hydrolase-like protein	GO:0016787	CG11309-PA						PF00561				G3DSA:3.40.50.1820	SSF53474									
aly207479.1	Unknown	GO:0005737,GO:0045842,GO:0051726,GO:0007444,GO:0000090,GO:0030162,GO:0090302,GO:0022008,GO:0005680	CG10850-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.1	Unknown		n/a																				
aly208.10	Unknown	GO:0021782,GO:0017016,GO:0045467,GO:0045742,GO:0045743,GO:0042803,GO:0007165	CG8965-PA				SM00314,SM00314		PF00788,PF00788	PS50200,PS50200				SSF54236,SSF54236									
aly208.11	Voltage-dependent L-type calcium channel subunit beta-2	GO:1901385,GO:0006810,GO:0042383,GO:0005887,GO:0005262,GO:0007268,GO:0051928,GO:0005246,GO:0070588,GO:0006816,GO:0007601,GO:0007528,GO:0005891,GO:0070509,GO:0005515,GO:0005886,GO:0007411,GO:0005245	CG42403-PL				SM00326,SM00072		PF12052,PF00625	PS50002	PR01626,PR01626,PR01626,PR01626,PR01626,PR01626,PR01626,PR01626,PR01626		G3DSA:2.30.30.40,G3DSA:3.40.50.300	SSF50044,SSF52540			REACT_13685,REACT_18266						
aly208.12	Protein abrupt	GO:0016203,GO:0048666,GO:0007517,GO:0003676,GO:0007423,GO:0000122,GO:0003700,GO:0005634,GO:0044719,GO:0008039,GO:0016198,GO:0006355,GO:0048813,GO:0006351,GO:0005515,GO:0003677,GO:0007298,GO:0046872,GO:0016319	CG43860-PA				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695									
aly208.13	Unknown		n/a																				
aly208.14	Protein abrupt	GO:0016203,GO:0048666,GO:0007517,GO:0007423,GO:0000122,GO:0003700,GO:0005634,GO:0044719,GO:0008039,GO:0016198,GO:0006355,GO:0048813,GO:0006351,GO:0003676,GO:0003677,GO:0007298,GO:0046872,GO:0016319	CG43860-PA				SM00355,SM00355			PS50157,PS50157		PS00028		SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.15	Mitochondrial fission 1 protein	GO:0090141,GO:0005783,GO:0000266,GO:0051260,GO:0031307,GO:0010821,GO:0051561,GO:0005779,GO:0005778,GO:0016559,GO:0043653,GO:0016020,GO:0005777,GO:0005739,GO:0035584,GO:0007005,GO:2001244,GO:0043234,GO:0006626,GO:0090314,GO:0008053,GO:0043280,GO:0070584,GO:0000422,GO:0005829,GO:0007204,GO:0001836,GO:0005102,GO:0032471	CG17510-PC			PIRSF008835			PF14852,PF14853				G3DSA:1.25.40.10	SSF48452									
aly208.16	Ubiquitin-like-conjugating enzyme ATG3	GO:0019787,GO:0000422,GO:0043653,GO:0006914,GO:0019776,GO:0019777,GO:0000045,GO:0044804,GO:0015031,GO:0000153,GO:0016874,GO:0005829	CG6877-PA						PF10381,PF03986,PF03987														
aly208.17	Uncharacterized protein KIAA1109	GO:0051647,GO:0006629,GO:0016021,GO:0019915,GO:0005575,GO:0007283,GO:0001558,GO:0003674,GO:0060612,GO:0045444,GO:0005634,GO:0048488	CG42555-PJ						PF10479,PF10479,PF10479,PF10479						3557~3557								
aly208.18	Unknown		CG17687-PA										G3DSA:2.120.10.30,G3DSA:2.130.10.10	SSF50978									
aly208.19	Cilia- and flagella-associated protein 43	GO:0042995	CG17687-PA												263~311,488~508,549~583								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.2	Importin subunit alpha-4	GO:0008565,GO:0005737,GO:0008022,GO:0005643,GO:0005634,GO:0006606,GO:0017022,GO:0008320,GO:0009411,GO:0005488,GO:0007095,GO:0051533	CG9423-PA			PIRSF005673	SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185		PF01749,PF00514,PF00514,PF00514,PF00514,PF00514,PF00514,PF00514,PF161866	PS51214,PS50176,PS50176			G3DSA:1.25.10.10	SSF48371									
aly208.20	Unknown		n/a																				
aly208.21	Group XV phospholipase A2	GO:0070062,GO:0005543,GO:0005739,GO:0046470,GO:0005764,GO:0009062,GO:0047499,GO:0008374,GO:0004622,GO:0006672,GO:0006629	CG18858-PA						PF02450				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474										
aly208.22	TBC1 domain family member 20	GO:0005783,GO:0019068,GO:0005789,GO:0002088,GO:0030173,GO:0072520,GO:0006888,GO:0043547,GO:0032313,GO:1902953,GO:0044829,GO:0070309,GO:0005096,GO:0031965,GO:0005097,GO:0017137,GO:0007283,GO:0046726,GO:0001675,GO:0007030,GO:0034389,GO:0090110,GO:0008584,GO:0043010	CG17883-PA						PF00566	PS50086			G3DSA:1.10.8.270	SSF47923	220~240								
aly208.23	Unknown		n/a												5~25								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.24	Unknown	GO:0006030,GO:0005576,GO:0008061	CG8192-PA						PF01607	PS50940			G3DSA:2.170.140.10	SSF57625	120~143								
aly208.25	Unknown		n/a																				
aly208.26	Metallophosphoesterase 1	GO:0070971,GO:0016787,GO:0006888,GO:0005793,GO:0005794,GO:0005801,GO:0006470,GO:0016021,GO:0006506,GO:0033116,GO:0030145,GO:0008081,GO:0034235,GO:0016791	CG8889-PE						PF00149				G3DSA:3.60.21.10	SSF56300									
aly208.27	Unknown		CG4497-PA																				
aly208.28	G2/mitotic-specific cyclin-B3	GO:0000910,GO:0000079,GO:0035186,GO:0005634,GO:0000281,GO:0019901,GO:0016538,GO:0007052,GO:0005515,GO:0035561,GO:0007067,GO:0010389	CG5814-PA			PIRSF001771	SM00385,SM00385		PF02984,PF00134				G3DSA:1.10.472.10,G3DSA:1.10.472.10	SSF47954,SSF47954									
aly208.29	Peroxisome biogenesis factor 1	GO:0005737,GO:0016558,GO:0008022,GO:0007031,GO:0070062,GO:0021782,GO:0007422,GO:0006625,GO:0005829,GO:0042623,GO:0005777,GO:0043231,GO:0005778,GO:0060152,GO:0008152,GO:0032403,GO:0048137,GO:0005524,GO:0007417	CG6760-PA				SM00382,SM00382		PF09262,PF00004,PF00004				G3DSA:1.10.8.60,G3DSA:3.10.330.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF54585,SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.3	Cytoplasmic protein NCK1	GO:0006930,GO:0007409,GO:0030159,GO:0030032,GO:0033137,GO:0050852,GO:0042110,GO:1903676,GO:0012506,GO:0048010,GO:0007411,GO:0005783,GO:0005070,GO:0036493,GO:0030838,GO:0005634,GO:0030971,GO:0000164,GO:0071074,GO:1990441,GO:0005737,GO:0008286,GO:0006469,GO:0042102,GO:0070262,GO:0060548,GO:0045087,GO:0005158,GO:0007264,GO:0046627,GO:0004860,GO:1902237,GO:0005911,GO:0005886,GO:0007520,GO:1903912,GO:0050839,GO:0051707,GO:0038096,GO:0007015,GO:0030674,GO:0005840,GO:0008093,GO:0005829,GO:0045944,GO:0005515,GO:1903679,GO:0005102,GO:1903898,GO:0007172	CG3727-PB			PIRSF037874	SM00326,SM00326,SM00326,SM00252		PF00018,PF00018,PF00018,PF00017	PS50002,PS50002,PS50002,PS50001	PR00401,PR00401,PR00401,PR00401,PR00452,PR00452,PR00452,PR00452,PR00499,PR00499,PR00499,PR00499		G3DSA:2.30.30.40,G3DSA:2.30.30.40,G3DSA:3.30.505.10,G3DSA:2.30.30.40	SSF55550,SSF50044,SSF50044,SSF50044			REACT_18266,REACT_16888						
aly208.30	Transcription factor SOX-14	GO:0043565,GO:0006909,GO:0000122,GO:0003700,GO:0005634,GO:0006355,GO:0045892,GO:0006351	CG7345-PB				SM00398		PF00505	PS50118			G3DSA:1.10.30.10	SSF47095									
aly208.31	Transcription factor SOX-14	GO:0043565,GO:0000122,GO:0003700,GO:0005634,GO:0006355,GO:0008301,GO:0006351,GO:0045892	CG32139-PC				SM00398		PF00505	PS50118			G3DSA:1.10.30.10	SSF47095									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.32	SOX domain-containing protein dichaete	GO:0035120,GO:0003677,GO:0007411,GO:0007417,GO:0005737,GO:0043565,GO:0000122,GO:0005634,GO:0014019,GO:0060810,GO:0003730,GO:0002168,GO:0010468,GO:0008134,GO:0008301,GO:0045893,GO:0007350,GO:0007442,GO:0007420,GO:0009950,GO:0003700,GO:0070983,GO:0003705,GO:0006355,GO:0006357,GO:0045944	CG5893-PA				SM00398		PF00505	PS50118			G3DSA:1.10.30.10	SSF47095										
aly208.33	Viral cathepsin	GO:0003674,GO:0035071,GO:0035220,GO:0045169,GO:0005575,GO:0048102,GO:0004197,GO:0008150,GO:0004869,GO:0006508,GO:0008234,GO:0022416	CG12163-PA				SM00848,SM00645		PF00112,PF00112,PF08246		PR00705,PR00705,PR00705	PS00640,PS00139,PS00639	G3DSA:3.90.70.10,G3DSA:3.90.70.10	SSF54001									
aly208.34	Transcription factor Sox-21-B	GO:0043565,GO:0000122,GO:0003700,GO:0005634,GO:0006355,GO:0008301,GO:0006351,GO:0002088,GO:0045892	CG32139-PC				SM00398		PF00505	PS50118			G3DSA:1.10.30.10	SSF47095									
aly208.35	Unknown		n/a																				
aly208.36	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.37	Unknown	GO:0004867	n/a				SM00131		PF00014				G3DSA:4.10.410.10	SSF57362									
aly208.38	Leucine-rich repeat neuronal protein 2	GO:0035147,GO:0007424,GO:0016477,GO:0016021,GO:0008045,GO:0007476,GO:0004872,GO:0005515,GO:0005886,GO:0007155,GO:0007436,GO:0007165	CG11280-PB				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00082		PF00560,PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly208.39	Unknown		n/a																				
aly208.4	Transcription elongation factor SPT5	GO:0032044,GO:0008023,GO:0000122,GO:0000176,GO:0005634,GO:0005705,GO:0032784,GO:0005703,GO:0005700,GO:0032785,GO:0007052,GO:0007549,GO:0045944,GO:0006351,GO:0005515,GO:0006368,GO:0007095,GO:0046982,GO:0032786,GO:0035101	CG7626-PA			PIRSF036945	SM01104,SM00738,SM00739,SM00739,SM00739,SM00739,SM00739		PF00467,PF00467,PF03439,PF11942				G3DSA:2.30.30.30	SSF50104									
aly208.40	Translationally controlled tumor protein homolog	GO:0005737,GO:0005088,GO:0045793,GO:0031573,GO:0071480,GO:0040018,GO:0033129,GO:0005085,GO:0005700,GO:0007095,GO:0005634,GO:0006302	CG4800-PA						PF00838		PR01653,PR01653,PR01653	PS01002,PS01003	G3DSA:2.170.150.10	SSF51316									
aly208.41	Zinc finger protein 776	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG7372-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157	PR00929,PR00929,PR00929	PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57716,SSF57667,SSF57667	673~700								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.42	Patronin	GO:0005737,GO:0005819,GO:0007026,GO:0051013,GO:0005813,GO:0051011,GO:0030496,GO:0005515,GO:0000022,GO:0005874,GO:0008017	CG33130-PI				SM01051		PF11971,PF08683,PF17095	PS50021,PS51508			G3DSA:1.10.418.10	SSF47576,SSF50346	607~641,1112~1139								
aly208.43	Unknown		n/a																				
aly208.44	Mitochondrial import inner membrane translocase subunit Tim13	GO:0015031,GO:0005743,GO:0046872	CG34132-PA						PF02953				G3DSA:1.10.287.810	SSF144122									
aly208.45	U11/U12 small nuclear ribonucleoprotein 25 kDa protein	GO:0005737,GO:0005654,GO:0045171,GO:0005634,GO:0005575,GO:0008150,GO:0005689,GO:0003674,GO:0008380,GO:0006397	CG34313-PA										G3DSA:3.10.20.90	SSF54236									
aly208.46	Unknown	GO:0043234,GO:0003682,GO:0006357,GO:0005634,GO:0006355,GO:0000791,GO:0005515,GO:0003677,GO:0046872	CG8092-PC				SM00355,SM00355			PS50157		PS00028,PS00028			50~77								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.47	Tyrosine-protein phosphatase non-receptor type 23	GO:0006470,GO:1903393,GO:0035335,GO:0043162,GO:0051225,GO:0005737,GO:0036064,GO:0031982,GO:0016023,GO:0005634,GO:0005654,GO:0045742,GO:2000643,GO:0060271,GO:0019901,GO:1903387,GO:0070062,GO:0002775,GO:0004725,GO:0010633,GO:0040008,GO:0045752,GO:0015031,GO:0005768,GO:0005769	CG9311-PA				SM01041		PF00102,PF03097,PF13949	PS51180,PS50055			G3DSA:1.25.40.280,G3DSA:1.20.140.50,G3DSA:1.20.140.50,G3DSA:1.20.120.560,G3DSA:3.90.190.10	SSF52799	692~712,565~585								
aly208.48	Unknown		n/a																				
aly208.49	Protein spire	GO:0030036,GO:0051639,GO:0007304,GO:0005737,GO:0045010,GO:0051493,GO:0003779,GO:0048471,GO:0048477,GO:0005856,GO:0030029,GO:0008017,GO:0030659,GO:0007315,GO:0005938,GO:0005886,GO:0045451,GO:0007015,GO:0016192,GO:0007316,GO:0030717,GO:0005515,GO:0015031	CG10076-PA				SM00750		PF16474	PS51082,PS51082,PS51377													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.5	Long-chain-fatty-acid--CoA ligase 4	GO:0016020,GO:0005783,GO:0022008,GO:0030307,GO:0031957,GO:0005789,GO:0019432,GO:0035338,GO:0044281,GO:0007411,GO:0060136,GO:0035282,GO:0006629,GO:0005737,GO:0005778,GO:0070062,GO:0016021,GO:0005811,GO:0010890,GO:0004467,GO:0060996,GO:0005524,GO:0015908,GO:0007584,GO:0047676,GO:0003824,GO:0008152,GO:0007268,GO:0001676,GO:0044255,GO:0032307,GO:0008610,GO:0007399,GO:0043025,GO:0044233,GO:0070672,GO:0005741	CG8732-PB						PF00501			PS00455	G3DSA:3.40.50.980,G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.30.300.30	SSF56801,SSF56801										
aly208.50	Storkhead-box protein 1	GO:0033138,GO:1901858,GO:0010800,GO:0010629,GO:0010628,GO:0003674,GO:0008045,GO:0007067,GO:0061418,GO:0051301,GO:0005737,GO:1904031,GO:0005730,GO:0005813,GO:0005634,GO:0005654,GO:0010468,GO:0006351,GO:0008284,GO:0010971,GO:1902882,GO:0051881,GO:0071500,GO:0005575,GO:0000977,GO:0010821	CG10573-PA						PF10264						856~876								
aly208.51	Unknown		n/a												5~25								
aly208.52	Phosphatidate cytidylyltransferase, photoreceptor-specific	GO:0006655,GO:0016049,GO:0005783,GO:0007430,GO:0016056,GO:0043052,GO:0005635,GO:0007601,GO:0019915,GO:0005789,GO:0007602,GO:0060439,GO:0010883,GO:0005887,GO:0005886,GO:0004605,GO:0016024,GO:0016021,GO:0005790	CG7962-PA			PIRSF018269			PF01148			PS01315				00564+2.7.7.41		PWY-5667,PWY-5981	UPA00557				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.53	Unknown	GO:0031637,GO:0008083,GO:0007399,GO:0005121,GO:0008045,GO:0005576,GO:0021556,GO:0008063,GO:0007411,GO:0010941	CG9972-PA																				
aly208.54	Unknown		n/a																				
aly208.55	DNA N6-methyl adenine demethylase	GO:0008270,GO:0003677	CG43444-PF						PF02008	PS51058													
aly208.56	DNA N6-methyl adenine demethylase	GO:0008270,GO:0003677	CG43444-PF						PF12851,PF12851						250~341,1174~1194								
aly208.57	Decaprenyl-diphosphate synthase subunit 2	GO:0006744,GO:0000010,GO:0050878,GO:0051290,GO:0005739,GO:0008299,GO:1990234,GO:0050347	CG10585-PA						PF00348				G3DSA:1.10.600.10	SSF48576,SSF48576									
aly208.58	Glutamate synthase [NADH], amyloplastic	GO:0015930,GO:0050660,GO:0051538,GO:0097054,GO:0051536,GO:0004355,GO:0006541,GO:0016040,GO:0006807,GO:0010181,GO:0009501,GO:0005506,GO:0006537,GO:0055114	CG9674-PF			PIRSF000187		TIGR01317	PF04898,PF01645,PF00310,PF01493,PF07992,PF14691	PS51278	PR00419,PR00419,PR00419,PR00419		G3DSA:3.60.20.10,G3DSA:3.50.50.60,G3DSA:3.20.20.70,G3DSA:2.160.20.60,G3DSA:3.20.20.70,G3DSA:1.10.1060.10,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF56235,SSF51971,SSF46548,SSF51395,SSF51971,SSF69336	1518~1541	00910+1.4.1.14,00250+1.4.1.14		PWY-6963	UPA00634,UPA00045				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.59	Vitamin K-dependent gamma-carboxylase	GO:0008488,GO:0016021,GO:0017187,GO:0018214,GO:0005789	CG13927-PA				SM00752		PF05090				G3DSA:2.60.120.10	SSF51182		00130+4.1.1.90							
aly208.6	Serine/threonine-protein phosphatase BSU1	GO:0016787,GO:0009742,GO:0016311,GO:0006470,GO:0005634,GO:0004722,GO:0046872,GO:0032880	CG8822-PA				SM00156		PF00149	PS50222	PR00114,PR00114,PR00114,PR00114,PR00114,PR00114,PR00114	PS00125,PS00018	G3DSA:1.10.238.10,G3DSA:3.60.21.10,G3DSA:1.10.238.10	SSF56300,SSF47473									
aly208.60	Elongation of very long chain fatty acids protein 6	GO:0005783,GO:0016021,GO:0030497,GO:0005789,GO:0009922,GO:0007283,GO:0030176,GO:0016740,GO:0042759,GO:0019367	CG3971-PA																				
aly208.61	Unknown		n/a																				
aly208.62	Unknown		n/a												38~58								
aly208.63	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly208.64	Unknown		n/a																				
aly208.65	Unknown		n/a												10~89								
aly208.7	Sentrin-specific protease 1	GO:0004175,GO:0032435,GO:0097190,GO:0016926,GO:0008233,GO:0005925,GO:0005737,GO:0044267,GO:0005637,GO:0005634,GO:0005654,GO:0010724,GO:0071456,GO:0006508,GO:0060997,GO:0021952,GO:0006919,GO:0043687,GO:0031965,GO:0016929,GO:0016485,GO:0016925,GO:0004843,GO:0005643,GO:0045944	CG12359-PA						PF02902	PS50600			G3DSA:3.30.310.130,G3DSA:3.30.310.130	SSF54001	415~439								
aly208.8	N-acetylserotonin O-methyltransferase-like protein	GO:0005737,GO:0008171	CG9515-PA	MF_00528		PIRSF006305		TIGR00172	PF02545				G3DSA:3.90.950.10	SSF52972									
aly208.9	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2080.1	Gastric triacylglycerol lipase	GO:0005576,GO:0004806,GO:0006629,GO:0016042	CG6113-PC						PF04083				G3DSA:3.40.50.1820	SSF53474									
aly2080.2	GDP-D-glucose phosphorylase 1	GO:0005737,GO:0016787,GO:0016779,GO:0005085,GO:0000166,GO:0003824,GO:0080048,GO:0006006	CG3552-PA										G3DSA:3.30.428.10										
aly2080.3	Unknown		n/a						PF10545	PS51029													
aly2080.4	Probable cytochrome P450 301a1, mitochondrial	GO:0007490,GO:0004497,GO:0020037,GO:0016705,GO:0005739,GO:0031966,GO:0005506,GO:0055114,GO:0009055	CG8587-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463		G3DSA:1.10.630.10	SSF48264	333~353		REACT_13433						
aly2080.5	Probable cytochrome P450 49a1	GO:0004497,GO:0016705,GO:0020037,GO:0016020,GO:0005739,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG18377-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly2080.6	Keratin-associated protein 16-1	GO:0007015,GO:0005214,GO:0045095,GO:0007160,GO:0016324,GO:0003383,GO:0016476	CG5847-PA				SM00241			PS51034													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2080.7	Unknown		n/a																				
aly20848.1	Exportin-7-B	GO:0005737,GO:0005049,GO:0005643,GO:0005634,GO:0008536,GO:0006611,GO:0005488,GO:0006886	CG33180-PF											SSF48371									
aly2085.1	Titin	GO:0035206,GO:0007498,GO:0030017,GO:0005875,GO:0051301,GO:0007062,GO:0007517,GO:0007519,GO:0031674,GO:0003779,GO:0030018,GO:0016203,GO:0008307,GO:0045214,GO:0000794,GO:0007520,GO:0007522,GO:0005863,GO:0007525,GO:0040011,GO:0004687,GO:0007076	CG1915-PP				SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408		PF06582,PF06582,PF06582,PF06582,PF06582,PF06582,PF06582,PF06582,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679	PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726	1799~1819								
aly2085.2	Twitchin	GO:0018107,GO:0018105,GO:0031672,GO:0017022,GO:0004674,GO:0046872,GO:0005524	CG14964-PB				SM00408,SM00408,SM00060,SM00060,SM00409,SM00409		PF00041,PF00041,PF07679,PF07679	PS50835,PS50853,PS50835,PS50853	PR00014,PR00014,PR00014,PR00014		G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF49265,SSF49265									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2085.3	Cytosol aminopeptidase	GO:0005737,GO:0004177,GO:0030145,GO:0006508,GO:0008235,GO:0016319	CG6372-PA						PF02789,PF00883		PR00481,PR00481,PR00481,PR00481,PR00481		G3DSA:3.40.630.10,G3DSA:3.40.220.10	SSF52949,SSF53187		00480+3.4.11.1		PWY-5988,PWY-6018					
aly2085.4	Glycosyltransferase 25 family member	GO:0005575,GO:0008475,GO:0016757,GO:0005788,GO:0009103	CG31915-PA						PF01755,PF13704					SSF53448									
aly2085.5	Locomotion-related protein Hikaru genki	GO:0007155,GO:0043083,GO:0005576,GO:0043025,GO:0008039	CG2040-PA				SM00032,SM00032,SM00032,SM00032		PF00084,PF00084,PF00084,PF00084	PS50923,PS50835,PS50923,PS50923,PS50923			G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.60.40.10,G3DSA:2.10.70.10	SSF48726,SSF57535,SSF57535,SSF57535,SSF57535									
aly2085.6	Heparanase	GO:0030203,GO:0030200,GO:0030305,GO:0007160,GO:0061042,GO:0044281,GO:0051897,GO:0043202,GO:0005634,GO:0005654,GO:0005576,GO:0051798,GO:0004566,GO:0045545,GO:0051797,GO:0005975,GO:0043231,GO:0010575,GO:0045121,GO:0033690,GO:0005764,GO:0005765,GO:0006029,GO:0046983,GO:0006027,GO:0030194	n/a						PF03662				G3DSA:3.20.20.80	SSF51445,SSF51445									
aly2085.7	Peptidyl-prolyl cis-trans isomerase FKBP14	GO:0006457,GO:0005615,GO:0007444,GO:0005788,GO:0016020,GO:0008587,GO:0046716,GO:0018208,GO:0005528,GO:0022416,GO:0005509,GO:0003755,GO:0008593,GO:0002121,GO:0005783	CG9847-PD				SM00054,SM00054		PF13499,PF00254	PS50222,PS50059,PS50222		PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:3.10.50.40	SSF54534,SSF47473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2087.1	Cytochrome c oxidase assembly protein COX15 homolog	GO:1902600,GO:0016021,GO:0070069,GO:0008535,GO:0005743,GO:0006784,GO:0016627,GO:0055114	CG3803-PA						PF02628										UPA00269				
aly2087.10	Organic cation transporter protein	GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0008513,GO:0016021	CG7458-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly2087.11	Solute carrier family 22 member 1	GO:0005333,GO:0005277,GO:0006855,GO:0015651,GO:0005329,GO:0010248,GO:0005215,GO:0016021,GO:0016020,GO:0051260,GO:0016323,GO:0048241,GO:0015101,GO:0044281,GO:0005887,GO:0015874,GO:0015872,GO:0015695,GO:0005886,GO:0008513,GO:0055085	CG7442-PA						PF07690	PS50850		PS00216,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly2087.12	Organic cation transporter protein	GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0008513,GO:0016021	CG7458-PA						PF07690	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly2087.13	Solute carrier family 22 member 1	GO:0005215,GO:0016021,GO:0016323,GO:0015101,GO:0008513,GO:0055085	CG7458-PA						PF00083			PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly2087.14	Organic cation transporter protein	GO:0055085,GO:0006811,GO:0006915,GO:0008513,GO:0022857,GO:0016021	CG7442-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	549~550,316~343								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2087.15	Organic cation transporter-like protein	GO:0030307,GO:0016021,GO:0007390,GO:0015695,GO:0040018,GO:0015101,GO:0008513,GO:0055085	CG7442-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	322~347								
aly2087.16	Organic cation transporter protein	GO:0005215,GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0008513,GO:0016021	CG7442-PA						PF00083	PS50850		PS00216,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly2087.17	Potassium channel subfamily K member 9	GO:0008021,GO:0005267,GO:0005249,GO:0071804,GO:0071805,GO:0006813,GO:0016021,GO:0016020,GO:0030322,GO:0046331,GO:0022841,GO:0005887,GO:0005886,GO:0005252	CG9194-PA						PF07885,PF07885		PR01333,PR01333		G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324									
aly2087.18	Opioid growth factor receptor	GO:0005737,GO:0005634,GO:0016020,GO:0004872,GO:0040008	n/a																				
aly2087.19	Unknown	GO:0005252,GO:0046331,GO:0016021,GO:0005267,GO:0071805	CG9194-PA										G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324									
aly2087.2	Ubiquitin domain-containing protein 2	GO:0005575,GO:0008150,GO:0003674,GO:0005737	CG1172-PA						PF16455						179~191								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2087.20	Organic cation transporter protein	GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0008513,GO:0016021	CG7442-PA						PF07690	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly2087.21	Unknown	GO:0008513	CG7448-PC																				
aly2087.22	Solute carrier family 22 member 6	GO:0005901,GO:0097254,GO:0070062,GO:0016021,GO:0051260,GO:0042803,GO:0005215,GO:0015711,GO:0016323,GO:0005887,GO:0005886,GO:0043252,GO:0055085,GO:0043234,GO:0015301,GO:0008514,GO:0031427,GO:0015347,GO:0031404,GO:0008513,GO:0005452,GO:0015742	CG7458-PA						PF07690	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly2087.23	Solute carrier family 22 member 3	GO:0015844,GO:0019534,GO:0051615,GO:0005329,GO:0015697,GO:0032098,GO:0016021,GO:0015695,GO:0015872,GO:0098779,GO:0015101,GO:0005887,GO:0051608,GO:0008513,GO:0055085,GO:0015651	CG7458-PA						PF00083	PS50850		PS00216,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly2087.24	Major facilitator superfamily domain-containing protein 8	GO:0005765,GO:0016021,GO:0055085	CG8596-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly2087.25	Unknown	GO:0005811	CG7630-PA						PF16020														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2087.26	Exocyst complex component 1	GO:0000145,GO:0016081,GO:0016080,GO:0006887,GO:0005546,GO:0015031	CG3885-PA						PF09763,PF09763						173~200,89~109								
aly2087.27	PiggyBac transposable element-derived protein 3		n/a						PF13843														
aly2087.28	PiggyBac transposable element-derived protein 3		n/a						PF13843														
aly2087.29	Prefoldin subunit 2	GO:0005737,GO:0044267,GO:0051087,GO:0006457,GO:0070062,GO:0005730,GO:0051084,GO:0005634,GO:0006458,GO:0044183,GO:0051082,GO:0005654,GO:0005739,GO:0016272,GO:0048477,GO:0051495,GO:0006909	CG6302-PA						PF01920				G3DSA:1.10.287.370	SSF46579	22~42								
aly2087.3	Alpha-ketoglutarate-dependent dioxygenase alkB homolog 6	GO:0016706,GO:0005737,GO:0005634,GO:0046872,GO:0055114	CG6144-PB						PF13532				G3DSA:2.60.120.590	SSF51197									
aly2087.30	Molybdenum cofactor biosynthesis protein 1	GO:0006777,GO:0051539,GO:0061597,GO:0003824,GO:0019008,GO:0046872,GO:0005525	CG33048-PC					TIGR00581	PF04055,PF06463,PF01967				G3DSA:3.20.20.70,G3DSA:3.30.70.640	SSF102114,SSF55040		00790+4.1.99.18		PWY-6823	UPA00344				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2087.31	Unknown		n/a																				
aly2087.32	Transmembrane protease serine 6	GO:0004252,GO:0042730,GO:0006879,GO:0005615,GO:0016021,GO:0033619,GO:0055072,GO:0045892,GO:0097264,GO:0005886,GO:0045944,GO:0030514,GO:0006508	n/a						PF00089				G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2087.33	Unknown		n/a																				
aly2087.4	Cytosol aminopeptidase	GO:0005737,GO:0004177,GO:0070062,GO:0030145,GO:0005739,GO:0005622,GO:0005654,GO:0006508,GO:0008233,GO:0005925,GO:0008235	CG4439-PA						PF00883		PR00481,PR00481,PR00481		G3DSA:3.40.630.10,G3DSA:3.40.630.10	SSF53187		00480+3.4.11.1		PWY-5988,PWY-6018					
aly2087.5	Calmodulin	GO:0051383,GO:0042052,GO:0046716,GO:0031476,GO:0031475,GO:0005875,GO:0005737,GO:0016028,GO:0016062,GO:0016061,GO:0016060,GO:0005814,GO:0000922,GO:0005509,GO:0007099,GO:0032036,GO:0006468,GO:0007605,GO:0072499,GO:0030048,GO:0007052,GO:0005819,GO:2001020,GO:0031489,GO:0070855,GO:0016059,GO:0016056,GO:0030496,GO:0051533,GO:0005513,GO:0046331,GO:0005516,GO:0005515	CG8472-PA				SM00054,SM00054,SM00054,SM00054		PF13499,PF13499	PS50222,PS50222,PS50222,PS50222		PS00018,PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2087.6	Unknown		n/a																				
aly2087.7	Unknown		n/a																				
aly2087.8	Tetratricopeptide repeat protein 7B	GO:0022008	CG8325-PA												69~89								
aly2087.9	Unknown	GO:0022008	CG8325-PA																				
aly2089.1	ADP-ribosylation factor-like protein 6	GO:0005737,GO:0005856,GO:0042384,GO:0070121,GO:0060170,GO:0007601,GO:0007368,GO:0007369,GO:0003924,GO:0033339,GO:0005622,GO:0046872,GO:0008593,GO:0005929,GO:0032402,GO:0007264,GO:0005525	CG7735-PA				SM00177,SM00178	TIGR00231	PF00025	PS51417	PR00328,PR00328		G3DSA:3.40.50.300	SSF52540									
aly20891.1	Unknown		n/a						PF16028														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly20891.2	Unknown	GO:0004686,GO:0045793,GO:0071011,GO:0005829,GO:0006468,GO:0000398,GO:0004672,GO:0006417,GO:0071013,GO:0005524	CG1609-PC												271~291								
aly2090.1	Gonadotropin-releasing hormone receptor	GO:0004930,GO:0097004,GO:0007186,GO:0016021,GO:0005886,GO:0007218,GO:0097003,GO:0005887,GO:0008188,GO:0016500,GO:0035237	CG10698-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly2091.1	Serine-enriched protein	GO:0005575,GO:0008150,GO:0003674	CG18471-PA				SM00875,SM00225		PF07707,PF00651	PS50097			G3DSA:3.30.710.10,G3DSA:3.30.710.10	SSF54695,SSF54695									
aly2091.2	Unknown		CG33143-PF																				
aly2091.3	Pro-Pol polyprotein	GO:0006310,GO:0046718,GO:0075713,GO:0075732,GO:0004523,GO:0003887,GO:0015074,GO:0004190,GO:0003723,GO:0042025,GO:0003964,GO:0030430,GO:0046872,GO:0019012	n/a						PF00665	PS50994			G3DSA:3.30.420.10	SSF53098									
aly2091.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2091.5	Unknown		n/a																				
aly209478.1	Unknown		n/a																				
aly2095.1	Unknown	GO:0005575,GO:0003674,GO:0006886,GO:0007476,GO:0017137	CG43340-PM												398~418								
aly2095.2	UPF0553 protein C9orf64 homolog	GO:0005575,GO:0003674,GO:0008150	CG9752-PA						PF10343														
aly2095.3	Nucleoporin Nup43	GO:0019221,GO:0034605,GO:0019083,GO:0010827,GO:0003674,GO:0044281,GO:0007059,GO:0051028,GO:0007067,GO:0051301,GO:0044267,GO:0007264,GO:0008645,GO:0005635,GO:0015758,GO:0010467,GO:0019058,GO:0000278,GO:0043687,GO:0007077,GO:0016925,GO:0055085,GO:0000777,GO:0005975,GO:0031080,GO:1900034,GO:0005829,GO:0005515,GO:0015031,GO:0016032	CG7671-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320			PS50294,PS50082			G3DSA:2.130.10.10	SSF50978										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2095.4	Rho GTPase-activating protein 28	GO:0051056,GO:0005829,GO:0005096,GO:0005622,GO:0005654,GO:0007165,GO:0007264,GO:0030054	CG17082-PB										G3DSA:1.10.555.10				REACT_11044						
aly2095.5	Uncharacterized protein CXorf65 homolog		n/a						PF15874														
aly2095.6	Unknown		n/a																				
aly2096.1	Endochitinase	GO:0005975,GO:0005615,GO:0000272,GO:0005576,GO:0008061,GO:0004568,GO:0006030,GO:0006032	CG9307-PA				SM00494,SM00636		PF01607,PF00704	PS50940		PS01095	G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.10.50.10,G3DSA:2.170.140.10	SSF57625,SSF51445,SSF51445,SSF54556		00520+3.2.1.14		PWY-6902					
aly2096.10	Unknown	GO:0036064,GO:0000242,GO:0035058,GO:0050954,GO:0051297,GO:0005814,GO:0007098,GO:0007338,GO:0005813,GO:0007288,GO:0008356,GO:0007099	CG2919-PA												182~216,416~464,261~302,796~827,839~894,484~532,314~334,916~950,17~51,545~565,576~649								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2096.11	Aminomethyltransferase, mitochondrial	GO:0004047,GO:0005960,GO:0005811,GO:0006546,GO:0005739,GO:0008483	CG6415-PA			PIRSF006487		TIGR00528	PF01571,PF08669				G3DSA:3.30.70.1400,G3DSA:3.30.1360.120,G3DSA:3.30.1360.120,G3DSA:2.40.30.110	SSF103025,SSF101790		00260+2.1.2.10,00670+2.1.2.10							
aly2096.12	COX assembly mitochondrial protein 2 homolog	GO:0005739	CG42375-PA						PF08583,PF01597				G3DSA:2.40.50.100	SSF51230									
aly2096.13	Sarcalumenin	GO:0033018,GO:0003924,GO:0006816,GO:0005509,GO:0005525	CG9297-PB						PF16880,PF00350	PS51718			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	230~270,309~340,682~702								
aly2096.14	DNA-directed RNA polymerases I, II, and III subunit RPABC2	GO:0005736,GO:0005666,GO:0007095,GO:0003677,GO:0006360,GO:0005665,GO:0006351,GO:0006366,GO:0003899,GO:0006383	CG1163-PA			PIRSF000778,PIRSF500154			PF01192			PS01111	G3DSA:3.90.940.10	SSF63562		00240+2.7.7.6,00230+2.7.7.6							
aly2096.15	40S ribosomal protein S27	GO:0022627,GO:0005811,GO:0005622,GO:0003735,GO:0046872,GO:0006412,GO:0005840	CG10423-PB	MF_00371					PF01667			PS01168	G3DSA:2.20.25.100	SSF57829									
aly2096.16	Putative riboflavin kinase	GO:0005737,GO:0008531,GO:0009398,GO:0009231,GO:0046872,GO:0005524	CG2846-PA				SM00904		PF01687				G3DSA:2.40.30.30	SSF82114	103~137								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2096.17	Unknown		n/a																				
aly2096.18	Unknown		n/a																				
aly2096.19	Unknown		n/a										G3DSA:1.20.58.70	SSF46984									
aly2096.2	Pleckstrin homology domain-containing family A member 7	GO:0005737,GO:0005813,GO:0070097,GO:0005915,GO:0045218,GO:0090136	CG34383-PI				SM00233		PF00169	PS50003			G3DSA:2.30.29.30	SSF50729	1392~1419,294~324,1309~1329								
aly2096.20	F-box/WD repeat-containing protein 4	GO:0042733,GO:0051216,GO:0060173,GO:0016055,GO:0002053,GO:0005515	CG33969-PC										G3DSA:2.130.10.10	SSF101908									
aly2096.21	Uncharacterized protein B0303.7	GO:0005575,GO:0008150,GO:0003674,GO:0005515	CG7129-PA				SM00326,SM00326		PF00018,PF00018	PS50002,PS50002	PR00499,PR00499,PR00499,PR004499,PR00452,PR00452,PR00452		G3DSA:2.30.30.40,G3DSA:2.30.30.40	SSF50044,SSF50044									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2096.22	Cysteine-rich hydrophobic domain-containing protein 2	GO:0006893,GO:0005886,GO:0005798,GO:0005622	CG5938-PB						PF10256														
aly2096.23	Larval cuticle protein A3A	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG15006-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2096.24	Larval cuticle protein A2B	GO:0040003,GO:0005214,GO:0008011,GO:0008010,GO:0031012,GO:0042302	CG3818-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2096.25	Cuticle protein	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG6240-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2096.26	Cuticle protein	GO:0040003,GO:0005214,GO:0008010,GO:0031012,GO:0022008,GO:0042302	CG1331-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2096.27	Cuticle protein	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG1330-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2096.28	Tetratricopeptide repeat protein 25	GO:0005575,GO:0008150,GO:0003674,GO:0005515	CG13502-PA							PS50293,PS50005			G3DSA:1.25.40.10	SSF48452	279~299								
aly2096.29	Unknown		n/a																				
aly2096.3	Unknown		n/a																				
aly2096.30	Cuticle protein	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG6240-PA						PF00379,PF00379	PS51155,PS51155	PR00947,PR00947,PR00947	PS00233,PS00233											
aly2096.31	Larval cuticle protein A2B	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG1330-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2096.32	Cuticle protein	GO:0040003,GO:0005214,GO:0008010,GO:0031012,GO:0042008,GO:0042302	CG1331-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2096.33	Male-specific lethal 3 homolog	GO:0031936,GO:0072487,GO:0007549,GO:0035064,GO:0035206,GO:0006325,GO:0016456,GO:0005634,GO:0000805,GO:0006366,GO:0043984,GO:0005654,GO:0003700,GO:0003677,GO:0003682,GO:0005694,GO:0007275,GO:0009047,GO:0003729	CG8631-PA				SM00298		PF11717,PF05712	PS51640			G3DSA:2.30.30.270	SSF54160									
aly2096.34	Histone acetyltransferase type B catalytic subunit	GO:0043234,GO:0006348,GO:0045089,GO:0043967,GO:0006336,GO:0005634,GO:0006335,GO:0004402,GO:0005654,GO:0000790,GO:0010485,GO:0016573,GO:0050829,GO:0016363,GO:0007584,GO:0016568	CG2051-PB			PIRSF038084			PF10394				G3DSA:3.90.360.10,G3DSA:3.40.630.30	SSF55729									
aly2096.35	E3 ubiquitin-protein ligase KCMF1	GO:0015459,GO:0016874,GO:0008270	CG11984-PD				SM00291		PF00569,PF05605	PS50135		PS01357		SSF57850									
aly2096.36	SAP domain-containing ribonucleoprotein	GO:0016607,GO:0048190,GO:0035071,GO:0006355,GO:0000346,GO:0048102,GO:0003723,GO:0003676,GO:0003677,GO:0006417,GO:0006406,GO:0006351	CG8149-PA				SM00513		PF02037	PS50800			G3DSA:1.10.720.30	SSF68906									
aly2096.37	Probable methyltransferase BTM2 homolog	GO:0005575,GO:0003674,GO:0016433,GO:0008150	CG3570-PA	MF_03044					PF11968				G3DSA:3.40.50.150	SSF53335									
aly2096.38	Embryonic stem cell-specific 5-hydroxymethylcytosine-binding protein	GO:0008233,GO:0003677	CG11986-PA						PF02586				G3DSA:3.90.1680.10	SSF143081									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2096.39	Unknown		CG11983-PA																				
aly2096.4	Aurora kinase C	GO:0051255,GO:0008608,GO:0000780,GO:0031616,GO:0007067,GO:0005876,GO:0005737,GO:0005819,GO:0051321,GO:0006325,GO:0000281,GO:0004674,GO:0004712,GO:0004672,GO:0032465,GO:0032133,GO:0005524,GO:0048599,GO:0006468,GO:0035174,GO:0016572,GO:0000793,GO:0007052,GO:0007076,GO:0022008,GO:0051233,GO:0000775,GO:0000776,GO:0000910,GO:0000070,GO:0007283,GO:0030496,GO:0035404,GO:0009966	CG6620-PA						PF00069	PS50011			G3DSA:1.10.510.10	SSF56112										
aly2096.40	Protein SHC1	GO:0005737,GO:0005628,GO:0071555,GO:0030437,GO:0008047,GO:0005515,GO:0006031,GO:0043085	n/a				SM00671,SM00671		PF08238,PF08238				G3DSA:1.25.40.10	SSF81901										
aly2096.41	Scaffold attachment factor B1	GO:0042445,GO:0003682,GO:0000381,GO:0001047,GO:0030520,GO:0005634,GO:0000166,GO:0005654,GO:0045944,GO:0006351,GO:0003676,GO:0040007,GO:0016363,GO:0044822,GO:0003729	CG6995-PB				SM00360,SM00513		PF02037,PF00076	PS50102,PS50800			G3DSA:3.30.70.330,G3DSA:1.10.720.30	SSF54928,SSF68906	438~487								
aly2096.42	Coiled-coil domain-containing protein 115	GO:0005764,GO:0005768	CG14671-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2096.43	Glycoprotein 3 alpha-L-fucosyltransferase A	GO:0018392,GO:0005797,GO:0006486,GO:0007399,GO:0036071,GO:0016021,GO:0016020,GO:0008417,GO:0000138,GO:0033932,GO:0005886,GO:0032580,GO:0046920	CG6869-PA						PF00852,PF17039					SSF53756					UPA00378				
aly2096.44	Peroxisomal biogenesis factor 3	GO:0043234,GO:0032994,GO:0005779,GO:0007031,GO:0016021,GO:0005783,GO:0016557,GO:0003333,GO:0005777,GO:0008289,GO:0015171,GO:0005654,GO:0005778,GO:0045046,GO:0005829,GO:1903146	CG6859-PA						PF04882,PF04882														
aly2096.45	Mitochondrial import inner membrane translocase subunit Tim8 A	GO:0015450,GO:0006626,GO:0005739,GO:0005743,GO:0008270,GO:0005744,GO:0015031	CG1728-PB						PF02953				G3DSA:1.10.287.810	SSF144122									
aly2096.46	Proteasome assembly chaperone 2	GO:0000502,GO:0005634,GO:0043248	CG12321-PA						PF09754					SSF159659									
aly2096.47	Unknown		n/a																				
aly2096.48	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2096.49	Unknown		n/a																				
aly2096.5	Putative hydroxypyruvate isomerase	GO:0046487,GO:0008903,GO:0005576	CG2227-PA			PIRSF006241			PF01261				G3DSA:3.20.20.150	SSF51658		00630+5.3.1.22							
aly2096.50	Unknown		CG34383-PI																				
aly2096.51	Aurora kinase B	GO:0048132,GO:0000920,GO:0008608,GO:0000780,GO:0090307,GO:0031616,GO:0005876,GO:0005737,GO:0031577,GO:0005819,GO:0051321,GO:0006325,GO:0000281,GO:0004674,GO:0004672,GO:0032465,GO:0032467,GO:0046872,GO:0032133,GO:0005524,GO:0006468,GO:0035174,GO:0016572,GO:0007052,GO:0007076,GO:0022008,GO:0051233,GO:0000775,GO:0000776,GO:0000910,GO:0043988,GO:0000070,GO:0030496,GO:0009966	CG6620-PA				SM00220		PF00069	PS50011		PS00107	G3DSA:3.30.200.20	SSF56112										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2096.6	Ecdysone 20-monooxygenase	GO:0016020,GO:0007494,GO:0004501,GO:0020037,GO:0008258,GO:0016705,GO:0007391,GO:0031966,GO:0005739,GO:0007295,GO:0045456,GO:0005506,GO:0007417,GO:0007298,GO:0055114,GO:0009055	CG13478-PB						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly2096.7	Pseudouridine-5'-phosphatase	GO:0016787,GO:0070062,GO:1990738,GO:0042060,GO:0009117,GO:0008152,GO:0046872	CG15441-PA					TIGR01509	PF00702				G3DSA:3.40.50.1000	SSF56784									
aly2096.8	Probable pseudouridine-5'-phosphatase	GO:0016787,GO:1990738,GO:0042060,GO:0009117,GO:0008152,GO:0046872	CG15441-PA					TIGR01509	PF13419				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF56784									
aly2096.9	Pseudouridine-5'-phosphatase	GO:0016787,GO:0070062,GO:1990738,GO:0042060,GO:0009117,GO:0008152,GO:0046872	CG15441-PA					TIGR01509	PF13419				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF56784									
aly20976.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly21.1	Unknown		n/a						PF15868	PS51257													
aly21.10	DNA mismatch repair protein Mlh3	GO:0003696,GO:0032390,GO:0032389,GO:0019237,GO:0005634,GO:0003682,GO:0006298,GO:0007144,GO:0030983,GO:0001673,GO:0008104,GO:0032300,GO:0007140,GO:0016887,GO:0000795,GO:0007130,GO:0007131,GO:0005712,GO:0032407,GO:0003697,GO:0005524	CG11482-PA						PF13589				G3DSA:3.30.565.10	SSF55874									
aly21.11	Unknown		n/a																				
aly21.12	Unknown		n/a																				
aly21.13	Glutathione S-transferase 1, isoform C	GO:0005737,GO:0004364,GO:0018833,GO:0006749	CG17639-PB						PF00043,PF13417	PS50404,PS50405			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF47616,SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly21.14	Angiotensin-converting enzyme	GO:0009897,GO:0016020,GO:0008144,GO:0008238,GO:0010629,GO:0060047,GO:0008217,GO:0043171,GO:0008233,GO:0050435,GO:0008237,GO:0005737,GO:1903597,GO:0032092,GO:0042447,GO:0070062,GO:0031434,GO:0010608,GO:0016021,GO:0004180,GO:0001822,GO:0003779,GO:2000170,GO:1902033,GO:0061098,GO:0006508,GO:1900086,GO:0051019,GO:0032091,GO:0008240,GO:0008241,GO:0007283,GO:0071838,GO:0005886,GO:0060177,GO:0002446,GO:0005615,GO:0005768,GO:0003084,GO:0050482,GO:0031404,GO:0005764,GO:0031711,GO:0004175,GO:0003081,GO:0008270	CG17988-PB						PF01401		PR00791,PR00791,PR00791,PR00791,PR00791,PR00791			SSF55486	741~741,777~114									
aly21.15	Solute carrier family 46 member 3	GO:0016021,GO:0055085,GO:0070062	CG15890-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly21.16	Unknown	GO:0005737,GO:0019010	CG10527-PA				SM00696,SM00696		PF11901														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly21.17	Protein toll	GO:0009897,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0035007,GO:0008063,GO:0006955,GO:0007416,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0002229,GO:0006952,GO:0042802,GO:0016201,GO:0009880,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005887,GO:0005886,GO:0007155,GO:0007352,GO:0043234,GO:0007507,GO:0009950,GO:0009620,GO:0004888,GO:0045944,GO:0005515,GO:0030097,GO:0045610,GO:0005769,GO:0007165	CG5490-PC				SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF13306	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.40.50.10140,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52047,SSF52200									
aly21.2	Roundabout homolog 2	GO:0005887,GO:0001657,GO:0030425,GO:0030424,GO:0050925,GO:0008046,GO:0004872,GO:0008045,GO:0007411,GO:0001656,GO:0022409,GO:0003151,GO:0007432,GO:0031982,GO:0016021,GO:0008406,GO:0070062,GO:0021891,GO:0071666,GO:0001964,GO:0007417,GO:0043025,GO:0042802,GO:0031987,GO:0035385,GO:2000274,GO:0072499,GO:0009986,GO:0035050,GO:0044295,GO:0008038,GO:0032870,GO:0046716,GO:0009649,GO:0005886,GO:0007156,GO:0008201,GO:0007420,GO:0043234,GO:0007427,GO:0031290,GO:0030673,GO:0050773,GO:0050772,GO:0048854,GO:0070983,GO:0016199,GO:0048813,GO:0005515,GO:0051964,GO:0061364	CG13521-PA				SM00408,SM00408,SM00408,SM00408,SM00060,SM00060,SM00409,SM00409,SM00409		PF00041,PF07679,PF07679,PF07679,PF07679	PS50835,PS50835,PS50835,PS50835,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF49265,SSF49265,SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly21.3	Roundabout homolog 1	GO:0005887,GO:0008285,GO:0030275,GO:0030425,GO:0030424,GO:0050925,GO:0021836,GO:0004872,GO:0008045,GO:0007411,GO:0022409,GO:0003151,GO:0007432,GO:0031982,GO:0016021,GO:0006919,GO:0008406,GO:0021891,GO:0071666,GO:0001964,GO:0070100,GO:0043025,GO:0002042,GO:0031987,GO:0035385,GO:0033600,GO:2000274,GO:0072499,GO:0009986,GO:0035050,GO:0044295,GO:0008038,GO:0046716,GO:0009649,GO:0005886,GO:0060763,GO:0007156,GO:0008201,GO:0043234,GO:0007427,GO:0030673,GO:0050773,GO:0050772,GO:0048854,GO:0070983,GO:0016199,GO:0005737,GO:0048813,GO:0042802,GO:0005515	CG13521-PA				SM00060,SM00060,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408		PF00041,PF07679,PF07679,PF07679,PF07679	PS50853,PS50853,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF49265,SSF49265,SSF48726,SSF48726,SSF48726									
aly21.4	Unknown		n/a						PF15868														
aly21.5	Uncharacterized protein C6orf203 homolog	GO:0003723,GO:0005739	CG4884-PA							PS50889			G3DSA:3.10.290.10	SSF55174									
aly21.6	DNA helicase MCM9	GO:0006974,GO:0007276,GO:0000724,GO:0005634,GO:0097362,GO:0000398,GO:0004386,GO:0008266,GO:0005524,GO:0007292,GO:0003677,GO:0005681	CG6011-PA				SM00382,SM00500,SM00350		PF00493,PF08799,PF02840	PS50051	PR01657,PR01657,PR01657,PR01657,PR01657		G3DSA:1.20.940.10,G3DSA:3.40.50.300,G3DSA:2.40.50.140,G3DSA:2.40.50.140	SSF52540,SSF50249,SSF158230,SSF47938	1139~1139,43~70								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly21.7	Chymotrypsin-2	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG31269-PB				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly21.8	DNA mismatch repair protein MLH3	GO:0000710,GO:0006298,GO:0097587,GO:0016887,GO:0007131,GO:0005634,GO:0005524	n/a											SSF118116									
aly21.9	Unknown		n/a																				
aly210.1	PTB domain-containing adapter protein ced-6	GO:0005737,GO:0016319,GO:0016322,GO:0005575,GO:0005515,GO:0043277	CG11804-PD				SM00462		PF00640	PS01179			G3DSA:2.30.29.30	SSF50729	186~213								
aly210.2	Unknown		n/a																				
aly210.3	Cyclin-T	GO:0007015,GO:0006468,GO:0008023,GO:0008024,GO:0000278,GO:0016538,GO:0005634,GO:0032783,GO:0005703,GO:0005700,GO:0019901,GO:0006355,GO:0008360,GO:0006351,GO:0009408,GO:0008353,GO:0000079	CG6292-PB				SM00385		PF00134				G3DSA:1.10.472.10	SSF47954,SSF47954	329~354,545~565								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly210.4	KAT8 regulatory NSL complex subunit 2	GO:0000123,GO:0006325,GO:0005634,GO:0043981,GO:0043984,GO:0005654,GO:0043982,GO:0007095,GO:0022008,GO:0044545	CG18041-PC						PF13891,PF13891						299~319								
aly210.5	Enhancer of polycomb homolog 1	GO:0032777,GO:0000785,GO:0035267,GO:0000123,GO:0000122,GO:0006325,GO:0005634,GO:0005654,GO:0045814,GO:0043967,GO:0043968,GO:0031965,GO:0045892,GO:0045893,GO:0035886,GO:0005725,GO:0070983,GO:0005700,GO:0005701,GO:0045944,GO:0006351,GO:0040008	CG7776-PE						PF10513														
aly210.6	Unknown		n/a																				
aly2101.1	MICOS complex subunit Mic10	GO:0003674,GO:0016021,GO:0008150,GO:0005739,GO:0005743	CG41128-PB						PF04418														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2101.10	Aryl hydrocarbon receptor	GO:0032922,GO:0036011,GO:0007165,GO:0004871,GO:0003677,GO:0070888,GO:0005737,GO:0000122,GO:0005634,GO:0048800,GO:0006366,GO:0048814,GO:0045892,GO:0045893,GO:0007469,GO:0003700,GO:0010092,GO:0003705,GO:0045676,GO:0006355,GO:0006351,GO:0046982	CG6993-PC				SM00086	TIGR00229	PF00989,PF08447	PS50112			G3DSA:3.30.450.20,G3DSA:3.30.450.20	SSF55785,SSF55785										
aly2101.11	Unknown		n/a																				
aly2101.12	Unknown	GO:0005575,GO:0007476,GO:0003674,GO:0008150,GO:0005615	CG6301-PA						PF05335						58~78,93~127,177~204								
aly2101.13	Unknown	GO:0043195,GO:0005615,GO:0097367,GO:0050807,GO:0005576,GO:0008061,GO:0043083,GO:0006030,GO:0007274,GO:0007416	CG7549-PE						PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly2101.14	MAP7 domain containing protein 2	GO:0031987,GO:0005737,GO:0045177,GO:0015630,GO:0040023,GO:0048741,GO:0005874,GO:0008017,GO:0060632,GO:0005198,GO:0000226,GO:2000574	CG14998-PF												23~68								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2101.15	Unknown		n/a												449~469,78~98,270~332,118~154,171~200								
aly2101.16	Tachykinins	GO:0007218,GO:0005184,GO:0007608,GO:0005326,GO:0007268,GO:0007217,GO:0007610,GO:0007628,GO:0071861,GO:0006836,GO:0005102,GO:0005615	CG14734-PB												128~148								
aly2101.17	Putative peptidyl-prolyl cis-trans isomerase dodo	GO:0005634,GO:0007173,GO:0000413,GO:0003755	CG17051-PA				SM00456		PF00639,PF00397	PS50198,PS50020		PS01159	G3DSA:3.10.50.40,G3DSA:2.20.70.10	SSF54534,SSF51045									
aly2101.18	Unknown		n/a																				
aly2101.19	COMM domain-containing protein 4	GO:0005737,GO:0005634,GO:0005575,GO:0006355,GO:0003674,GO:0006351,GO:0008150	CG34039-PB						PF07258						178~208								
aly2101.2	Unknown		n/a						PF14924						29~49								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2101.20	E3 ubiquitin-protein ligase TRAIP	GO:0005730,GO:0007346,GO:0010804,GO:0051276,GO:0008283,GO:0005057,GO:0061630,GO:0006915,GO:0006952,GO:0008270,GO:0032688,GO:0048471,GO:0016874,GO:0007165	CG5140-PA				SM00184		PF13639	PS50089			G3DSA:3.30.40.10	SSF57850	136~163,710~97,205~253								
aly2101.21	E3 ubiquitin-protein ligase TRAIP	GO:0007346,GO:0051276,GO:0005730,GO:0005057,GO:0061630,GO:0010804,GO:0006952,GO:0016567,GO:0004842,GO:0007165,GO:0005515,GO:0032688,GO:0035556,GO:0016874,GO:0048471,GO:0008270	CG5140-PA				SM00184		PF13639	PS50089			G3DSA:3.30.40.10	SSF57850	110~137,611~95,149~190,212~246								
aly2101.22	C2 domain-containing protein 5	GO:0032587,GO:0065002,GO:0005544,GO:0038028,GO:0030659,GO:0005509,GO:0005886,GO:0032869,GO:0031340,GO:0090314,GO:0010828,GO:0005938	CG6454-PC				SM00239		PF00168	PS50004			G3DSA:2.60.40.150	SSF117782,SSF49562	930~950								
aly2101.23	Myosuppression	GO:0010459,GO:0007218,GO:0005184,GO:0005615,GO:0060457,GO:0005576,GO:0045822,GO:0071855,GO:0045986,GO:0008344	CG6440-PA																				
aly2101.24	Serine protease 55	GO:0004252,GO:0005829,GO:0016021,GO:0006508	CG32755-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2101.25	Src substrate cortactin	GO:0007301,GO:0005905,GO:0048041,GO:0007298,GO:0005925,GO:0048260,GO:0030054,GO:0005856,GO:0001726,GO:0070064,GO:0070864,GO:0031532,GO:0006886,GO:0030027,GO:0002102,GO:0008360,GO:0097581,GO:0005886,GO:0030041,GO:0030516,GO:0043234,GO:0007010,GO:0007420,GO:0043197,GO:0048870,GO:0030863,GO:0006898,GO:0030838,GO:0048812	CG3637-PA						PF02218,PF02218,PF02218,PF02218,PF02218,PF02218	PS51090,PS51090,PS51090,PS51090,PS51090,PS51090,PS50002			G3DSA:2.30.30.40	SSF50044	313~344,48~68								
aly2101.26	Acyl-CoA synthetase short-chain family member 3, mitochondrial	GO:0003987,GO:0005739,GO:0005524,GO:0008152	CG6432-PA						PF16177,PF13193,PF00501				G3DSA:3.30.300.30,G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:3.40.50.980	SSF56801									
aly2101.27	C2 domain-containing protein 5	GO:0032587,GO:0065002,GO:0005544,GO:0038028,GO:0030659,GO:0005509,GO:0005886,GO:0032869,GO:0031340,GO:0090314,GO:0010828,GO:0005938	CG6454-PC																				
aly2101.3	Unknown		n/a												11~31								
aly2101.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2101.5	Growth arrest-specific protein 8	GO:0005737,GO:0005794,GO:0048870,GO:0031514,GO:0030317,GO:0003674,GO:0005874	CG14271-PB						PF13851						124~166,283~334,37~57,168~195,395~415,248~271,60~100								
aly2101.6	Protein tipE	GO:0045433,GO:0034605,GO:0005886,GO:0035725,GO:0006814,GO:0017080,GO:0005887,GO:0005248,GO:0002028	CG1232-PA						PF16972,PF16972														
aly2101.7	Protein tipE	GO:0045433,GO:0016021,GO:0005248,GO:0035725,GO:0006814,GO:0017080,GO:0005887,GO:0005886,GO:0034605,GO:0002028	CG15004-PB						PF16972,PF16972														
aly2101.8	Unknown	GO:0017080,GO:0016021,GO:0002028	CG18676-PA																				
aly2101.9	B2 protein (Fragment)	GO:0005549,GO:0007606,GO:0005615,GO:0032504,GO:0005576	CG8462-PA				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly2103.1	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C		n/a						PF13637	PS50088,PS50088,PS50297			G3DSA:1.25.40.20	SSF48403									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2103.2	Unknown		n/a												112~132								
aly2103.3	T-complex protein 1 subunit eta	GO:0006457,GO:0070062,GO:0042623,GO:1901998,GO:0044297,GO:0051082,GO:0031122,GO:0002199,GO:0007052,GO:0005739,GO:0007339,GO:0005832,GO:0022008,GO:0005874,GO:0005875,GO:0005524	CG8351-PA					TIGR02345	PF00118		PR00304,PR00304,PR00304	PS00995	G3DSA:3.30.260.10,G3DSA:3.30.260.10,G3DSA:1.10.560.10,G3DSA:1.10.560.10,G3DSA:3.50.7.10	SSF54849,SSF54849,SSF52029,SSF48592,SSF48592			REACT_17015						
aly2103.4	Zinc finger protein 569	GO:0045931,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0008270,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178,GO:0006351	CG14938-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667,SSF57667,SSF57667									
aly2103.5	Zinc finger and BTB domain-containing protein 48	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG2202-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:2.10.110.10	SSF57667,SSF57667,SSF57667									
aly2103.6	Zinc finger protein 345	GO:0031936,GO:0043565,GO:0000122,GO:0003700,GO:0005634,GO:0006366,GO:0005700,GO:0045892,GO:0005515,GO:0003677,GO:0000785,GO:0046872,GO:0006383,GO:0006359,GO:0043035	CG8573-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly2103.7	Thioredoxin-related transmembrane protein 2 homolog	GO:0016021,GO:0005623,GO:0005575,GO:0008150,GO:0003674,GO:0045454	CG11007-PA						PF00085				G3DSA:3.40.30.10	SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly21059.1	Ras-related protein Rab-5B	GO:0007264,GO:0031982,GO:0007422,GO:0055037,GO:0003924,GO:0032482,GO:0019003,GO:0045202,GO:0005886,GO:0015031,GO:0005525,GO:0031901,GO:0016192	CG3870-PA				SM00175	TIGR00231	PF00071	PS51419	PR00449,PR00449		G3DSA:3.40.50.300	SSF52540									
aly2107.1	Retinal guanylyl cyclase 2	GO:0006468,GO:0016021,GO:0046982,GO:0004383,GO:0016020,GO:0005622,GO:0005575,GO:0042803,GO:0004672,GO:0035556,GO:0005525,GO:0050908,GO:0005524,GO:0006182	CG34357-PC				SM00044		PF07701,PF07714,PF00211	PS50011,PS50125			G3DSA:3.30.70.1230,G3DSA:1.10.510.10	SSF56112,SSF55073	656~687	00230+4.6.1.2							
aly2107.10	Unknown	GO:0030246	CG14866-PB										G3DSA:3.10.100.10	SSF56436	181~201								
aly2107.11	DnaJ homolog subfamily C member 3	GO:0005737,GO:0051603,GO:0016020,GO:0070062,GO:0030968,GO:0005829,GO:0051087,GO:0005788,GO:0004860,GO:0006469,GO:0043066,GO:0051787,GO:0005515,GO:1903912,GO:1903561,GO:0005790	CG8286-PA				SM00028,SM00028,SM00028,SM00028,SM00028,SM00271		PF00515,PF13371,PF00226,PF13181,PF13414,PF07719	PS50005,PS50005,PS50293,PS50293,PS50005,PS50005,PS50076,PS50005,PS50005	PR00625,PR00625,PR00625,PR00625,PR00625		G3DSA:1.10.287.110,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452,SSF46565	368~388								
aly2107.12	60S ribosomal protein L35a	GO:0042273,GO:0000049,GO:0070062,GO:0022625,GO:0044822,GO:0016020,GO:0005739,GO:0005622,GO:0003735,GO:0006364,GO:0006412,GO:0005840	CG2099-PA						PF01247			PS01105		SSF50447									
aly2107.13	Cytochrome P450 6k1	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG8859-PA						PF00067		PR00385,PR00385,PR00385,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2107.14	Protein FAM43A	GO:0005515	CG8312-PA				SM00462		PF14719				G3DSA:2.30.29.30	SSF50729	509~529,413~433								
aly2107.15	Unknown	GO:0046872,GO:0003676	CG11966-PA																				
aly2107.16	Nanos homolog 2	GO:0042078,GO:0008270,GO:0035282,GO:0007275,GO:0008354,GO:0005737,GO:0005634,GO:0001709,GO:0043066,GO:0045835,GO:0006402,GO:0048477,GO:1900153,GO:0016321,GO:0007281,GO:0008595,GO:0007283,GO:0007314,GO:0045892,GO:0048471,GO:0048134,GO:0030718,GO:0007280,GO:0000932,GO:0048813,GO:0003723,GO:0005515,GO:0017148,GO:0006378,GO:0003729,GO:0045495	CG5637-PA						PF05741	PS51522					165~185								
aly2107.17	Peroxiredoxin 1	GO:0006974,GO:0005829,GO:0016209,GO:0004601,GO:0007281,GO:0004602,GO:0042744,GO:0005875,GO:0008379,GO:0042594,GO:0008354,GO:0007155,GO:0008340,GO:0045454,GO:0006979,GO:0055114	CG1633-PE						PF00578,PF10417	PS51352			G3DSA:3.40.30.10	SSF52833		00480+1.11.1.15							
aly2107.18	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2107.2	Diamine acetyltransferase 2	GO:0005737,GO:0004145,GO:0009447,GO:0008080	CG4210-PA						PF00583	PS51065,PS51186			G3DSA:3.40.630.30	SSF55729									
aly2107.3	Transcription factor BCFI	GO:0003700,GO:0043565,GO:0005634,GO:0006351,GO:0008270	n/a																				
aly2107.4	GATA-binding factor 6-A	GO:0061320,GO:0007498,GO:0030154,GO:0060047,GO:0008270,GO:0043565,GO:0042440,GO:0007510,GO:0000122,GO:0005634,GO:0008407,GO:0000983,GO:0000981,GO:0002805,GO:0007389,GO:0035051,GO:0035050,GO:0022416,GO:0045892,GO:0045893,GO:0001103,GO:0007350,GO:0007179,GO:0001085,GO:0007507,GO:0007398,GO:0003700,GO:0007391,GO:0006355,GO:0045944,GO:0006351,GO:0005515,GO:0048542,GO:0046982,GO:0010002	CG3978-PA				SM00401,SM00401		PF00320,PF00320	PS50114,PS50114	PR00619,PR00619	PS00344,PS00344	G3DSA:3.30.50.10,G3DSA:3.30.50.10	SSF57716,SSF57716									
aly2107.5	LINE-1 retrotransposable element ORF2 protein	GO:0006310,GO:0032199,GO:0032197,GO:0009036,GO:0090305,GO:0003964,GO:0046872	n/a						PF00078					SSF56672									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2107.6	GATA-binding factor A	GO:0061320,GO:0007498,GO:0030154,GO:0060047,GO:0008270,GO:0043565,GO:0042440,GO:0007510,GO:0000122,GO:0005634,GO:0008407,GO:0000983,GO:0000981,GO:0002805,GO:0007389,GO:0035051,GO:0035050,GO:0022416,GO:0045892,GO:0045893,GO:0001103,GO:0007350,GO:0007179,GO:0001085,GO:0007507,GO:0007398,GO:0003700,GO:0007391,GO:0006355,GO:0045944,GO:0006351,GO:0005515,GO:0048542,GO:0046982,GO:0010002	CG3978-PA				SM00401,SM00401		PF00320,PF00320	PS50114,PS50114	PR00619,PR00619	PS00344,PS00344	G3DSA:3.30.50.10,G3DSA:3.30.50.10	SSF57716,SSF57716									
aly2107.7	Diamine acetyltransferase 2	GO:0005737,GO:0032920,GO:0032919,GO:0070062,GO:0008080,GO:0009447,GO:0046204,GO:0004145,GO:0032918	CG4210-PA						PF00583	PS51186			G3DSA:3.40.630.30	SSF55729									
aly2107.8	Zinc finger protein 681	GO:0006351,GO:0003700,GO:0005634,GO:0006355,GO:0000790,GO:0002230,GO:0008270,GO:0005515,GO:0003677,GO:0046872,GO:0043035	CG2711-PA				SM00355,SM00355,SM00355,SM00355,SM00355		PF12874	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.50.10	SSF57667,SSF57667,SSF57667	98~118								
aly2107.9	Protocadherin-23	GO:0007424,GO:0016339,GO:0016020,GO:0005509,GO:0005887,GO:0005886,GO:0007156,GO:0016021	CG13664-PD				SM00112,SM00112		PF00028,PF00028	PS50268,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205		G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49313,SSF49313									
aly210720.1	Transposable element Tc3 transposase	GO:0015074,GO:0005634,GO:0004803,GO:0006313,GO:0003677	n/a						PF13358														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly21085.1	Zinc finger and BTB domain-containing protein 49	GO:0005737,GO:0008285,GO:0006351,GO:0001223,GO:0043565,GO:0005634,GO:0007050,GO:0045944,GO:0000977,GO:0003677,GO:0046872,GO:0008134,GO:0008270	CG14711-PA				SM00355,SM00355,SM00355		PF12874	PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60	SSF57667									
aly21087.1	Copper-transporting ATPase 1	GO:0060003,GO:0043085,GO:0005783,GO:0048085,GO:0007595,GO:0005886,GO:0048812,GO:0051353,GO:0048066,GO:0000302,GO:0002082,GO:0002164,GO:0043524,GO:0001836,GO:0007626,GO:0006825,GO:0010043,GO:0010041,GO:0010273,GO:0042421,GO:0006568,GO:0021702,GO:0032767,GO:0005737,GO:0016020,GO:0001701,GO:0051542,GO:0016532,GO:0016021,GO:0005770,GO:0048813,GO:0000166,GO:0030198,GO:0007005,GO:0043005,GO:0030141,GO:0015677,GO:0021954,GO:0005375,GO:0005507,GO:0043025,GO:0010468,GO:0005524,GO:0048554,GO:0005794,GO:0004008,GO:0048471,GO:0006878,GO:0042428,GO:0048553,GO:0030140,GO:0046034,GO:0006584,GO:0016323,GO:0042417,GO:0034220,GO:0048251,GO:0051216,GO:0055065,GO:0042093,GO:0021860,GO:0031069,GO:0006570,GO:0043473,GO:0046872,GO:0055085,GO:0018205,GO:0005829,GO:0005802,GO:0042415,GO:0015679,GO:0031526,GO:0001974,GO:0030199,GO:0042414,GO:0043588,GO:0048286,GO:0019430,GO:0001568	CG1886-PB						PF00122													
aly2109.1	Heat shock 70 kDa protein cognate 5	GO:0070584,GO:0006457,GO:0000422,GO:0005811,GO:0005739,GO:0010918,GO:0051082,GO:0016887,GO:0009408,GO:0005875,GO:0005524	CG8542-PB						PF00012		PR00301,PR00301,PR00301,PR00301,PR00301,PR00301	PS00297,PS00329	G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.30.30,G3DSA:3.90.640.10,G3DSA:3.30.420.40,G3DSA:3.30.420.40	SSF53067,SSF53067	312~332								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2109.2	Cell death specification protein 2	GO:0043565,GO:0003700,GO:0005634,GO:0006915,GO:0001012,GO:0006355,GO:0006351,GO:0043068,GO:0042803	CG7786-PA						PF07716				G3DSA:1.20.5.170	SSF57959									
aly2109.3	ATP synthase subunit beta, mitochondrial	GO:0045261,GO:0015986,GO:0015992,GO:0015991,GO:0000275,GO:0005811,GO:0005739,GO:0005743,GO:0046933,GO:0046331,GO:0008553,GO:0005524	CG11154-PD	MF_01347			SM00382	TIGR01039	PF02874,PF00006,PF00306			PS00152	G3DSA:1.10.1140.10,G3DSA:2.40.10.170,G3DSA:3.40.50.300	SSF52540,SSF50615,SSF47917		00195+3.6.3.14,00190+3.6.3.14		PWY-7219					
aly2109.4	Putative serine protease 29	GO:0004252,GO:0005576,GO:0006508	CG5390-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2109.5	Tryptase	GO:0004252,GO:0005576,GO:0006508	CG40160-PA				SM00020		PF00089	PS50240	PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2109.6	Unknown		n/a																				
aly2109.7	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005576,GO:0005886,GO:0006508	CG5390-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly210977.1	Unknown		n/a																				
aly2111.1	ATP-binding cassette sub-family D member 2	GO:0043190,GO:0042626,GO:0005778,GO:0016021,GO:0043231,GO:0006635,GO:0005215,GO:0005829,GO:0005777,GO:0042760,GO:0000038,GO:0042803,GO:0055085,GO:0005524,GO:0032000	CG2316-PB						PF06472	PS51257,PS50929			G3DSA:3.40.50.300	SSF90123,SSF52540									
aly2111.2	Inhibin beta B chain	GO:2001235,GO:0032924,GO:0032927,GO:0005160,GO:0046676,GO:0007411,GO:0032869,GO:0045444,GO:0044320,GO:0008083,GO:0009612,GO:0007179,GO:0048471,GO:0042803,GO:0048599,GO:0060279,GO:0046881,GO:0046882,GO:0009267,GO:0048178,GO:0040007,GO:0005576	CG16987-PB				SM00204		PF00019	PS51362	PR00669,PR00669,PR00669	PS00250	G3DSA:2.10.90.10	SSF57501									
aly2114.1	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0030672,GO:0016021,GO:0007268,GO:0008513,GO:0022857,GO:0001669,GO:0006836,GO:0055085,GO:0030054	CG15221-PB						PF00083				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly2114.2	Unknown	GO:0050662,GO:0044237,GO:0003824	CG5854-PA						PF01370				G3DSA:3.40.50.720	SSF51735,SSF51735									
aly2114.3	Zinc finger protein 26	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12874,PF13912,PF13912,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2114.4	BTB/POZ domain-containing protein 17	GO:0007517,GO:0009306,GO:0005829,GO:0048813,GO:0005576,GO:0003674	CG1841-PB				SM00875,SM00225		PF07707,PF00651	PS50097			G3DSA:3.30.710.10,G3DSA:1.50.10.20	SSF54695									
aly2114.5	Peptidyl-prolyl cis-trans isomerase FKBP4	GO:0031111,GO:0006457,GO:0031115,GO:0031072,GO:0034605,GO:0005789,GO:0006825,GO:0050908,GO:0005874,GO:0005737,GO:0000413,GO:0070062,GO:0030521,GO:0016027,GO:0030850,GO:0005739,GO:0046661,GO:0005654,GO:0005528,GO:0003755,GO:0048471,GO:0043025,GO:0005524,GO:0005525,GO:0006463,GO:0044822,GO:0044295,GO:0010977,GO:0061077,GO:0031503,GO:0030674,GO:0018208,GO:0007422,GO:1900034,GO:0005829,GO:0051924,GO:0005515,GO:0007566	CG4535-PA				SM00028,SM00028		PF00515,PF00254,PF00254	PS50059,PS50005,PS50293,PS50293,PS50059,PS50005			G3DSA:1.25.40.10,G3DSA:3.10.50.40,G3DSA:3.10.50.40	SSF54534,SSF54534,SSF48452									
aly21158.1	Unknown		n/a										G3DSA:3.30.530.20										
aly21159.1	Unknown		n/a																				
aly2116.1	Facilitated trehalose transporter Tret1-2 homolog	GO:0005355,GO:0035428,GO:0015992,GO:0016021,GO:0016020,GO:0046323,GO:0005887,GO:0005886,GO:0005351,GO:0055085	CG1213-PA					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473			REACT_15518						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2116.10	U3 small nucleolar ribonucleoprotein protein IMP4	GO:0032040,GO:0042134,GO:0034457,GO:0005730,GO:0030532,GO:0006364,GO:0030515	CG11920-PA				SM00879		PF04427	PS50833			G3DSA:3.40.50.10480,G3DSA:3.40.50.10480	SSF52954									
aly2116.2	Erythroid differentiation-related factor 1	GO:0006355,GO:0005634,GO:0006351	CG6511-PA												581~601								
aly2116.3	Zinc finger protein on ecdysone puffs	GO:0071011,GO:0005694,GO:0005634,GO:0005703,GO:0000398,GO:0003697,GO:0003727,GO:0003677,GO:0048024,GO:0046872,GO:0071013,GO:0005875	CG6143-PB				SM00355,SM00355,SM00355							SSF57667									
aly2116.4	Unknown		n/a										G3DSA:1.10.1780.10		63~97								
aly2116.5	Y+L amino acid transporter 2	GO:0015297,GO:1902475,GO:0016020,GO:0015171,GO:0015807,GO:0015179,GO:0005887,GO:0016323,GO:0003333	CG1607-PC			PIRSF006060			PF13520														
aly2116.6	NADPH-dependent diflavin oxidoreductase 1	GO:0050661,GO:0050660,GO:0016709,GO:0036245,GO:0005829,GO:0048471,GO:0016226,GO:0003958,GO:0008150,GO:0010181,GO:0005506,GO:0008219,GO:0055114,GO:0016491	CG13667-PB	MF_03178					PF00175,PF00258,PF00667	PS51384,PS50902	PR00369,PR00369,PR00369,PR00369,PR00371,PR00371,PR00371,PR00371,PR00371,PR00371,PR00371		G3DSA:3.40.50.360,G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:3.40.50.80,G3DSA:1.20.990.10	SSF52343,SSF63380,SSF52218									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2116.7	THO complex subunit 3	GO:0016607,GO:0005794,GO:0043231,GO:0005875,GO:0005654,GO:0046784,GO:0003723,GO:0005515,GO:0000346,GO:0000445,GO:0008380,GO:0006406,GO:0006397	CG9615-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF08662	PS50082,PS50082,PS50294,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10	SSF50978									
aly2116.8	TATA box-binding protein-associated factor RNA polymerase I subunit B	GO:0001189,GO:0005730,GO:0001164,GO:0001187,GO:1901838,GO:0005668,GO:0046872	CG6241-PA						PF11781														
aly2116.9	Unknown		n/a																				
aly21198.1	Unknown		n/a												3~86								
aly212078.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2124.1	Transcriptional activator cubitus interruptus	GO:0035217,GO:0035277,GO:0035224,GO:0001077,GO:0003677,GO:0008544,GO:0000980,GO:0002385,GO:0005737,GO:0007346,GO:0007367,GO:0060914,GO:0000122,GO:0005634,GO:0016020,GO:0030707,GO:0006366,GO:0030858,GO:0046872,GO:0048477,GO:0042803,GO:0048666,GO:0048592,GO:0035017,GO:0035301,GO:0001205,GO:0007350,GO:0043234,GO:0044212,GO:0007224,GO:0003700,GO:0006355,GO:0048813,GO:0048100,GO:0045944,GO:0000977,GO:0005515,GO:1900087	CG2125-PA				SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										
aly2124.2	Dual specificity protein phosphatase 3	GO:0016791,GO:0050868,GO:0006470,GO:0050860,GO:0000188,GO:0043508,GO:0046329,GO:0035335,GO:0043409,GO:0005737,GO:0070062,GO:0005634,GO:0005654,GO:0033549,GO:0045931,GO:0008138,GO:0019901,GO:0001772,GO:0005829,GO:0004721,GO:0070373,GO:0004725	CG14211-PB				SM00195		PF00782	PS50054,PS50056		PS00383	G3DSA:3.90.190.10	SSF52799										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2124.3	Twitchin	GO:0005737,GO:0018107,GO:0006468,GO:0004687,GO:0007498,GO:0031672,GO:0018105,GO:0004674,GO:0008307,GO:0005200,GO:0045214,GO:0005524,GO:0005515,GO:0046872,GO:0030018	CG32019-PF				SM00408,SM00409,SM00220,SM00060		PF00041,PF07679,	PS50853,PS50853,PS50853,PS50835,PS50835,PS50853,PS50853,PS50835,PS50853,PS50853,PS50835,PS50853,PS50853,PS50835,PS50853,PS50853,PS50853,PS50853,PS50853,PS50835,PS50853,PS50853,PS50853,PS50011,PS50835,PS50835,PS50853,PS50835,PS50853,PS50853,PS50853,PS50835,PS50835,PS50835,PS50853,PS50835,PS50853,PS50835,PS50853,PS50835,PS50853,PS50835,PS50835,PS50835,PS50835,PS50853,PS50853,PS50853,PS50853,PS50835,PS50853,PS50853,PS50835,PS50853,PS50835,PS50853,PS50853,PS50853,PS50835,PS50835,PS50835,PS50835,PS50853,PS50835,PS50853,PS50835,PS50835,PS50853,PS50853	PR00014,PR00014,PR00014,PR00014	PS00108,PS00107	G3DSA:2.60.40.10,G3DSA:1.10.510.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.30.200.20,G3DSA:2.60.40.1	SSF49265,SSF49265,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF56112,SSF49265,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF49265,SSF49265,SSF49265,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF49265,SSF48726,SSF49265,SSF49265,SSF48726,SSF49265,SSF49265,SSF48726,SSF48726,SSF48726,SSF49265,SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726	9158~9160,834~871,884~932								
aly2124.4	Transcription factor castor	GO:0016319,GO:0048699,GO:0007417,GO:0021782,GO:0006355,GO:0003700,GO:0005634,GO:0014019,GO:0009791,GO:0007419,GO:0006357,GO:0045892,GO:0006351,GO:0003677,GO:0046872,GO:0007402,GO:0040034	CG2102-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028											
aly2124.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2127.1	Potassium channel subfamily K member 1	GO:0005267,GO:0005272,GO:0071805,GO:0016021,GO:1902937,GO:0035725,GO:0034705,GO:0060075,GO:0005887,GO:0022841,GO:0005252,GO:0046982,GO:0005768,GO:0005242	CG9361-PA						PF07885,PF07885		PR01586,PR01586,PR01586,PR01586,PR01333,PR01333,PR01096,PR01096,PR01096		G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324,SSF81324									
aly2127.10	Unknown		n/a																				
aly2127.11	Exostosin-2	GO:0030206,GO:0005783,GO:0008101,GO:0005789,GO:0008375,GO:0007275,GO:0006486,GO:0016021,GO:0031227,GO:0015020,GO:0046872,GO:0030210,GO:0005794,GO:0050508,GO:0050509,GO:0007224,GO:0016055,GO:0006044,GO:0000139,GO:0015012,GO:0005515,GO:0015014,GO:0006024	CG8433-PB						PF09258				G3DSA:3.90.550.10	SSF53448									
aly2127.2	Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66	GO:0034720,GO:0005634,GO:0070544,GO:0005575,GO:0016706,GO:0051864,GO:0032453,GO:0008150,GO:0006351,GO:0045892,GO:0003674,GO:0005506	CG2982-PB				SM00558		PF08007	PS51184			G3DSA:2.60.120.650	SSF51197									
aly2127.3	Protein PBDC1		CG7519-PA						PF04669				G3DSA:1.10.3560.10										
aly2127.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2127.5	60S ribosomal protein L26	GO:0015934,GO:0005840,GO:0022625,GO:0003735,GO:0007052,GO:0000022,GO:0006412	CG6846-PA				SM00739	TIGR01080	PF00467,PF16906			PS01108	G3DSA:2.30.30.30	SSF50104			REACT_13698,REACT_15380,REACT_6167,REACT_17015,REACT_1762,REACT_71						
aly2127.6	Unknown		n/a																				
aly2127.7	Muscarinic acetylcholine receptor DM1	GO:0007606,GO:0007200,GO:0016021,GO:0016907,GO:0007207,GO:0045211,GO:0030054,GO:0005887,GO:0007213,GO:0007271,GO:0007186,GO:0008227,GO:0007197,GO:0045202	CG4356-PB						PF00001	PS50262	PR00243,PR00243,PR00243,PR00243,PR00243,PR00243,PR00243,PR00243,PR00243,PR00237,PR00237,PR00237,PR002	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly2127.8	Unknown	GO:0031110	n/a						PF00836						88~108								
aly2127.9	Serum response factor homolog	GO:0007424,GO:0006366,GO:0045165,GO:0035154,GO:0007430,GO:0033613,GO:0035209,GO:0005634,GO:0030154,GO:0007476,GO:0008586,GO:0035220,GO:0007475,GO:0001077,GO:0045944,GO:0030431,GO:0003677,GO:0046983,GO:0007614,GO:0002168	CG3411-PA				SM00432		PF00319	PS50066	PR00404,PR00404,PR00404	PS00350		SSF55455			REACT_21303						
aly2128.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly213.1	Unknown		n/a																				
aly213.10	Unknown		n/a																				
aly213.11	Cuticle protein 2	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG9079-PA						PF00379	PS51155													
aly213.2	RNA polymerase II-associated protein 3	GO:0008283,GO:0007446,GO:0007444,GO:0051087,GO:0004722,GO:0005515,GO:0046529	CG13570-PA				SM00028,SM00028,SM00028		PF13877,PF13414	PS50005,PS50293,PS50005,PS50005			G3DSA:1.25.40.10	SSF48452	25~45								
aly213.3	Cuticle protein 3	GO:0040003,GO:0005615,GO:0032504,GO:0005214,GO:0008010,GO:0031012,GO:0042302	CG18348-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly213.4	Cuticle protein 3	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG8634-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly213.5	Cuticle protein 3	GO:0040003,GO:0005615,GO:0032504,GO:0005214,GO:0008010,GO:0031012,GO:0042302	CG18348-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly213.6	Pupal cuticle protein 36a	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG8638-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly213.7	Unknown		n/a																				
aly213.8	Pupal cuticle protein 27	GO:0040003,GO:0005214,GO:0008011,GO:0008010,GO:0031012,GO:0042302	CG7673-PA						PF00379	PS51155		PS00233											
aly213.9	Cuticle protein 3	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG6956-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2130.1	Slit homolog 1 protein	GO:0007424,GO:0007420,GO:0035151,GO:0035159,GO:0051964,GO:0048843,GO:0021510,GO:0043395,GO:0005509,GO:0005515,GO:0008045,GO:0005615	CG8561-PB				SM00365,SM00369,SM00369		PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13306,PF13306,PF13306	PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52058,SSF52058,SSF52058,SSF52058,SSF52058,SSF52058	2024~2044								
aly2130.10	Ceramide-1-phosphate transfer protein	GO:0005737,GO:0005794,GO:0005548,GO:0005543,GO:1902389,GO:1902388,GO:1902387,GO:0005640,GO:0046836,GO:0005886,GO:0051861,GO:0017089,GO:0005829,GO:0010008	CG30392-PA						PF08718				G3DSA:1.10.3520.10	SSF110004									
aly2130.11	NF-kappa-B essential modulator	GO:0019730,GO:0006963,GO:0006964,GO:0008063,GO:0050829,GO:0042803,GO:0051650,GO:0005737,GO:0072686,GO:0007250,GO:0005634,GO:0000922,GO:0001782,GO:0008384,GO:0046872,GO:0043123,GO:0045089,GO:0070530,GO:0006974,GO:0008385,GO:0030163,GO:0006955,GO:0051092,GO:0051607,GO:0000151,G	CG16910-PB						PF11577,PF16516				G3DSA:1.20.5.990		315~342,208~267,117~151,180~200,543~563,280~307,501~521								
aly2130.12	CHH-like protein	GO:0005179,GO:0007218,GO:0007623,GO:0005615,GO:0046331,GO:0005184,GO:0005576	CG13586-PF						PF01147,PF01147		PR00550,PR00550,PR00550	PS01250	G3DSA:1.10.2010.10,G3DSA:1.10.2010.10	SSF81778,SSF81778									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2130.13	Peroxisomal leader peptide-processing protease	GO:0004252,GO:0031998,GO:0051260,GO:0016020,GO:0005777,GO:0002020,GO:0016485,GO:0006508,GO:0042802	CG3589-PA						PF13365				G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494,SSF50494									
aly2130.14	Unknown		n/a																				
aly2130.15	Unknown		n/a																				
aly2130.16	ATP-binding cassette sub-family A member 3	GO:0043190,GO:0042626,GO:0006810,GO:0005615,GO:0006869,GO:0097208,GO:0005215,GO:0016021,GO:0016020,GO:0042493,GO:0097233,GO:0005886,GO:0055085,GO:0005524	CG1718-PB						PF00005			PS00211	G3DSA:3.40.50.300	SSF52540									
aly2130.17	Unknown		n/a																				
aly2130.18	ATP-binding cassette sub-family A member 3	GO:0043190,GO:0042626,GO:0006810,GO:0005615,GO:0006869,GO:0097208,GO:0005215,GO:0016021,GO:0016020,GO:0042493,GO:0097233,GO:0016887,GO:0005886,GO:0055085,GO:0005524	CG6052-PA						PF00005				G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2130.19	Thioredoxin domain-containing protein 6	GO:0005737,GO:0005856,GO:0006228,GO:0005622,GO:0006241,GO:0004550,GO:0005524,GO:0006662,GO:0015035,GO:0045454,GO:0006183	CG18130-PA						PF15928						108~128,269~324								
aly2130.2	Leucine-rich repeat-containing G-protein coupled receptor 4	GO:0007424,GO:0050710,GO:0005887,GO:0035151,GO:0090263,GO:0035159,GO:0016055,GO:0034122,GO:0004888,GO:0048511,GO:0007283,GO:0046849,GO:0005515,GO:0008045,GO:0007186,GO:0030282,GO:0001649	CG8561-PB				SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058								
aly2130.20	Unknown		n/a																				
aly2130.21	ABC transporter A family member 4	GO:0043190,GO:0042626,GO:0043231,GO:0006869,GO:0005215,GO:0016021,GO:0006810,GO:0031288,GO:0055085,GO:0005524	CG1718-PB				SM00382		PF12698,PF00005,PF00005	PS50893		PS00211	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									
aly2130.22	ATP-binding cassette sub-family A member 3	GO:0043190,GO:0042626,GO:0006810,GO:0005615,GO:0006869,GO:0097208,GO:0005215,GO:0016021,GO:0016020,GO:0042493,GO:0097233,GO:0005886,GO:0055085,GO:0005524	CG1718-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2130.23	UMP-CMP kinase	GO:0005737,GO:0006221,GO:0006207,GO:0009142,GO:0046939,GO:0004127,GO:0004550,GO:0006165,GO:0009041,GO:0005634,GO:0005524	CG6092-PA	MF_03172,MF_00235				TIGR01359	PF00406		PR00094,PR00094,PR00094,PR00094,PR00094	PS00113	G3DSA:3.40.50.300	SSF52540		00240+2.7.4.14,00230+2.7.4.3		PWY-7219,PWY-7176	UPA00588				
aly2130.24	Translation elongation factor 2	GO:0005737,GO:0003746,GO:0005829,GO:0005811,GO:0003924,GO:0006412,GO:0007052,GO:0000022,GO:0006414,GO:0005875,GO:0005525	CG2238-PD				SM00838,SM00889	TIGR00231	PF00679,PF03764,PF03144,PF00009,PF14492	PS51722	PR00315,PR00315,PR00315,PR00315	PS00301	G3DSA:2.40.30.10,G3DSA:3.30.70.240,G3DSA:3.90.1430.10,G3DSA:3.40.50.300,G3DSA:3.30.230.10,G3DSA:3.30.70.870	SSF52540,SSF54980,SSF54211,SSF50447,SSF54980									
aly2130.25	Elongation of very long chain fatty acids protein 7	GO:0009922,GO:0005783,GO:0016021,GO:0030497,GO:0005789,GO:0005575,GO:0016740,GO:0034626,GO:0022008,GO:0042761,GO:0019367	CG5326-PA						PF01151							00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					
aly2130.26	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 11	GO:0016021,GO:0055114,GO:0005747,GO:0005739	CG9350-PA																				
aly2130.27	RNA exonuclease 4	GO:0008408,GO:0005730,GO:0004527,GO:0090305,GO:0006364,GO:0003676,GO:0005634	CG6833-PA				SM00479		PF00929				G3DSA:3.30.420.10	SSF53098	160~160								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2130.3	Unknown	GO:0006662,GO:0015035,GO:0045454	CG18130-PA						PF15928				G3DSA:3.40.30.10										
aly2130.4	Eukaryotic translation initiation factor 3 subunit J	GO:0005737,GO:0005852,GO:0016282,GO:0006446,GO:0033290,GO:0022008,GO:0006413,GO:0001731,GO:0003743	CG12131-PA						PF08597				G3DSA:1.10.246.60		26~46,108~128								
aly2130.5	Unknown		n/a						PF16087														
aly2130.6	Protein PF14_0175	GO:0016021,GO:0003677	CG12964-PC												871~898,757~860								
aly2130.7	Oxysterol-binding protein-related protein 9	GO:0005737,GO:0005794,GO:0006869,GO:0008142,GO:0008289,GO:0031902	CG1513-PA				SM00233		PF00169,PF01237	PS50003		PS01013	G3DSA:2.30.29.30	SSF50729,SSF144000									
aly2130.8	Protein yellow	GO:0005737,GO:0060179,GO:0016853,GO:0048082,GO:0006583,GO:0048065,GO:0048066,GO:0048067,GO:0005576,GO:0042438,GO:0070451	CG4182-PA						PF03022		PR01366,PR01366,PR01366,PR01366		G3DSA:2.120.10.30	SSF63829,SSF63829	372~372								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2130.9	RING finger and CHY zinc finger domain-containing protein 1	GO:0005737,GO:0016607,GO:0032436,GO:0004842,GO:0002039,GO:0005634,GO:0000151,GO:0005654,GO:0016567,GO:0051865,GO:0042787,GO:0008270,GO:0031398,GO:0016874,GO:0042803	CG16947-PA				SM00184		PF05495,PF14599	PS50089,PS51270,PS51266			G3DSA:3.30.40.10,G3DSA:2.20.28.10	SSF161219,SSF57850,SSF161245									
aly2133.1	Unknown	GO:0005575,GO:0008150,GO:0004930,GO:0016020,GO:0003674	CG44153-PA						PF00431	PS01180			G3DSA:2.60.120.290	SSF49854									
aly213475.1	Glutamate receptor ionotropic, kainate 3	GO:0043197,GO:0035235,GO:0015277,GO:0006811,GO:0060025,GO:0007216,GO:0005234,GO:0045211,GO:0001640,GO:0004970,GO:0005886,GO:0016021,GO:0030054,GO:0007196	CG5621-PC				SM00918		PF10613				G3DSA:3.40.190.10	SSF53850									
aly21383.1	Solute carrier family 28 member 3	GO:0015855,GO:0006810,GO:0015389,GO:0015864,GO:0016020,GO:0006863,GO:0015860,GO:0005415,GO:0005887,GO:0015390,GO:0001895,GO:0072531,GO:0001882	CG8083-PA						PF07662								REACT_1698,REACT_15518						
aly214.1	Presenilins-associated rhomboid-like protein, mitochondrial	GO:0004252,GO:0004175,GO:0016021,GO:0090201,GO:2000377,GO:0005739,GO:0030162,GO:0005743,GO:0008053,GO:1903214,GO:1903146,GO:0016485,GO:0006508,GO:0005634,GO:2001243	CG8972-PA						PF01694				G3DSA:1.20.1540.10	SSF144091									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly214.10	Regulating synaptic membrane exocytosis protein 2	GO:0008021,GO:0061669,GO:0042391,GO:0005083,GO:0048167,GO:0010628,GO:0019933,GO:1903861,GO:0048791,GO:0007274,GO:0044325,GO:0030054,GO:0030073,GO:0070062,GO:0006886,GO:0048786,GO:0046872,GO:0017156,GO:0017157,GO:2000463,GO:0017137,GO:0007269,GO:0097151,GO:0070073,GO:0016192,GO:0042734,GO:0016079,GO:0005622	CG33547-PF				SM00239,SM00239,SM00228		PF02318,PF00168,PF00168,PF00595	PS50916,PS50106,PS50004,PS50004,PS50178			G3DSA:2.30.42.10,G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:3.30.40.10	SSF49562,SSF49562,SSF57903,SSF50156	1748~1748								
aly214.11	Host cell factor	GO:0045927,GO:0005671,GO:0043966,GO:0000123,GO:0043967,GO:0003700,GO:0003713,GO:0005634,GO:0004402,GO:0048188,GO:0045893,GO:0016573,GO:0051568,GO:0006338,GO:0003682,GO:0044666,GO:0007049,GO:0044665	CG1710-PB				SM00060,SM00060						G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265										
aly214.12	Small integral membrane protein 8	GO:0005575,GO:0003674,GO:0016021,GO:0008150	CG32448-PB						PF14937														
aly214.13	Rab-like protein 6	GO:0045175,GO:0005737,GO:0007264,GO:0016192,GO:0005730,GO:0005813,GO:0055037,GO:0031254,GO:0003924,GO:0045178,GO:0032482,GO:0046331,GO:0045202,GO:0007295,GO:0015031,GO:0005634,GO:0043025,GO:0031982,GO:0005525	CG17060-PA				SM00175		PF00071	PS51419	PR00449,PR00449		G3DSA:3.40.50.300	SSF52540,SSF52540	238~258								
aly214.14	F-box/LRR-repeat protein 6	GO:0005654,GO:2000060,GO:0031647,GO:0032093,GO:0005515	CG13213-PC				SM00367,SM00367,SM00367,SM00367		PF12937	PS50181			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047,SSF52047,SSF52047									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly214.15	Unknown	GO:0007443,GO:0007442,GO:0008104,GO:0035071,GO:0048567,GO:0002009,GO:0007422,GO:0008406,GO:0007391,GO:0007390,GO:0035262,GO:0048102,GO:0008360,GO:0035297,GO:0007435,GO:0046329,GO:0046328,GO:0007394,GO:0007417	CG12437-PA						PF15891														
aly214.16	Zinc finger CCCH-type with G patch domain-containing protein	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG4709-PA				SM00443		PF01585	PS50174,PS50103					421~448,510~547,1~32								
aly214.17	FK506-binding protein 15	GO:0016020,GO:0006897,GO:0010923,GO:0030426,GO:0030424,GO:0006457,GO:0005769	n/a										G3DSA:1.20.58.60		406~426,256~276,445~472,353~373								
aly214.18	Zinc finger protein 622	GO:0005737,GO:0005794,GO:0008631,GO:0005730,GO:0044822,GO:0033674,GO:0043410,GO:0046330,GO:0043065,GO:0008270,GO:0003676,GO:0046872	CG6769-PB				SM00451,SM00451,SM00355,SM00355,SM00355,SM00355		PF12756,PF12171			PS00028,PS00028		SSF57667,SSF57667	45~65								
aly214.19	Unknown		n/a																				
aly214.2	S-formylglutathione hydrolase	GO:0005737,GO:0005794,GO:0070062,GO:0016023,GO:0005654,GO:0046294,GO:0052689,GO:0016788,GO:0018738,GO:0005886,GO:0047374	CG4390-PB					TIGR02821	PF00756				G3DSA:3.40.50.1820	SSF53474		00680+3.1.2.12		PWY-1801					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly214.20	Arginase-2, mitochondrial	GO:0004053,GO:0000050,GO:0005739,GO:0006941,GO:0034641,GO:0006525,GO:0019547,GO:0001657,GO:0005759,GO:0046872,GO:0006809,GO:0044281	CG18104-PA					TIGR01229	PF00491	PS51409	PR00116,PR00116,PR00116,PR00116,PR00116	PS01053	G3DSA:3.40.800.10	SSF52768		00330+3.5.3.1	REACT_13	PWY-4984,PWY-6305,PWY-6922,PWY-31	UPA00158				
aly214.21	Unknown		n/a						PF00089				G3DSA:2.40.10.10	SSF50494									
aly214.22	Odorant receptor 4	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0004984	CG17911-PA						PF02949														
aly214.23	Unknown		n/a										G3DSA:3.30.60.30										
aly214.24	Unknown		CG10936-PA						PF01390	PS50024				SSF82671	1122~1142								
aly214.25	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly214.26	Lipoprotein lipase	GO:0034361,GO:0042627,GO:0016042,GO:0005575,GO:0004465,GO:0005886,GO:0009749,GO:0016298,GO:0008201,GO:0031225	CG6472-PB						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly214.27	Unknown		n/a																				
aly214.28	Unknown		n/a																				
aly214.3	Protein Mpv17	GO:0005778,GO:0000002,GO:0016021,GO:0042592,GO:0005743,GO:0003674	CG11077-PA						PF04117														
aly214.4	DnaJ homolog subfamily C member 5 homolog	GO:0031987,GO:0008021,GO:0006457,GO:0016192,GO:0016191,GO:0048854,GO:0006887,GO:0001964,GO:0061177,GO:0061176,GO:0007269,GO:0016079,GO:0043195,GO:0005886	CG6395-PB				SM00271		PF00226	PS50076	PR00625,PR00625,PR00625,PR00625		G3DSA:1.10.287.110	SSF46565									
aly214.5	Acetylcholine receptor subunit alpha-L1	GO:0006810,GO:0016021,GO:0005230,GO:0016020,GO:0005892,GO:0045211,GO:0004889,GO:0007271,GO:0006811,GO:0030054	CG11822-PA						PF02931				G3DSA:1.20.120.370,G3DSA:2.70.170.10	SSF63712,SSF90112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly214.6	Unknown		n/a						PF00079				G3DSA:3.30.497.10	SSF56574									
aly214.7	Antichymotrypsin-2	GO:0060570,GO:0005783,GO:0005576,GO:0030162,GO:0004867,GO:0010951,GO:0004869,GO:0010955,GO:0005615	CG9453-PB				SM00093		PF00079				G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574									
aly214.8	Serine protease inhibitor 3/4 (Fragment)	GO:0060570,GO:0005783,GO:0005576,GO:0030162,GO:0004867,GO:0010951,GO:0004869,GO:0010955,GO:0005615	CG9453-PB				SM00093		PF00079				G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574,SSF56574									
aly214.9	Cytochrome c oxidase subunit 6A2, mitochondrial	GO:0004129,GO:0005743,GO:0006091,GO:0005751	CG30093-PA						PF02046			PS01329	G3DSA:4.10.95.10	SSF81411									
aly214261.1	Coatomer subunit epsilon	GO:0006891,GO:0006890,GO:0006888,GO:0005198,GO:0005654,GO:0015031,GO:0030126,GO:0005875	CG9543-PA						PF04733														
aly21430.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2144.1	Unknown		n/a																				
aly2145.1	Zinc finger MIZ domain-containing protein 1	GO:0005737,GO:0016607,GO:0001701,GO:0007569,GO:0048589,GO:0048096,GO:0006351,GO:0048146,GO:0048844,GO:0005654,GO:0001570,GO:0003007,GO:0045944,GO:0008270,GO:0007296,GO:0043231	CG7958-PB						PF02891	PS51044			G3DSA:3.30.40.10						UPA00886				
aly21473.1	Facilitated trehalose transporter Tret1-1	GO:0005355,GO:0035428,GO:0015992,GO:0015771,GO:0016021,GO:0016020,GO:0046323,GO:0008643,GO:0022857,GO:0015574,GO:0005887,GO:0005886,GO:0005351,GO:0055085	CG30035-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly2148.1	Small nuclear ribonucleoprotein Sm D3	GO:0007067,GO:0007417,GO:0007517,GO:0005634,GO:0034709,GO:0030182,GO:0071011,GO:0071013,GO:0000387,GO:0034715,GO:0007052,GO:0034719,GO:0045451,GO:0007422,GO:0005829,GO:0030532,GO:0000398,GO:0071208,GO:0005687,GO:0048542,GO:0005685,GO:0005681,GO:0045495	CG8427-PA				SM00651		PF01423				G3DSA:2.30.30.100	SSF50182									
aly2148.10	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	GO:0006744,GO:0008757,GO:0005739,GO:0043334,GO:0031314,GO:0008425,GO:0008168,GO:0032259	CG2453-PA	MF_01813				TIGR01934	PF01209	PS51608		PS01183	G3DSA:3.40.50.150	SSF53335		00130+2.1.1.163		PWY-5849,PWY-5895,PWY-5891,PWY-5890,PWY-5892,PWY-5844,PWY-5839	UPA00079				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2148.11	Serine/arginine rich splicing factor 9	GO:0008380,GO:0005515,GO:0005730,GO:0071011,GO:0005634,GO:0044822,GO:0003998,GO:0000166,GO:0005654,GO:0006376,GO:0003676,GO:0048025,GO:0007095,GO:0022008,GO:0006397,GO:0071013,GO:0005681,GO:0003729	CG6987-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928										
aly2148.12	Dynein light chain 2, cytoplasmic	GO:0005856,GO:0005737,GO:0007017,GO:0042623,GO:0007018,GO:0003774,GO:0008152,GO:0005868,GO:0030286,GO:0005874,GO:0005875	CG5450-PA						PF01221			PS01239	G3DSA:3.30.740.10	SSF54648			REACT_578						
aly2148.13	Unknown		n/a																				
aly2148.14	Phenoloxidase subunit 1	GO:0006952,GO:0036264,GO:0036263,GO:0005615,GO:0006583,GO:0042417,GO:0005576,GO:0008152,GO:0004503,GO:0046872	CG8193-PA						PF03722,PF03723,PF00372		PR00187,PR00187,PR00187,PR00187	PS00210,PS00498,PS00209	G3DSA:1.20.1370.10,G3DSA:1.10.1280.10,G3DSA:2.60.40.1520	SSF48056,SSF81296,SSF48050										
aly2148.15	Phenoloxidase subunit 1	GO:0006952,GO:0036264,GO:0036263,GO:0005615,GO:0006583,GO:0042417,GO:0005576,GO:0008152,GO:0004503,GO:0046872	CG8193-PA						PF03722,PF00372,PF03723		PR00187,PR00187,PR00187,PR00187	PS00210,PS00209	G3DSA:1.10.1280.10,G3DSA:2.60.40.1520,G3DSA:1.20.1370.10	SSF48050,SSF48056,SSF81296										
aly2148.16	Phenoloxidase subunit 1	GO:0006952,GO:0036264,GO:0036263,GO:0005615,GO:0006583,GO:0042417,GO:0005576,GO:0008152,GO:0004503,GO:0046872	CG8193-PA						PF03722,PF03723,PF03723,PF00372		PR00187,PR00187,PR00187,PR00187	PS00210,PS00498,PS00209	G3DSA:1.10.1280.10,G3DSA:1.20.1370.10,G3DSA:2.60.40.1520,G3DSA:2.60.40.1520	SSF81296,SSF48050,SSF48056										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2148.17	Phenoloxidase subunit 1	GO:0006952,GO:0036264,GO:0036263,GO:0005615,GO:0006583,GO:0042417,GO:0005576,GO:0008152,GO:0004503,GO:0046872	CG8193-PA						PF03722,PF03723,PF00372		PR00187,PR00187,PR00187,PR00187	PS00210,PS00498,PS00209	G3DSA:1.10.1280.10,G3DSA:1.20.1370.10,G3DSA:2.60.40.1520	SSF81296,SSF48056,SSF48050									
aly2148.18	Unknown		n/a																				
aly2148.19	Calcium/calmodulin-dependent protein kinase kinase 2	GO:0005737,GO:0006468,GO:0045859,GO:0004683,GO:0004713,GO:0005634,GO:0019722,GO:0000165,GO:0018108,GO:0005622,GO:0004674,GO:0005509,GO:0045893,GO:0004672,GO:0042995,GO:0046777,GO:0005524,GO:0005516	CG17698-PF				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112,SSF56112									
aly2148.2	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG4576-PA						PF01757														
aly2148.3	Unknown		n/a																				
aly2148.4	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG9447-PC						PF01757														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2148.5	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG4576-PA						PF01757														
aly2148.6	Unknown		CG4658-PB				SM00584		PF07534														
aly2148.7	Peroxisome assembly protein 12	GO:0005779,GO:0007031,GO:0016558,GO:0006625,GO:0005777,GO:0008022,GO:0008270,GO:0007286,GO:0048137	CG3639-PA			PIRSF038074	SM00184		PF04757				G3DSA:3.30.40.10	SSF57850									
aly2148.8	Unknown		n/a																				
aly2148.9	Protein GUCD1		CG13760-PC						PF09778														
aly21483.1	Aristaless-related homeobox protein	GO:0048666,GO:0042463,GO:0006351,GO:0042052,GO:0042051,GO:0043565,GO:0003700,GO:0005634,GO:0003322,GO:0021539,GO:0006355,GO:0001077,GO:0045893,GO:0003677,GO:0042803	CG2819-PA				SM00389		PF00046	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly21483.2	Unknown		n/a																				
aly21488.1	Unknown		n/a																				
aly2149.1	Unknown		n/a																				
aly2149.2	TBC1 domain family member 1	GO:0005178,GO:0032313,GO:0009986,GO:0005096,GO:0005097,GO:0005515,GO:0005634,GO:0033627	CG1093-PA				SM00164,SM00462		PF00640,PF11830,PF00566	PS50086,PS01179			G3DSA:2.30.29.30,G3DSA:1.10.8.270	SSF47923,SSF50729									
aly2149.3	Unknown	GO:0003677	CG8359-PA				SM00595,SM00595		PF10545,PF10545,PF02944	PS51031,PS51029,PS51029													
aly2149.4	Unknown		n/a				SM00595		PF02944,PF10545	PS51029,PS51031													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2149.5	Unknown		CG8281-PA				SM00595		PF10545	PS51029					71~91								
aly215.1	ATP-binding cassette sub-family G member 1	GO:0009897,GO:0034375,GO:0034374,GO:0055037,GO:0017127,GO:0030301,GO:0034041,GO:0055099,GO:0042987,GO:1901998,GO:0055091,GO:0005548,GO:0042626,GO:0033993,GO:0016021,GO:0005739,GO:0005654,GO:0034436,GO:0034437,GO:0010745,GO:0010875,GO:0005524,GO:0033700,GO:0005794,GO:0005215,GO:0006810,GO:0042803,GO:0043531,GO:0005886,GO:0010872,GO:0042632,GO:0043691,GO:0010033,GO:0008203,GO:0043190,GO:0019534,GO:0043231,GO:0032367,GO:0006355,GO:0033344,GO:0045542,GO:0046982,GO:0005768,GO:0010888	CG32091-PB				SM00382		PF01061,PF00005	PS50893		PS00211	G3DSA:3.40.50.300	SSF52540										
aly215.10	Unknown		n/a																				
aly215.11	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly215.12	Zinc finger and BTB domain-containing protein 24	GO:0006909,GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12071-PD				SM00355,SM00355,SM00355,SM00355		PF12230	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:2.60.120.10	SSF81995,SSF57667	292~322,46~79								
aly215.13	Unknown	GO:0000122,GO:0005634,GO:0003677,GO:0008270,GO:0008407	CG10309-PB				SM00868		PF07776					SSF57716									
aly215.14	Nucleoside diphosphate kinase homolog 5	GO:0042384,GO:1902176,GO:0006228,GO:0036126,GO:0005622,GO:0007283,GO:0006241,GO:0004550,GO:0005524,GO:0006165,GO:0007286,GO:0021591,GO:0003351,GO:0006183,GO:0009116	CG5310-PA				SM00562		PF05186,PF00334				G3DSA:3.30.70.141	SSF54919		00230+2.7.4.6,00240+2.7.4.6		PWY-7210,PWY-7198,PWY-7176,PWY-7220,PWY-7184,PWY-7187,PWY-7205,PWY-7224,PWY-7197,PWY-7226,PWY-						
aly215.15	Sulfated glycoprotein 1	GO:0033227,GO:0005615,GO:0045169,GO:0005764,GO:0046836,GO:0006665	CG12070-PA				SM00162,SM00162,SM00741,SM00741,SM00741,SM00741,SM00741		PF02199,PF02199,PF03489,PF03489,PF03489,PF03489,PF03489,PF05184,PF05184,PF05184,PF05184,PF05184	PS50015,PS51110,PS50015,PS50015,PS50015,PS50015,PS50015,PS50015,PS51110	PR01797,PR01797,PR01797,PR01797,PR01797,PR01797,PR01797		G3DSA:1.10.225.10,G3DSA:1.10.225.10,G3DSA:1.10.225.10,G3DSA:1.10.225.10,G3DSA:1.10.225.10,G3DSA:1.10.225.10,G3DSA:1.10.225.10,G3DSA:1.10.225.10	SSF47862,SSF47862,SSF47862,SSF47862,SSF47862,SSF47862,SSF47862,SSF47862,SSF47862									
aly215.16	Unknown	GO:0043565,GO:0003700,GO:0005634,GO:0048813,GO:0006357,GO:0005667	CG1447-PE																				
aly215.17	Pituitary homeobox homolog Ptx1	GO:0043565,GO:0003700,GO:0005634,GO:0048813,GO:0006357,GO:0006351,GO:0005667,GO:0003677	CG1447-PE			PIRSF000563	SM00389		PF03826,PF00046	PS50803,PS50071		PS00027	G3DSA:1.10.10.60	SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly215.18	Progestin and adipoQ receptor family member 3	GO:0005794,GO:0034067,GO:0016021,GO:0033137,GO:0000139,GO:0043407,GO:0010977,GO:0004872,GO:0001933	CG7530-PA						PF03006														
aly215.19	Ubiquitin-conjugating enzyme E2-17 kDa	GO:0001751,GO:0007067,GO:0001745,GO:0061630,GO:0000209,GO:0007140,GO:0004842,GO:0005875,GO:0042787,GO:0048477,GO:0005524,GO:0016322,GO:0008054,GO:0007286,GO:0048132,GO:0022008,GO:0016874,GO:0061631,GO:0030718,GO:0031625,GO:0051276,GO:0031647,GO:0045676,GO:0016567,GO:0006511,GO:0005515	CG7425-PA				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				
aly215.2	Malate dehydrogenase, cytoplasmic	GO:0019674,GO:0051287,GO:0006734,GO:0006099,GO:0005737,GO:0044262,GO:0070062,GO:0043209,GO:0005813,GO:0005811,GO:0005777,GO:0005739,GO:0003824,GO:0046331,GO:0055114,GO:0005615,GO:0005975,GO:0016615,GO:0016616,GO:0005829,GO:0006107,GO:0030060,GO:0006108,GO:1903146	CG5362-PA	MF_01517		PIRSF000102		TIGR01759,TIGR01758	PF02866,PF00056			PS00068	G3DSA:3.90.110.10,G3DSA:3.40.50.720	SSF51735,SSF56327		00630+1.1.1.37,00680+1.1.1.37,00720+1.1.1.37,00710+1.1.1.37,00620+1.1.1.37,00270+1.1.1.37,00020+1.1.1.37	REACT_474	PWY-561,PWY-5913,PWY-1622,PWY-7383,PWY-5392,PWY-6969,PWY-6728,PWY-7115,PWY-5690					
aly215.20	Cadherin-23	GO:0007424,GO:0016021,GO:0032420,GO:0051480,GO:0050896,GO:0016339,GO:0016020,GO:0007601,GO:0006816,GO:0050953,GO:0007605,GO:0005509,GO:0005887,GO:0005886,GO:0050957,GO:0007156,GO:0005829,GO:0045494	CG3389-PB				SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112		PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028	PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313	1753~1767								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly215.21	Tyrosine-protein phosphatase non-receptor type 13	GO:0016332,GO:0008105,GO:0005080,GO:0045197,GO:0045196,GO:0035003,GO:0007163,GO:0007043,GO:0007294,GO:0035335,GO:0007309,GO:0007298,GO:0007299,GO:0008356,GO:0040001,GO:0007416,GO:0045175,GO:0002009,GO:0045177,GO:0035089,GO:0070062,GO:0030709,GO:0045176,GO:0045179,GO:0000281,GO:0051490,GO:0030027,GO:0060446,GO:0006470,GO:0055059,GO:0005737,GO:0043005,GO:0016324,GO:0016325,GO:0070300,GO:0016327,GO:0044297,GO:0008594,GO:0045186,GO:0005914,GO:0005913,GO:0005938,GO:0005886,GO:0072002,GO:0014066,GO:0036312,GO:0001738,GO:2000040,GO:0045167,GO:0007377,GO:0090175,GO:0035091,GO:0004725,GO:0005856,GO:0005915,GO:0090250,GO:0007314,GO:0005515,GO:0043296,GO:0005634,GO:0005912	CG5055-PB				SM00228,SM00228,SM00228		PF00595,PF00595,PF16063	PS50106,PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156,SSF50156									
aly215.22	Unknown		n/a																				
aly215.3	Leucine-rich PPR motif-containing protein, mitochondrial	GO:0016020,GO:0048487,GO:0051028,GO:0042645,GO:0005874,GO:0005737,GO:0005654,GO:0005637,GO:0005634,GO:0047497,GO:0005739,GO:0030529,GO:0000961,GO:0034518,GO:0003730,GO:0048471,GO:0044822,GO:0006351,GO:0005856,GO:0008017,GO:0070129,GO:0000794,GO:0031625,GO:0005640,GO:0003697,GO:0006355,GO:0003723	CG10302-PA						PF12854	PS51375,PS51375,PS51375,PS51375,PS51375,PS51375,PS51375,PS51375			G3DSA:1.25.40.10,G3DSA:1.25.40.10											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly215.4	Unknown		n/a																				
aly215.5	Unknown	GO:0015630,GO:0030715,GO:0030720,GO:0051017,GO:0008407,GO:0051663,GO:0003674,GO:0016325,GO:0006403,GO:0046843	CG43162-PD												217~237								
aly215.6	WW domain-containing oxidoreductase	GO:0005737,GO:0010165,GO:0006915,GO:0016614,GO:0016055,GO:2000377,GO:0005515,GO:0050829,GO:0010212,GO:0016491	CG7221-PA				SM00456,SM00456		PF00106,PF00397	PS50020,PS50020	PR00081,PR00081,PR00081		G3DSA:3.40.50.720,G3DSA:2.20.70.10,G3DSA:2.20.70.10	SSF51045,SSF51735,SSF51045									
aly215.7	Unknown	GO:0016021,GO:0055085,GO:0008513	CG15221-PB										G3DSA:1.20.1250.20										
aly215.8	Synaptic vesicle glycoprotein 2A	GO:0008021,GO:0005783,GO:0006836,GO:0031594,GO:0004872,GO:0005737,GO:0016021,GO:0048786,GO:0043005,GO:0006874,GO:0006629,GO:0005215,GO:0006810,GO:0019901,GO:0005911,GO:0007268,GO:0043195,GO:0055085,GO:0030672,GO:0022857,GO:0016298,GO:0045202	CG31272-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly215.9	Synaptic vesicle glycoprotein 2A	GO:0048786,GO:0030672,GO:0006629,GO:0005215,GO:0016021,GO:0006810,GO:0031594,GO:0022857,GO:0004872,GO:0005911,GO:0006874,GO:0045202,GO:0043195,GO:0006836,GO:0016298,GO:0055085,GO:0005783	CG31272-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly215169.1	Aldo-keto reductase AKR2E4	GO:0008106,GO:0035220,GO:0022416,GO:0055114,GO:0008202,GO:0016491	CG2767-PA						PF00248			PS00063	G3DSA:3.20.20.100	SSF51430									
aly21519.1	Proclotting enzyme	GO:0006508,GO:0045087,GO:0005576,GO:0042381,GO:0004252	CG31217-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly21519.2	Low-density lipoprotein receptor (Fragment)	GO:0005794,GO:0034362,GO:0016021,GO:0006897,GO:0004252,GO:0045087,GO:0005770,GO:0005769,GO:0006869,GO:0005905,GO:0005509,GO:0005515,GO:0005886,GO:0005764,GO:0006508,GO:0009986,GO:0008203	CG31217-PA				SM00192,SM00192,SM00192,SM00192		PF00057,PF00057,PF00057,PF00057	PS50068,PS50068,PS50068,PS50068	PR00261,PR00261,PR00261,PR00261	PS01209,PS01209,PS01209	G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10	SSF57424,SSF57424,SSF57424,SSF57424									
aly21535.1	Protein PET100 homolog, mitochondrial	GO:0033617,GO:0016021,GO:0005739	CG14483-PA						PF09803														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly21535.2	Major facilitator superfamily domain-containing protein 9	GO:0005215,GO:0016021,GO:0055085	n/a										G3DSA:1.20.1250.20	SSF103473									
aly2154.1	Pancreatic triacylglycerol lipase (Fragment)	GO:0004806,GO:0008970,GO:0016042,GO:0005575,GO:0005576,GO:0022008,GO:0046872,GO:0016298	CG6277-PA						PF00151,PF00151,PF00151,PF00151		PR00821,PR00821,PR00821		G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474,SSF53474,SSF53474									
aly2154.10	General odorant-binding protein 69a	GO:0005549,GO:0005615,GO:0032504,GO:0007606,GO:0008145,GO:0005550,GO:0005576	CG8462-PA				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly2154.11	Adenylate cyclase type 2	GO:0045121,GO:0007268,GO:0030425,GO:0004016,GO:0007165,GO:0034199,GO:0035556,GO:0008543,GO:0005737,GO:0071377,GO:0003091,GO:0016021,GO:0016020,GO:0016849,GO:0007188,GO:0007189,GO:0006112,GO:0009190,GO:0006171,GO:0005524,GO:0045087,GO:0006833,GO:0007173,GO:0005886,GO:0048011,GO:0008179,GO:0055085,GO:0046872,GO:0007202,GO:0005622,GO:0007193,GO:0046982,GO:0044281	CG5712-PA				SM00044,SM00044		PF16214,PF00211,PF00211	PS50125,PS50125		PS00452	G3DSA:3.30.70.1230,G3DSA:3.30.70.1230	SSF55073,SSF55073	376~396								
aly2154.12	Leucine-rich repeat neuronal protein 2	GO:0016021,GO:0007476,GO:0003674,GO:0004872,GO:0005515,GO:0007155,GO:0042981,GO:0007165	CG34368-PC				SM00082,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365		PF13306,PF00560,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2154.13	Unknown		n/a												52~67								
aly2154.14	Lipase member H-A	GO:0016020,GO:0052689,GO:0016042,GO:0005575,GO:0005576,GO:0016298	CG10116-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly2154.15	Lipase member I	GO:0005615,GO:0008970,GO:0016020,GO:0052689,GO:0016042,GO:0005575,GO:0005576,GO:0004620,GO:0005886,GO:0022008,GO:0016298,GO:0008201	CG6277-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly2154.2	Pancreatic lipase-related protein 2	GO:0009395,GO:0047714,GO:0004806,GO:0005615,GO:0008970,GO:0016042,GO:0005575,GO:0005509,GO:0019376,GO:0004620,GO:0016298,GO:0047372	CG6271-PA						PF00151,PF00151,PF00151		PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474,SSF53474									
aly2154.3	Unknown		CG15239-PA						PF15998														
aly2154.4	Unknown	GO:0005488	CG15239-PA						PF15998					SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2154.5	Unknown	GO:0005575,GO:0003674,GO:0008150	CG34038-PB						PF15998														
aly2154.6	Unknown	GO:0005575,GO:0003674,GO:0008150	CG34038-PB						PF15998														
aly2154.7	Unknown		CG8568-PA						PF15998														
aly2154.8	N-alpha-acetyltransferase 35, NatC auxiliary subunit	GO:0005737,GO:0008284,GO:0031417,GO:0043066,GO:0003674,GO:0048659,GO:0032006,GO:0008150,GO:0001756,GO:0048514	CG4065-PA						PF04112						206~229,454~474								
aly2154.9	Unknown		n/a																				
aly2159.1	Caspase	GO:0097200,GO:0010165,GO:0097194,GO:0097153,GO:1990525,GO:0035070,GO:0035103,GO:0012501,GO:0006915,GO:0016322,GO:0005737,GO:0046672,GO:0004197,GO:0046668,GO:0048515,GO:0045476,GO:0010623,GO:0006508,GO:2001269	CG7788-PA				SM00115		PF00656	PS50207,PS50208	PR00376,PR00376,PR00376,PR00376,PR00376	PS01121,PS01122	G3DSA:3.40.50.1460	SSF52129									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly21598.1	Unknown		n/a																				
aly216.1	Matrix metalloprotein ase-16	GO:0035202,GO:0097094,GO:0030425,GO:0031012,GO:0001503,GO:0008270,GO:0048701,GO:0008237,GO:0030574,GO:0016021,GO:0005509,GO:0006508,GO:0048477,GO:0046529,GO:0004222,GO:0042060,GO:0046331,GO:0005886,GO:0060348,GO:0040037,GO:0007424,GO:0007426,GO:0001958,GO:0007561,GO:0002218,GO:0035988,GO:0071711,GO:0034769	CG1794-PB				SM00235,SM00120,SM00120,SM00120,SM00120		PF01471,PF00413,PF00045,PF00045,PF00045	PS51642,PS51642,PS51642,PS51642	PR00138,PR00138,PR00138,PR00138,PR00138		G3DSA:3.40.390.10,G3DSA:2.110.10.10	SSF50923,SSF47090,SSF55486	852~852								
aly216.10	Armadillo repeat-containing protein 5	GO:0005737,GO:0000221,GO:0046961,GO:0015991	CG7837-PA				SM00185,SM00185,SM00185,SM00185,SM00225		PF00651	PS50097			G3DSA:1.25.10.10,G3DSA:3.30.710.10	SSF54695,SSF48371,SSF48371,SSF48371	1061~1063								
aly216.11	Mitochondrial inner membrane protein COX18	GO:0008565,GO:0051204,GO:0051205,GO:0020037,GO:0016021,GO:0016705,GO:0008535,GO:0031305,GO:0005743,GO:0015031,GO:0005506,GO:0055114	CG4942-PA						PF00067,PF02096		PR00463,PR00463,PR00463		G3DSA:1.10.630.10	SSF48264	43~63		REACT_13433						
aly216.12	Cytochrome P450 315a1, mitochondrial	GO:0007417,GO:0016020,GO:0007494,GO:0020037,GO:0008258,GO:0016705,GO:0007391,GO:0031966,GO:0005739,GO:0006697,GO:0008045,GO:0005506,GO:0009055,GO:0055114,GO:0042768	CG14728-PA						PF00067				G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.13	26S proteasome non-ATPase regulatory subunit 2	GO:0004175,GO:0005838,GO:0070062,GO:0022624,GO:0008283,GO:0043161,GO:0030234,GO:0016020,GO:0042176,GO:0007052,GO:0006508,GO:0000022,GO:0008540	CG7762-PA			PIRSF015965			PF01851,PF01851				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371	22~42,936~940		REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045						
aly216.14	PRKR-interacting protein 1 homolog	GO:0005730	CG8441-PA						PF06658						94~131								
aly216.15	Enolase	GO:0000015,GO:0005737,GO:0005811,GO:0000287,GO:0004634,GO:0005886,GO:0006096	CG17654-PD	MF_00318		PIRSF001400		TIGR01060	PF03952,PF00113		PR00148,PR00148,PR00148,PR00148,PR00148,PR00148	PS00164	G3DSA:3.20.20.120,G3DSA:3.30.390.10	SSF54826,SSF51604		00680+4.2.1.11,00010+4.2.1.11	REACT_474	PWY-1042,PWY-2221,PWY-1622,PWY-6901,PWY-7218,PWY-6886,PWY-5723,PWY-6142,PWY-5484,PWY-7124,PWY-	UPA00109				
aly216.16	Unknown	GO:0005575,GO:0008150,GO:0003674	CG44242-PB						PF10937														
aly216.17	Phosphonates-binding periplasmic protein	GO:0042916,GO:0043190,GO:0042597,GO:0042917	n/a						PF12974					SSF53850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.18	THO complex subunit 5 homolog	GO:0043234,GO:0005737,GO:0051028,GO:0005730,GO:0030154,GO:0016607,GO:0003674,GO:0006406,GO:0000347,GO:0000228,GO:0006397,GO:0008380,GO:0007140,GO:0003723	CG2980-PA						PF09766														
aly216.19	Serine/threonine-protein kinase unc-51	GO:0019894,GO:0009267,GO:0035069,GO:0016236,GO:0034273,GO:0050804,GO:0051124,GO:0030516,GO:0050808,GO:0007411,GO:0046777,GO:0032880,GO:0040024,GO:0045138,GO:0007409,GO:0008088,GO:0004674,GO:0010508,GO:0043005,GO:0004672,GO:0016477,GO:0010506,GO:0005524,GO:0006468,GO:0006914,GO:0016301,GO:0012501,GO:0008361,GO:0001558,GO:0045476,GO:0043277,GO:0008340,GO:0034599,GO:0030424,GO:0006979,GO:0006897,GO:0040014,GO:0043025,GO:0009792,GO:0032007	CG10967-PB				SM00220		PF12063,PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112,SSF56112									
aly216.2	Cytochrome c oxidase assembly protein COX19	GO:0005758,GO:0005829,GO:0009060,GO:0033617	CG42496-PA						PF06747				G3DSA:1.10.810.10	SSF47072									
aly216.20	Density-regulated protein homolog	GO:0008284,GO:0035076,GO:0046628,GO:0002188,GO:0045948,GO:0003743,GO:0006413,GO:0003729	CG9099-PB					TIGR01159	PF01253	PS50296			G3DSA:3.30.780.10	SSF55159									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.21	Septin-4	GO:0000910,GO:0005856,GO:0031105,GO:0005940,GO:0007420,GO:0030382,GO:0031514,GO:0097227,GO:0036126,GO:0003924,GO:0005739,GO:0043065,GO:0043209,GO:0051301,GO:0031398,GO:0007286,GO:2001244,GO:0042995,GO:0048240,GO:0007049,GO:0005525	CG9699-PA			PIRSF006698			PF00735	PS51719			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	376~403								
aly216.22	Carboxypeptidase M	GO:0004181,GO:0004185,GO:0008270,GO:0005886,GO:0006508,GO:0031225	CG4678-PE				SM00631		PF13620,PF00246		PR00765,PR00765,PR00765,PR00765	PS00133,PS00132	G3DSA:2.60.40.1120,G3DSA:3.40.630.10	SSF49464,SSF53187									
aly216.23	Replication factor C subunit 5	GO:0005634,GO:0017111,GO:0005663,GO:0046331,GO:0006260,GO:0006261,GO:0003677,GO:0022008,GO:0005875,GO:0005524	CG5313-PA				SM00382		PF08542,PF00004				G3DSA:3.40.50.300,G3DSA:1.10.8.60,G3DSA:1.20.272.10	SSF52540,SSF48019			REACT_152,REACT_216,REACT_22172,REACT_383,REACT_1538						
aly216.24	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1	GO:0004483,GO:0080009,GO:0005634,GO:0097309,GO:0006370,GO:0003676,GO:0008168,GO:0032259	CG6379-PA				SM00443		PF01585,PF01728	PS50174,PS51613			G3DSA:3.40.50.150	SSF53335				PWY-7379					
aly216.25	THO complex subunit 4-A	GO:0005737,GO:0016607,GO:0071011,GO:0003713,GO:0071013,GO:0031965,GO:0000398,GO:0000166,GO:0005654,GO:0003723,GO:0003676,GO:0051028,GO:0006397,GO:0008380,GO:0003729	CG1101-PA				SM00360		PF13865,PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly216.26	Methyltransferase-like protein 16	GO:0005575,GO:0008168,GO:0032259,GO:0003676	CG7544-PA			PIRSF037350			PF05971				G3DSA:3.40.50.150	SSF53335	364~384								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.27	Unknown		n/a																				
aly216.28	Histone RNA hairpin-binding protein	GO:0005737,GO:0005634,GO:0008334,GO:0006398,GO:0007076,GO:0003723,GO:0035613,GO:0007275,GO:0007049,GO:0003729	CG11886-PA						PF15247														
aly216.29	High mobility group protein 20A	GO:0006355,GO:0005634,GO:0006351,GO:0003677	CG9418-PA				SM00398		PF00505	PS50118			G3DSA:1.10.30.10	SSF47095	234~271								
aly216.3	Probable RNA binding protein 19	GO:0005737,GO:0005730,GO:0040019,GO:0005634,GO:0016020,GO:0044822,GO:0004386,GO:0005654,GO:0003676,GO:0000166,GO:0005694,GO:0007275,GO:0003729	CG3335-PA				SM00360,SM00360,SM00360,SM00360,SM00360,SM00360		PF00076,PF00076,PF00076,PF00076,PF00076,PF00076	PS50102,PS50102,PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928,SSF54928,SSF54928	113~137								
aly216.30	Exportin-6	GO:0016319,GO:0005737,GO:0005730,GO:0006611,GO:0006886,GO:0008565,GO:0008536,GO:0007629,GO:0007628,GO:0005654,GO:0048036,GO:0005886,GO:0005634,GO:0007614	CG3923-PC				SM00913		PF03810,PF08389	PS50166			G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371									
aly216.31	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.32	ADP-ribose pyrophosphatase, mitochondrial	GO:0016787,GO:0070062,GO:0046709,GO:0005739,GO:0046032,GO:0043262,GO:0047631	CG4098-PA						PF00293	PS51462			G3DSA:3.90.79.10	SSF55811									
aly216.33	Condensin complex subunit 1	GO:0005737,GO:0000070,GO:0005634,GO:0007052,GO:0000796,GO:0007076,GO:0000785,GO:0007067,GO:0005694,GO:0005829,GO:0051301	CG1911-PA			PIRSF017127			PF12717,PF12922				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371	561~581,435~455								
aly216.34	Translocon-associated protein subunit gamma	GO:0005786,GO:0044267,GO:0005784,GO:0016021,GO:0005811,GO:0006614,GO:0006412,GO:0010467,GO:0030176,GO:0006613	CG5885-PA						PF07074														
aly216.35	Metabotropic glutamate receptor	GO:0004930,GO:0015485,GO:0042734,GO:0038038,GO:0016021,GO:0045121,GO:0007216,GO:0007528,GO:0008066,GO:0051966,GO:0001642,GO:0001641,GO:0005886,GO:0005887,GO:0007186,GO:0072553,GO:0016595,GO:0007196	CG32447-PB						PF00003	PS50259													
aly216.36	CUE domain-containing protein 1	GO:0005515	CG12024-PA				SM00546		PF02845	PS51140			G3DSA:1.10.8.10	SSF46934	144~164								
aly216.37	Vacuolar fusion protein CCZ1 homolog	GO:0005765,GO:0016021,GO:0015205	CG14767-PC						PF03821,PF08217,PF08217														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.38	EF-hand domain-containing family member C2	GO:0051124,GO:0043195,GO:0043025,GO:0030425,GO:0048814,GO:0005874,GO:0005509	CG8959-PA				SM00676,SM00676,SM00676		PF06565,PF06565,PF06565	PS51336,PS51336,PS51336			G3DSA:1.10.238.10	SSF47473									
aly216.39	Dual oxidase maturation factor 1	GO:0008105,GO:2000379,GO:0007616,GO:0016021,GO:2000609,GO:0050727,GO:0045178,GO:0005789,GO:0045666,GO:0042743,GO:0005515,GO:0005886,GO:0015031,GO:0007611,GO:0006979,GO:0008355	CG4482-PA						PF10204														
aly216.4	Transmembrane 9 superfamily member 3	GO:0016021,GO:0005768	CG10590-PA						PF02990,PF02990														
aly216.40	Dual oxidase	GO:0042744,GO:0055114,GO:0042335,GO:0072593,GO:0019221,GO:0020037,GO:0048085,GO:0016021,GO:0016175,GO:0016174,GO:0035220,GO:0006979,GO:0051591,GO:0043066,GO:0012505,GO:0005509,GO:0008365,GO:0004601,GO:0002385,GO:0042742	CG3131-PC				SM00054,SM00054		PF03098,PF00036,PF08022,PF01794,PF08030	PS50222,PS50292,PS50222,PS51384,PS50222	PR00457,PR00457,PR00457,PR00457,PR00457	PS00018,PS00018	G3DSA:2.40.30.10,G3DSA:3.40.50.80,G3DSA:1.10.640.10,G3DSA:1.10.238.10	SSF63380,SSF47473,SSF48113,SSF52343									
aly216.41	Transcription factor 15	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003677,GO:0046983,GO:0007275	CG33557-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.42	Integrin alpha-PS1	GO:0007494,GO:0048567,GO:0050840,GO:0030154,GO:0035160,GO:0007160,GO:0004872,GO:0007411,GO:0005925,GO:0007414,GO:0007435,GO:0007432,GO:0007431,GO:0034446,GO:0007476,GO:0007475,GO:0009925,GO:0016477,GO:0033627,GO:0016203,GO:0016328,GO:0007608,GO:0007424,GO:0016324,GO:0008305,GO:0016337,GO:0005887,GO:0007155,GO:0007157,GO:0050839,GO:0007015,GO:0007427,GO:0007426,GO:0007229,GO:0046982	CG1771-PF				SM00191,SM00191,SM00191,SM00191		PF08441,PF01839,PF01839,PF01839	PS51470,PS51470,PS51470,PS51470,PS51470,PS51470,PS51470,PS51470	PR01185,PR01185,PR01185,PR01185,PR01185,PR01185,PR01185,PR01185	PS00242	G3DSA:2.130.10.130,G3DSA:2.60.40.1460,G3DSA:2.60.40.1510,G3DSA:2.60.40.1530,G3DSA:2.60.40.1530,G3DSA:1.20.5.930	SSF69318,SSF69179,SSF69179,SSF69179,SSF69179,SSF69179,SSF69179,SSF69179			REACT_13552							
aly216.43	Unknown		n/a																				
aly216.44	HEAT repeat-containing protein 6	GO:0044822,GO:0005488	CG16989-PA										G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371									
aly216.45	HEAT repeat-containing protein 6		CG16989-PA						PF13251					SSF48371,SSF48371									
aly216.46	Peptidyl-prolyl cis-trans isomerase-like 6	GO:0000413,GO:0006457,GO:0030532,GO:0071011,GO:0000398,GO:0003755,GO:0005681	CG17266-PA						PF00160	PS50072	PR00153,PR00153,PR00153,PR00153		G3DSA:2.40.100.10	SSF50891	351~371								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.47	ATP-binding cassette sub-family B member 6, mitochondrial	GO:0005783,GO:0005886,GO:0006779,GO:0031307,GO:0016887,GO:0042626,GO:0015232,GO:0016021,GO:0005739,GO:0005774,GO:0070574,GO:0046686,GO:0005524,GO:0005794,GO:0020037,GO:0005215,GO:0015439,GO:0015086,GO:0015562,GO:0055085,GO:0070062,GO:0043190,GO:0007420,GO:0015886,GO:0005743,GO:0043588,GO:0071585,GO:0005768	CG4225-PA				SM00382		PF00005,PF16185,PF00664	PS50893,PS50929		PS00211	G3DSA:3.40.50.300,G3DSA:1.20.1560.10	SSF52540,SSF90123									
aly216.48	G protein-coupled receptor kinase 1	GO:0006468,GO:0016060,GO:0035091,GO:0038032,GO:0007603,GO:0004674,GO:0008277,GO:0007165,GO:0004703,GO:0007474,GO:0001664,GO:0050254,GO:0007186,GO:0005524	CG40129-PB				SM00233,SM00220,SM00315,SM00133		PF00069,PF00615	PS50011,PS51285,PS50003,PS50132	PR00717,PR00717,PR00717,PR00717,PR00717	PS00108,PS00107	G3DSA:1.10.167.10,G3DSA:2.30.29.30,G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112,SSF48097,SSF50729	527~547								
aly216.49	Lysophospholipid acyltransferase 7	GO:0008654,GO:0016021,GO:0016020,GO:0071617,GO:0016746,GO:0030258	CG9526-PB																				
aly216.5	Transmembrane 9 superfamily member 3	GO:0016021,GO:0005768	CG10590-PA						PF02990														
aly216.50	Pyridoxal kinase	GO:0005737,GO:0046872,GO:0005524,GO:0009443,GO:0008478	CG4446-PB					TIGR00687	PF08543				G3DSA:3.40.1190.20	SSF53613		00750+2.7.1.35		PWY-7204,PWY-7282					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.51	Biogenesis of lysosome-related organelles complex 1 subunit 1	GO:0050808,GO:0031083,GO:0005515,GO:0008057,GO:0048489,GO:0007274,GO:0008355	CG30077-PB						PF06320														
aly216.52	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0060179,GO:0009744,GO:0046872,GO:0070328,GO:0006629,GO:0017105,GO:0019216,GO:0031410,GO:0006723,GO:0005811,GO:0005789,GO:0042593,GO:0042811,GO:0048047,GO:0004768,GO:0010506,GO:0016021,GO:0055114,GO:0005783	CG5887-PA						PF00487		PR00075,PR00075,PR00075,PR00075,PR00075,PR00075,PR00075												
aly216.53	Unknown	GO:0016772	CG13813-PA				SM00587		PF02958,PF02958				G3DSA:3.90.1200.10	SSF56112									
aly216.54	Kazrin	GO:0043234,GO:0005737,GO:0031424,GO:0005634,GO:0005856,GO:0045886,GO:0005515,GO:0007412,GO:0030057,GO:0001533,GO:0042803	CG11206-PC				SM00454,SM00454,SM00454		PF07647,PF00536,PF00536	PS50105,PS50105			G3DSA:1.10.150.50,G3DSA:1.10.150.50	SSF47769,SSF47769	274~329,341~361,210~244								
aly216.55	Unknown		CG3655-PC						PF01697	PS51257													
aly216.56	Intraflagellar transport protein 22 homolog	GO:0006996,GO:0030992,GO:0072372,GO:0097542,GO:0006886,GO:0003924,GO:0005622,GO:0032482,GO:0008152,GO:0005525	n/a						PF08477				G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.57	Protein suppressor of sable	GO:0005634,GO:0071027,GO:0005700,GO:0005654,GO:0045892,GO:0003723,GO:0035327,GO:0046872,GO:0003729	CG6222-PA				SM00356,SM00356,SM00356			PS50103,PS50103,PS50103			G3DSA:4.10.1000.10	SSF90229,SSF90229,SSF90229										
aly216.58	Ubiquitin conjugation factor E4 A	GO:0005737,GO:0034450,GO:0000151,GO:0016567,GO:0006511,GO:0016874,GO:0000209	CG11070-PA				SM00504		PF10408,PF04564	PS51698			G3DSA:3.30.40.10	SSF57850					UPA00143				
aly216.59	Glucocorticoid induced transcript 1 protein	GO:0005737	n/a						PF15388														
aly216.6	Notchless protein homolog 1	GO:0007219,GO:0005112,GO:0005515,GO:0005730	CG2863-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF00400,PF00400,PF08154	PS50294,PS50082,PS50082,PS50082,PS50082,PS50082,PS50082,PS50082	PR00319,PR00319,PR00319,PR00320,PR00320,PR00320	PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978									
aly216.60	DNA-directed RNA polymerase II 16 kDa polypeptide	GO:0016020,GO:0051124,GO:0043195,GO:0007095,GO:0016079,GO:0005326,GO:0048786,GO:0006366,GO:0005700,GO:0050804,GO:0046928,GO:0019905,GO:0003899,GO:0005665,GO:0022008,GO:0000166,GO:0007274,GO:0005705	CG43662-PF				SM00657		PF03874					SSF47819									
aly216.61	Cyclin-dependent kinase 2-interacting protein	GO:0005634,GO:0006260,GO:0051301,GO:0007049,GO:0006281	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.62	Unknown		n/a																				
aly216.63	Ubiquitin carboxyl-terminal hydrolase calypso	GO:0003682,GO:0004221,GO:0006342,GO:0005634,GO:0007385,GO:0005622,GO:0000790,GO:0006511,GO:0035522,GO:0035517,GO:0004843	CG8445-PB						PF01088		PR00707,PR00707,PR00707,PR00707		G3DSA:3.40.532.10	SSF54001									
aly216.64	Clustered mitochondria protein homolog	GO:0048312,GO:0005737,GO:0055059,GO:0072686,GO:0005852,GO:0051646,GO:0006413,GO:0003743	CG8443-PA						PF13424,PF15044,PF13374,PF12807,PF13236				G3DSA:1.25.40.10	SSF48452,SSF48452,SSF103107	923~943,1406~1426								
aly216.65	INO80 complex subunit E	GO:0006310,GO:0005730,GO:0006281,GO:0031011,GO:0005654,GO:0006355,GO:0006260,GO:0006351	CG18004-PA																				
aly216.66	AP-2 complex subunit alpha	GO:0008565,GO:0008021,GO:0016183,GO:0006897,GO:0016192,GO:0030100,GO:0006886,GO:0006901,GO:0015031,GO:0030135,GO:0030122,GO:0008104,GO:0005905,GO:0007269,GO:0005886,GO:0030131,GO:0045807,GO:0008356,GO:0022008,GO:0048488,GO:0048489	CG4260-PA			PIRSF037091	SM00809		PF02296,PF01602,PF02883				G3DSA:1.25.10.10,G3DSA:3.30.310.30,G3DSA:2.60.40.1030	SSF49348,SSF48371,SSF55711	22~42		REACT_13685,REACT_18266,REACT_6185,REACT_11061,REACT_9417						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.67	Protein phosphatase PTC7 homolog	GO:0003824,GO:0046872,GO:0004721	CG12091-PA				SM00332,SM00331		PF07228	PS51746			G3DSA:3.60.40.10	SSF81606									
aly216.68	Derlin-2	GO:0008284,GO:0030968,GO:0030307,GO:0005770,GO:0030970,GO:0001967,GO:0030176,GO:0003674,GO:0042742,GO:0030433,GO:0005769	CG14899-PA						PF04511					SSF144091									
aly216.69	Trafficking protein particle complex subunit 13	GO:0005575,GO:0003674,GO:0008150	CG4953-PA						PF06159														
aly216.7	Something about silencing protein 10	GO:0032040,GO:0005730,GO:0000462,GO:0003723,GO:0022008,GO:0016568	CG4202-PA						PF09368,PF04000						105~125								
aly216.70	Cytoplasmic phosphatidylinositol transfer protein 1	GO:0005737,GO:0015914,GO:0006810,GO:0008289,GO:0008526,GO:0007165	CG17818-PA						PF02121		PR00391,PR00391,PR00391,PR00391,PR00391		G3DSA:3.30.530.20	SSF55961									
aly216.71	Kallikrein 1-related peptidase b3	GO:0004252,GO:0070062,GO:0005057,GO:0005634,GO:0005576,GO:0006508,GO:0035556,GO:0046872	CG12386-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.72	Unknown		n/a																				
aly216.73	Calcium-binding protein E63-1	GO:0005737,GO:0035071,GO:0005634,GO:0048102,GO:0005509,GO:0005886	CG15855-PA				SM00054,SM00054,SM00054		PF13499,PF13499	PS50222,PS50222,PS50222		PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly216.74	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 6	GO:0008137,GO:0006120,GO:0003954,GO:0005747,GO:0006979,GO:0055114	CG7712-PA						PF05347														
aly216.75	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 6	GO:0008137,GO:0006120,GO:0003954,GO:0005747,GO:0006979,GO:0055114	CG7712-PA			PIRSF006643			PF05347														
aly216.76	Unknown		n/a						PF15995														
aly216.77	Unknown		n/a						PF15994														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.78	Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase	GO:0005737,GO:0008650,GO:0008033,GO:0001510,GO:0002128,GO:0008175,GO:0002181,GO:0008168	CG5220-PA	MF_01547,MF_03162					PF01728				G3DSA:3.40.50.150	SSF53335				PWY-6829					
aly216.79	Unknown		n/a																				
aly216.8	Cysteine-rich with EGF-like domain protein 2-A	GO:0005576,GO:0005509,GO:0005783	CG11377-PA				SM00179,SM00181,SM00181,SM00181,SM00261,SM00261			PS50026		PS00022,PS01248,PS01187	G3DSA:2.10.220.10	SSF57184									
aly216.80	Cytochrome P450 9e2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0048252,GO:0018685,GO:0005506,GO:0017143,GO:0055114,GO:0009055	CG10248-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly216.81	Putative methyltransferase NSUN6	GO:0008168,GO:0005730,GO:0003723,GO:0008649	CG11109-PB				SM00359		PF01472,PF01189	PS50890,PS51686	PR02008,PR02008,PR02008,PR02008,PR02008,PR02008	PS01153	G3DSA:2.30.130.10,G3DSA:3.40.50.150	SSF53335,SSF88697									
aly216.82	Dorsal-ventral patterning protein Sog	GO:0007362,GO:0040008,GO:0008083,GO:0007398,GO:0007378,GO:0016021,GO:0008586,GO:0007354,GO:0030512,GO:0035271,GO:0030509,GO:0007313,GO:0005515,GO:0005886,GO:0008293,GO:0005518,GO:0061328,GO:0030511,GO:0030510	CG9224-PA				SM00214,SM00214,SM00214		PF00093,PF00093,PF00093	PS50184,PS50184,PS50933,PS50933		PS01208		SSF57603,SSF57603,SSF57603									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.83	Serine--pyruvate aminotransferase, mitochondrial	GO:0051384,GO:0005782,GO:0008453,GO:0046724,GO:0019448,GO:0042853,GO:0005811,GO:0005777,GO:0005739,GO:0051591,GO:0042866,GO:0003824,GO:0009436,GO:0004760,GO:0030170,GO:0005759,GO:0016597,GO:0019265	CG3926-PA			PIRSF000524			PF00266				G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383		00440+2.6.1.37		PWY-6832					
aly216.84	Unknown		n/a																				
aly216.85	Unknown		n/a																				
aly216.86	Decorin	GO:0050840,GO:0031012,GO:0019800,GO:0001764,GO:0007411,GO:0022409,GO:0003151,GO:0007432,GO:0005615,GO:0008406,GO:0071666,GO:0010508,GO:0005509,GO:0008078,GO:0035385,GO:0030182,GO:2000274,GO:0044822,GO:0035050,GO:0048495,GO:0046331,GO:0050919,GO:0008201,GO:0008347,GO:0007427,GO:0007502,GO:0010632,GO:0016199,GO:0007509,GO:0005539,GO:0048813,GO:0005515,GO:0005578	CG43758-PF				SM00369,SM00369,SM00369		PF13855				G3DSA:3.80.10.10	SSF52058									
aly216.87	Superoxide dismutase [Cu-Zn]	GO:0005737,GO:0005507,GO:0005615,GO:0005634,GO:0005739,GO:0006979,GO:0019430,GO:0006801,GO:0009650,GO:0004784,GO:0046872,GO:0005829,GO:0055114,GO:0008270	CG9027-PE						PF00080		PR00068,PR00068,PR00068	PS00332,PS00087	G3DSA:2.60.40.200	SSF49329				PWY-6854					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly216.88	Putative nuclease HARBI1	GO:0005737,GO:0005813,GO:0005634,GO:0046872,GO:0004518	CG43088-PA						PF13359														
aly216.89	Protein RFT1 homolog	GO:0005319,GO:0034203,GO:0016021,GO:0005789,GO:0006869	CG3149-PA						PF04506														
aly216.9	Active breakpoint cluster region-related protein	GO:0005089,GO:0005886,GO:0030036,GO:0035025,GO:0035023,GO:0035556,GO:0032496,GO:0050766,GO:0050728,GO:0043547,GO:0050885,GO:0016020,GO:0005096,GO:0042472,GO:0060313,GO:0007030,GO:0045792,GO:0007420,GO:0005829,GO:0043314,GO:0005622,GO:0005575,GO:0002692,GO:0043114	CG40494-PE				SM00325,SM00233,SM00324		PF00621,PF00620,PF09036	PS50010,PS50238,PS50003		PS00741	G3DSA:1.20.900.10,G3DSA:2.30.29.30,G3DSA:2.30.29.30,G3DSA:2.60.40.150,G3DSA:4.10.280.30,G3DSA:1.10.555.10	SSF49562,SSF48065,SSF48350,SSF50729,SSF50729	25~45		REACT_14797,REACT_11044,REACT_11061						
aly216.90	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly21604.1	Cyclin-dependent kinase 5 activator 2	GO:0030426,GO:0030425,GO:0030424,GO:0021766,GO:0021722,GO:0001764,GO:0008045,GO:0004693,GO:0005737,GO:0045956,GO:0016533,GO:0043025,GO:0016534,GO:0006468,GO:0021819,GO:0008289,GO:0035011,GO:0007409,GO:0005886,GO:0008340,GO:0021549,GO:0008344,GO:0070059,GO:0000079	CG5387-PA						PF03261				G3DSA:1.10.472.10	SSF47954									
aly2163.1	Unknown		n/a																				
aly2163.2	Zinc finger and SCAN domain-containing protein 12	GO:0003700,GO:0005634,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG1832-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF13912,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667								
aly2163.3	Intron-binding protein aquarius	GO:0097157,GO:0071011,GO:0071013,GO:0016020,GO:0044822,GO:0000398,GO:0005654,GO:0005634	CG31368-PD						PF16399														
aly2163.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2163.5	Probable G-protein coupled receptor Mth-like 5	GO:0004930,GO:0016021,GO:0006950,GO:0042594,GO:0005886,GO:0008340,GO:0007186	CG6965-PB																				
aly2163.6	Probable G-protein coupled receptor Mth-like 3	GO:0004930,GO:0016021,GO:0006950,GO:0042594,GO:0005886,GO:0008340,GO:0007186	CG6530-PA						PF00002	PS50261				SSF81321									
aly2163.7	G-protein coupled receptor Mth2	GO:0004930,GO:0016021,GO:0016020,GO:0006950,GO:0004888,GO:0007166,GO:0005886,GO:0008340,GO:0007186	CG17061-PB							PS50261													
aly216410.1	Unknown		n/a						PF14529				G3DSA:3.30.40.10,G3DSA:3.60.10.10	SSF56219,SSF57903	156~183								
aly2165.1	Ciliogenesis-associated TTC17-interacting protein	GO:0005737,GO:0015629,GO:0005634,GO:0005886,GO:0030041,GO:0044782	CG13243-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2165.10	Photoreceptor-specific nuclear receptor	GO:0045924,GO:0007619,GO:0007617,GO:0007165,GO:0048047,GO:0008270,GO:0043401,GO:0008049,GO:0001078,GO:0004879,GO:0007530,GO:0042462,GO:0043565,GO:0030522,GO:0035206,GO:0000122,GO:0005634,GO:0005654,GO:0010467,GO:0006367,GO:0006366,GO:0008285,GO:0045872,GO:0007620,GO:0007601,GO:0007602,GO:0018991,GO:0018993,GO:0003700,GO:0003707,GO:0006355,GO:0045944,GO:0005667,GO:0060041	CG9019-PA				SM00430		PF00104		PR00398,PR00398,PR00398,PR00398,PR01282,PR01282,PR01282,PR01282,PR01282		G3DSA:1.10.565.10,G3DSA:1.10.565.10	SSF48508,SSF48508			REACT_71							
aly2165.11	Nuclear receptor subfamily 2 group E member 1	GO:0048047,GO:0043565,GO:0006351,GO:0018991,GO:0045924,GO:0018993,GO:0007619,GO:0003700,GO:0007617,GO:0005634,GO:0007620,GO:0003707,GO:0006355,GO:0008270,GO:0043401,GO:0035206,GO:0008049,GO:0001078,GO:0007275,GO:0004879,GO:0007530	CG9019-PA				SM00399		PF00105	PS51030	PR00047,PR00047,PR00047,PR00047	PS00031	G3DSA:3.30.50.10	SSF57716			REACT_71							
aly2165.12	Aminoacylase-1	GO:0004046,GO:0005737,GO:0070062,GO:0006520,GO:0046872,GO:0008237	CG6733-PA										G3DSA:3.40.630.10	SSF53187									
aly2165.13	Aminoacylase-1	GO:0004046,GO:0005737,GO:0006520,GO:0008237,GO:0046872	CG17109-PA									PS00758	G3DSA:3.40.630.10	SSF53187									
aly2165.14	Aminoacylase-1	GO:0004046,GO:0005737,GO:0006520,GO:0008237,GO:0046872	CG17110-PA			PIRSF036696			PF07687,PF01546			PS00759	G3DSA:3.30.70.360,G3DSA:3.40.630.10,G3DSA:3.40.630.10	SSF53187,SSF53187,SSF55031		00330+3.5.1.14							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2165.15	Broad-complex core protein isoforms 1/2/3/4/5	GO:0010629,GO:0003677,GO:0008219,GO:0007458,GO:0005634,GO:0007552,GO:0048808,GO:0046872,GO:0048477,GO:0071390,GO:0035075,GO:0035072,GO:0035071,GO:0035070,GO:0006914,GO:0048747,GO:0042332,GO:0040034,GO:0001752,GO:0003700,GO:0009608,GO:0007562,GO:0035193,GO:0006355,GO:0048813,GO:0045944,GO:0000977	CG11491-PP				SM00225		PF04500,PF00651	PS50097			G3DSA:3.30.710.10	SSF54695									
aly2165.16	Longitudinals lacking protein like	GO:0006351,GO:0001700,GO:0007435,GO:0031519,GO:0006357,GO:0003700,GO:0006342,GO:0005634,GO:0000794,GO:0005700,GO:0016458,GO:0007426,GO:0031208,GO:0045893,GO:0005515,GO:0003677,GO:0045892,GO:0035167,GO:0016568,GO:0042803	CG5738-PB						PF00651,PF04500	PS50097			G3DSA:3.30.710.10	SSF54695									
aly2165.17	L-2-hydroxyglutarate dehydrogenase, mitochondrial	GO:0005811,GO:0047545,GO:0005739,GO:0055114,GO:0016491	CG10639-PA						PF01266				G3DSA:3.30.9.10,G3DSA:3.30.9.10,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905									
aly2165.18	Post-GPI attachment to proteins factor 2	GO:0008565,GO:0016021,GO:0005789,GO:0006506,GO:0015031,GO:0000139	CG3876-PA						PF10277														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2165.19	Coiled-coil domain-containing protein KIAA1407 homolog		CG17258-PB												72~92,152~216								
aly2165.2	Transport and Golgi organization protein 1	GO:0070971,GO:0005794,GO:0007030,GO:0000137,GO:0009306,GO:0016021,GO:0006887,GO:0000139,GO:0003674,GO:0012505,GO:0051047,GO:0033363	CG11098-PA										G3DSA:2.30.30.40		755~775,793~932,1040~1074,1093~1120								
aly2165.20	Unknown	GO:0005794,GO:0018345,GO:0006888,GO:0008270,GO:0019706	CG17257-PB						PF01529														
aly2165.21	Unknown	GO:0005819,GO:0035186,GO:0030496,GO:0005634,GO:0031965,GO:0030707,GO:0000922,GO:0019901,GO:0007052,GO:0000070,GO:0005938,GO:0005813,GO:0007476,GO:0005876	CG9660-PA												1055~1082,1090~1110,1196~1223,1030~1050,1137~1188								
aly2165.22	Lipase member H-A	GO:0004806,GO:0006629,GO:0016020,GO:0052689,GO:0016042,GO:0005576	CG17292-PA						PF00151		PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly2165.23	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0055114	CG6142-PA						PF00732,PF05199			PS00624,PS00623	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905,SSF54373									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2165.24	Unknown		n/a																				
aly2165.25	WD repeat and FYVE domain-containing protein 3	GO:0005635,GO:0050807,GO:0016234,GO:0019898,GO:0031594,GO:0016239,GO:0007041,GO:0003831,GO:0005545,GO:0005737,GO:0016605,GO:0097635,GO:0048786,GO:0005776,GO:0035973,GO:0031396,GO:0046872,GO:0048749,GO:0031965,GO:0022416,GO:0012505,GO:0007409,GO:0008340,GO:0030424,GO:0016197	CG14001-PA																				
aly2165.3	Xanthine dehydrogenase	GO:0008762,GO:0004855,GO:0004854,GO:0005875,GO:0006650,GO:0050660,GO:0043546,GO:0006206,GO:0005777,GO:0006525,GO:0006568,GO:0005506,GO:0016491,GO:0048072,GO:0045471,GO:0016903,GO:0009115,GO:0008340,GO:0055114,GO:0009055,GO:0005829,GO:0051537,GO:0006144	CG7642-PA			PIRSF000127	SM01092,SM01008	TIGR02963,TIGR02965	PF02738,PF00111,PF00941,PF01799,PF01315,PF03450	PS51387,PS51085		PS00197,PS00559	G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:1.10.150.120,G3DSA:3.30.390.50,G3DSA:3.30.365.10,G3DSA:3.90.1170.50,G3DSA:3.30.465.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.43.10,G3DSA:3.10.20.30	SSF55447,SSF47741,SSF47741,SSF54665,SSF56176,SSF56003,SSF54292		00230+1.17.1.4+1.17.3.2,00983+1.17.3.2,00230+1.17.1.4,00232+1.17.3.2		PWY-5497,PWY-6596,PWY-6607,PWY-6606,PWY-6999,PWY-6608,PWY-5695,PWY-6538					
aly2165.4	Xanthine dehydrogenase	GO:0050660,GO:0043546,GO:0008762,GO:0006206,GO:0051537,GO:0005777,GO:0048072,GO:0006525,GO:0006568,GO:0005875,GO:0009115,GO:0004854,GO:0004855,GO:0008340,GO:0005506,GO:0009055,GO:0006144,GO:0055114,GO:0006650	CG7642-PA			PIRSF000127	SM01092,SM01008	TIGR02963	PF01799,PF01315,PF00111,PF00941,PF03450,PF02738	PS51085,PS51387		PS00197	G3DSA:3.90.1170.50,G3DSA:3.30.365.10,G3DSA:3.10.20.30,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.465.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.43.10,G3DSA:3.30.390.50,G3DSA:3.30.365.10,G3DSA:1.10.150.120	SSF56003,SSF56176,SSF54292,SSF54665,SSF55447,SSF47741		00230+1.17.1.4		PWY-5497,PWY-6596,PWY-6607,PWY-6606,PWY-6999,PWY-6608,PWY-5695,PWY-6538					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2165.5	Cytochrome c oxidase protein 20 homolog	GO:0005575,GO:0003674,GO:0016021,GO:0008150,GO:0031966	CG7620-PA						PF12597		PR02049,PR02049,PR02049,PR02049												
aly2165.6	Unknown		n/a																				
aly2165.7	Protein numb	GO:0055059,GO:0008104,GO:0061320,GO:0007419,GO:0003676,GO:0008356,GO:0045035,GO:0061382,GO:0007417,GO:0005737,GO:0050767,GO:0007219,GO:0005634,GO:0001709,GO:0045178,GO:0045746,GO:0016360,GO:0005112,GO:0005524,GO:0007622,GO:0035050,GO:0045180,GO:0005938,GO:0008593,GO:0007405,GO:0051642,GO:0008347,GO:0007400,GO:0007507,GO:0045165,GO:0007422,GO:0051960,GO:0005515,GO:0009786,GO:0045807,GO:0042694	CG3779-PA				SM00462		PF00640,PF06311	PS01179			G3DSA:2.30.29.30	SSF50729										
aly2165.8	WD repeat and FYVE domain-containing protein 3	GO:0005635,GO:0050807,GO:0016234,GO:0019898,GO:0031594,GO:0016239,GO:0007041,GO:0003831,GO:0005545,GO:0005737,GO:0016605,GO:0097635,GO:0048786,GO:0005776,GO:0035973,GO:0031396,GO:0046872,GO:0048749,GO:0031965,GO:0022416,GO:0012505,GO:0007409,GO:0008340,GO:0030424,GO:0016197	CG14001-PA				SM01026,SM00320,SM00320,SM00320,SM00320,SM00064		PF02138,PF14844,PF01363	PS50082,PS50178,PS50197,PS50294,PS50082		PS00678	G3DSA:1.10.1540.10,G3DSA:2.30.29.40,G3DSA:3.30.40.10,G3DSA:2.130.10.10	SSF57903,SSF49899,SSF81837,SSF50978,SSF50729,SSF48371,SSF48371,SSF48371	532~552									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2165.9	Cysteine and histidine-rich domain-containing protein	GO:0008361,GO:0046872,GO:0008270,GO:0050773,GO:0051298	CG6198-PA						PF04969,PF04968,PF04968	PS51401,PS51401,PS51203			G3DSA:2.60.40.790	SSF49764									
aly21692.1	Carbonic anhydrase 1	GO:0005737,GO:0006730,GO:0004089,GO:0008270	CG7820-PA						PF00194	PS51144		PS00162	G3DSA:3.10.200.10	SSF51069		00910+4.2.1.1		PWY-6142,PWY-241,PWY-7117,PWY-7115					
aly2174.1	Tyrosine-protein kinase receptor TYRO3	GO:0034446,GO:0005886,GO:0018108,GO:0005789,GO:0032940,GO:0003674,GO:0021885,GO:0005634,GO:0046777,GO:0050728,GO:0016021,GO:0005635,GO:0004714,GO:0004713,GO:0005524,GO:0006468,GO:0034122,GO:0007283,GO:0050914,GO:0043277,GO:0030168,GO:0035199,GO:0043491,GO:0070050,GO:0070527,G	CG13439-PA				SM00408,SM00408,SM00409,SM00409		PF07679,PF00047	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly21748.1	Unknown		n/a																				
aly21754.1	Unknown	GO:0016020,GO:0006486,GO:0008417	n/a						PF00852					SSF53756					UPA00378				
aly2178.1	Unknown		n/a						PF15430														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2178.10	Nucleolar complex protein 4 homolog A	GO:0022008,GO:0016021,GO:0031965,GO:0042254,GO:0005730	CG2875-PA						PF03914														
aly2178.11	Unknown		n/a																				
aly2178.12	High affinity copper uptake protein 1	GO:0006878,GO:0006825,GO:0016021,GO:0035434,GO:0015088,GO:0010038,GO:0005886,GO:0005375	CG7459-PA						PF04145														
aly2178.13	RNA polymerase II subunit B1 CTD phosphatase Rpap2	GO:0005737,GO:0070940,GO:0005730,GO:0005634,GO:0008420,GO:0009301,GO:0016591,GO:0046872	CG34183-PA						PF04181	PS51479													
aly2178.14	Folylpolyglutamate synthase, mitochondrial	GO:0005737,GO:0046901,GO:0006767,GO:0006766,GO:0007420,GO:0006139,GO:0005829,GO:0031100,GO:0004326,GO:0005739,GO:0005743,GO:0009058,GO:0001889,GO:0044281,GO:0005759,GO:0046655,GO:0006730,GO:0005524	CG2543-PA			PIRSF038895		TIGR01499	PF02875,PF08245			PS01011,PS01012	G3DSA:3.40.1190.10,G3DSA:3.40.1190.10,G3DSA:3.90.190.20	SSF53623,SSF53244	28~48	00790+6.3.2.17		PWY-2161	UPA00219,UPA00850				
aly2178.15	Adenylate kinase 8	GO:0006139,GO:0019205,GO:0005829,GO:0004127,GO:0004550,GO:0004017,GO:0006165,GO:0009142,GO:0005524	CG15543-PA						PF00406				G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2178.16	Heat shock 70 kDa protein cognate 3	GO:0012505,GO:0005783,GO:0005615,GO:0005811,GO:0005788,GO:0030431,GO:0016887,GO:0009408,GO:0016246,GO:0005875,GO:0005524,GO:0051298	CG4147-PE				SM01004		PF00012,PF00490,PF00490		PR00301,PR00301,PR00301,PR00301,PR00301,PR00301,PR00301,PR00301	PS00169,PS00297,PS00329,PS01036	G3DSA:3.30.30.30,G3DSA:3.20.20.70,G3DSA:3.90.640.10,G3DSA:1.20.1270.10,G3DSA:3.20.20.70,G3DSA:2.60.34.10,G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.30.420.40	SSF100920,SSF100934,SSF51569,SSF53067,SSF53067	558~585	00860+4.2.1.24		PWY-5189,PWY-5188	UPA00251				
aly2178.17	Unknown		n/a																				
aly2178.18	Histone-lysine N-methyltransferase EHMT1	GO:0018024,GO:0018027,GO:0018026,GO:0007616,GO:0007614,GO:0035220,GO:0016279,GO:0009790,GO:0002165,GO:0046974,GO:0008270,GO:0046976,GO:0046959,GO:0051567,GO:0008168,GO:0005737,GO:0006306,GO:0000122,GO:0005634,GO:0005654,GO:0070742,GO:0016571,GO:0005694,GO:0010468,GO:0035076,GO:0000791,GO:0045892,GO:0005886,GO:0008345,GO:0050775,GO:0070734,GO:0005705,GO:0002039,GO:0016568	CG2995-PB				SM00248,SM00248,SM00317,SM00468		PF05033,PF00856,PF12796	PS51257,PS50280,PS50088,PS50297			G3DSA:1.25.40.20,G3DSA:2.170.270.10,G3DSA:1.25.40.20,G3DSA:2.170.270.10	SSF48403,SSF48403,SSF82199		00310+2.1.1.43							
aly2178.19	Dual specificity protein kinase TTK	GO:0033046,GO:0033316,GO:0001666,GO:0007143,GO:0031577,GO:0007100,GO:0005819,GO:0000942,GO:0000705,GO:0004674,GO:0004712,GO:0043060,GO:0004672,GO:0051304,GO:0005524,GO:0004713,GO:0006468,GO:0000278,GO:0032837,GO:0007126,GO:0016321,GO:0000776,GO:0005813,GO:0007094,GO:0007093	CG7643-PB				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2178.2	Innexin inx1	GO:0010496,GO:0007399,GO:0016021,GO:0007632,GO:0007602,GO:0005886,GO:0055085,GO:0016323,GO:0005243,GO:0006811,GO:0005921	CG3039-PA						PF00876	PS51013	PR01262,PR01262,PR01262,PR01262,PR01262,PR01262												
aly2178.20	Spectrin alpha chain	GO:0005811,GO:0016337,GO:0008302,GO:0050807,GO:0030707,GO:0031594,GO:0007293,GO:0007009,GO:0003674,GO:0016199,GO:0007294,GO:0001738,GO:0007308,GO:0007274,GO:0002168,GO:0005856,GO:0045170,GO:0007026,GO:0030727,GO:0030721,GO:0003779,GO:0005509,GO:0051693,GO:0007417,GO:0042127,GO:0005794,GO:0042048,GO:0008017,GO:0060429,GO:0042062,GO:0016323,GO:0046331,GO:0005938,GO:0005886,GO:0045478,GO:0008091,GO:0048134,GO:0007010,GO:0008092,GO:0007560,GO:0048790,GO:0045169,GO:0008360,GO:0005516,GO:0005737	CG1977-PB				SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00054,SM00054,SM00326		PF13499,PF00018,PF08726,PF00435	PS50222,PS50222,PS50002	PR01887,PR01887,PR01887,PR00452,PR00452,PR00452	PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:2.30.30.40,G3DSA:1.10.238.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.5.170,G3DSA:1.20.58.60,G3DSA:1.20.58.60	SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF50044,SSF47473,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966	1900~1920,16~47,943~963,1436~1470,294~321,1649~1683,1216~1243,717~751,344~364,506~526								
aly2178.21	Protein vav	GO:0005089,GO:0005085,GO:0007520,GO:0032863,GO:0032864,GO:0035023,GO:0007411,GO:0035556,GO:0007417,GO:0043547,GO:0019992,GO:0016477,GO:0007424,GO:0072499,GO:0035011,GO:0008360,GO:0007409,GO:0007155,GO:0030676,GO:0007015,GO:0046872,GO:0007391,GO:0005622,GO:0005575,GO:0031532	CG7893-PC				SM00252,SM00326,SM00033,SM00233,SM00109,SM00325		PF00621,PF00307,PF00130,PF00017,PF00018,PF00169	PS50010,PS50021,PS50081,PS50002,PS50001,PS50003			G3DSA:1.10.418.10,G3DSA:2.30.30.40,G3DSA:3.30.505.10,G3DSA:3.30.60.20,G3DSA:1.20.900.10,G3DSA:2.30.29.30	SSF47576,SSF48065,SSF50729,SSF55550,SSF50044									
aly2178.22	Sulfiredoxin-1	GO:0005829,GO:0005575,GO:0055114,GO:0016667,GO:0032542,GO:0006979,GO:0005524	CG6762-PA			PIRSF017267	SM00470		PF02195				G3DSA:3.90.1530.10	SSF110849									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2178.23	Unknown		n/a																				
aly2178.24	Homeobox protein extradenticle	GO:0033613,GO:0000060,GO:0003677,GO:0005737,GO:0043565,GO:0007479,GO:0007432,GO:0005634,GO:0003713,GO:0007438,GO:0005515,GO:0008134,GO:0042659,GO:0007525,GO:0007420,GO:0007422,GO:0003700,GO:0003705,GO:0006355,GO:0006357,GO:0045944,GO:0006351,GO:0005667,GO:0001654,GO:0046982	CG8933-PB				SM00389		PF00046,PF03792	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689	161~181									
aly2178.25	Glycine--tRNA ligase	GO:0006426,GO:0005737,GO:0004812,GO:0004820,GO:0015966,GO:0005739,GO:0048813,GO:0006418,GO:0046983,GO:0005524	CG6778-PB				SM00991	TIGR00389	PF03129,PF00587,PF00458	PS51185,PS50862	PR01043,PR01043,PR01043,PR01043,PR01043,PR01043,PR01043	PS00762	G3DSA:3.40.50.800,G3DSA:1.10.287.10,G3DSA:3.30.930.10,G3DSA:3.30.930.10,G3DSA:3.30.930.10,G3DSA:3.30.930.10	SSF52954,SSF47060,SSF55681,SSF55681,SSF55681	164~198	00970+6.1.1.14	REACT_71						
aly2178.26	Pre-mRNA-splicing factor 38B	GO:0071011,GO:0044822,GO:0008380,GO:0000398,GO:0006397	CG1622-PA						PF03371														
aly2178.27	Unknown		n/a																				
aly2178.28	Surfeit locus protein 4 homolog	GO:0005789,GO:0016021,GO:0046331,GO:0012505,GO:0045169	CG6202-PA						PF02077			PS01339											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2178.29	Iron-sulfur protein NUBPL	GO:0070584,GO:0051539,GO:0032981,GO:0005739,GO:0000166,GO:0046872,GO:0005524	CG3262-PD						PF10609				G3DSA:3.40.50.300	SSF52540									
aly2178.3	Innexin inx7	GO:0005737,GO:0010496,GO:0072375,GO:0016021,GO:0007476,GO:0005886,GO:0006811,GO:0005243,GO:0005634,GO:0005921	CG2977-PA						PF00876	PS51013	PR01262,PR01262,PR01262,PR01262,PR01262												
aly2178.30	Uncharacterized protein C6orf136 homolog		CG16787-PA						PF10184														
aly2178.31	Unknown	GO:0032509,GO:0000813,GO:0043130	CG7192-PA						PF10240	PS51498													
aly2178.32	Casein kinase II subunit beta	GO:0016319,GO:0032927,GO:0030177,GO:0008062,GO:0010862,GO:0005737,GO:0070062,GO:0005634,GO:0061154,GO:0004674,GO:0004672,GO:0046872,GO:0033211,GO:0006468,GO:0007623,GO:0007622,GO:0019887,GO:0043537,GO:0045475,GO:0005886,GO:0022008,GO:0005956,GO:0031519,GO:0005829,GO:0016055,GO:0007249	CG15224-PE				SM01085		PF01214		PR00472,PR00472,PR00472,PR00472,PR00472,PR00472		G3DSA:1.10.1820.10,G3DSA:2.20.25.20	SSF57798									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2178.33	Unknown		n/a																				
aly2178.34	Protein SMG7	GO:0005737,GO:0051721,GO:0045111,GO:0000184,GO:0005634	n/a						PF10373					SSF48452									
aly2178.35	Protein SMG7	GO:0005737,GO:0051721,GO:0045111,GO:0000184,GO:0005829,GO:0010467,GO:0035303,GO:0005634,GO:0006406	n/a						PF10374					SSF48452									
aly2178.36	Protein roadkill	GO:0031648,GO:0007367,GO:0042067,GO:0048592,GO:0007349,GO:0045879,GO:0043065,GO:0016567,GO:0046330,GO:0046331,GO:0030162,GO:0005515,GO:0042308,GO:0001654,GO:0005634,GO:0042803	CG12537-PF				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695									
aly2178.37	Casein kinase II subunit beta	GO:0016319,GO:0005737,GO:0006468,GO:0007623,GO:0007622,GO:0019887,GO:0005634,GO:0016055,GO:0004674,GO:0005829,GO:0045475,GO:0008062,GO:0004672,GO:0022008,GO:0005956	CG15224-PE				SM01085		PF01214		PR00472,PR00472,PR00472,PR00472,PR00472,PR00472	PS01101	G3DSA:1.10.1820.10,G3DSA:2.20.25.20	SSF57798									
aly2178.38	Protein maternal effect lethal 26	GO:0005737,GO:0016567,GO:0016020,GO:0032154,GO:0000793,GO:0005938,GO:0044257,GO:0042802	n/a				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695,SSF54695									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2178.39	Golgi-associated plant pathogenesis-related protein 1	GO:0010634,GO:0070062,GO:0010718,GO:0000139,GO:0005575,GO:0005576,GO:0003674,GO:0008150,GO:0070374,GO:0042803	CG34049-PB				SM00198		PF00188		PR00837,PR00837,PR00837,PR00837,PR00838,PR00838,PR00838	PS01009	G3DSA:3.40.33.10	SSF55797									
aly2178.4	Innexin inx2	GO:0016324,GO:0010496,GO:0007440,GO:0042048,GO:0016021,GO:0016327,GO:0016331,GO:0055085,GO:0007293,GO:0005886,GO:0006811,GO:0007154,GO:0005243,GO:0030727,GO:0005921	CG4590-PA						PF00876	PS51013	PR01262,PR01262,PR01262,PR01262,PR01262,PR01262												
aly2178.40	40S ribosomal protein S23	GO:0022627,GO:0051297,GO:0005622,GO:0003735,GO:0015935,GO:0006412,GO:0051298,GO:0005840	CG8415-PB					TIGR00982	PF00164			PS00055	G3DSA:2.40.50.140	SSF50249									
aly2178.41	Receptor-mediated endocytosis protein 6 homolog	GO:0051056,GO:0016020,GO:0006897,GO:0005575,GO:0005096,GO:0005829,GO:0032794,GO:0005085,GO:0017112,GO:0005622,GO:0032483,GO:0007165,GO:0051223,GO:0043547	CG1657-PA						PF02204	PS51205				SSF109993									
aly2178.42	GTPase-activating protein and VPS9 domain-containing protein 1	GO:0051056,GO:0016020,GO:0006897,GO:0005575,GO:0005096,GO:0005829,GO:0032794,GO:0005085,GO:0017112,GO:0005622,GO:0032483,GO:0007165,GO:0051223,GO:0043087,GO:0005768,GO:0043547	CG1657-PA						PF00616	PS50018			G3DSA:1.10.506.10	SSF48350	1249~1249,26~50								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2178.43	Dual specificity mitogen-activated protein kinase kinase 7	GO:0048675,GO:0005829,GO:0034134,GO:0030032,GO:0007165,GO:0019899,GO:0071243,GO:0038123,GO:0009411,GO:0035006,GO:0034769,GO:0038124,GO:0008340,GO:0043507,GO:0008545,GO:0007298,GO:0034138,GO:0005737,GO:0007257,GO:0007254,GO:0030381,GO:0043652,GO:0005634,GO:0000287,GO:0000165,GO:0030707,GO:0004674,GO:0010508,GO:0004713,GO:0004672,GO:0035666,GO:0034162,GO:0034612,GO:0005524,GO:0046528,GO:0048666,GO:0006468,GO:0070328,GO:0033500,GO:0045087,GO:0006915,GO:0051017,GO:0019903,GO:0042060,GO:0071276,GO:0019901,GO:0002224,GO:0046330,GO:0051403,GO:0006970,GO:0045893,GO:0034142,GO:0034146,GO:0009408,GO:0034244,GO:0001736,GO:0002755,GO:0002756,GO:0038095,GO:0007395,GO:0007561,GO:0007391,GO:0005622,GO:0006357,GO:0046529,GO:0005515,GO:0004702,GO:0046844,GO:0034166,GO:0046847,GO:0045610,GO:0004708,GO:0046843	CG4353-PA				SM00220		PF00069	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF56112	3~23									
aly2178.44	Unknown		n/a																				
aly2178.45	Uridine-cytidine kinase 2	GO:0044211,GO:0043097,GO:0006909,GO:0016773,GO:0044206,GO:0006238,GO:0006206,GO:0055086,GO:0008152,GO:0004849,GO:0019206,GO:0005829,GO:0005524,GO:0044281	CG6364-PB										G3DSA:3.40.50.300										
aly2178.46	Probable uridine-cytidine kinase	GO:0044211,GO:0006909,GO:0016773,GO:0044206,GO:0016301,GO:0008152,GO:0004849,GO:0005524	CG6364-PB						PF00485		PR00988,PR00988,PR00988		G3DSA:3.40.50.300	SSF52540		00983+2.7.1.48,00240+2.7.1.48		PWY-7193	UPA00574,UPA00579				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2178.47	Multifunctional protein ADE2	GO:0005737,GO:0005829,GO:0007476,GO:0004639,GO:0004638,GO:0006189,GO:0002121,GO:0005524	CG3989-PA	MF_00137			SM01001		PF01259,PF00731			PS01057,PS01058	G3DSA:3.40.50.7700,G3DSA:3.30.200.20,G3DSA:3.30.470.20	SSF52255,SSF56104		00230+6.3.2.6		PWY-6123,PWY-6124,PWY-7234	UPA00074				
aly2178.48	Amidophosphoribosyltransferase	GO:0004044,GO:0051539,GO:0040016,GO:0006541,GO:0009113,GO:0006189,GO:0009116,GO:0006164,GO:0008340,GO:0046872,GO:0048477	CG10078-PB	MF_01931				TIGR01134	PF13522,PF00156	PS51278			G3DSA:3.40.50.2020,G3DSA:3.60.20.10	SSF56235,SSF53271		00230+2.4.2.14,00250+2.4.2.14		PWY-6121,PWY-6122,PWY-7282,PWY-6277	UPA00074				
aly2178.49	Probable Xaa-Pro aminopeptidase 3	GO:0004177,GO:0070062,GO:0003094,GO:0030145,GO:0005739,GO:0016485,GO:0006508,GO:0008235,GO:0008237	CG9581-PA				SM01011		PF05195,PF00557				G3DSA:3.40.350.10,G3DSA:3.90.230.10	SSF55920,SSF53092									
aly2178.5	Unknown		n/a																				
aly2178.50	Cysteine-rich with EGF-like domain protein 2	GO:0005576,GO:0005509,GO:0005515,GO:0005783	CG11377-PA				SM00181,SM00181,SM00181,SM00261,SM00261		PF11938	PS50026		PS01248,PS00022,PS01187	G3DSA:2.10.220.10	SSF57184									
aly2178.51	Unknown	GO:0045177,GO:0040005,GO:0008039,GO:0007475,GO:0008362,GO:0003674	CG2467-PC																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2178.52	Unknown	GO:0005089,GO:0016319,GO:0030833,GO:1900029,GO:0005544,GO:0005622,GO:0035022,GO:0035023	CG43947-PE						PF00621	PS50010			G3DSA:1.20.900.10	SSF48065,SSF50729									
aly2178.53	Regulator of G protein signaling loco	GO:0005089,GO:0016319,GO:0055059,GO:0000578,GO:0045179,GO:0005886,GO:0008105,GO:0007419,GO:0008277,GO:0007303,GO:0003015,GO:0035022,GO:0035023,GO:0008069,GO:0007049,GO:0005737,GO:0010001,GO:0030833,GO:0043547,GO:1900029,GO:0005057,GO:0019991,GO:0005544,GO:0016324,GO:0001965,GO:0060857,GO:0007186,GO:0038032,GO:0032291,GO:0005092,GO:0050790,GO:0005096,GO:0050832,GO:0014045,GO:0009786,GO:0007310,GO:0009408,GO:0006979,GO:0042594,GO:0030866,GO:0005622,GO:0005515	CG43947-PE						PF00595	PS50106			G3DSA:2.30.42.10	SSF50156									
aly2178.54	Unknown		n/a						PF16056														
aly2178.55	Unknown		n/a																				
aly2178.56	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2178.6	Probable ribosome production factor 1	GO:0042134,GO:0005730,GO:0030687,GO:0042254,GO:0000460,GO:0003723,GO:0000470,GO:0000027	CG6712-PA				SM00879		PF04427	PS50833			G3DSA:3.40.50.10480	SSF52954	29~49								
aly2178.7	Unknown		n/a																				
aly2178.8	Methyltransferase-like protein 6	GO:0008168	CG34195-PA			PIRSF037755			PF13489				G3DSA:3.40.50.150	SSF53335									
aly2178.9	116 kDa U5 small nuclear ribonucleoprotein component	GO:0005737,GO:0016607,GO:0008380,GO:0030532,GO:0071011,GO:0005829,GO:0016020,GO:0003924,GO:0005634,GO:0000398,GO:0005682,GO:0005654,GO:0006397,GO:0044822,GO:0015030,GO:0003746,GO:0006414,GO:0071013,GO:0005525	CG4849-PA				SM00889,SM00838	TIGR00231	PF14492,PF03764,PF00009,PF03144,PF00679,PF16004	PS51722	PR00315,PR00315,PR00315,PR00315,PR00315		G3DSA:3.30.70.240,G3DSA:2.40.30.10,G3DSA:3.30.230.10,G3DSA:3.30.70.870,G3DSA:3.40.50.300,G3DSA:3.90.1430.10	SSF54980,SSF54211,SSF50447,SSF52540,SSF54980									
aly218027.1	Probable cytochrome P450 301a1, mitochondrial	GO:0007490,GO:0004497,GO:0020037,GO:0016705,GO:0005739,GO:0031966,GO:0005506,GO:0055114,GO:0009055	CG8587-PA						PF00067				G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly21858.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2188.1	SKI family transcriptional corepressor 2	GO:0005737,GO:0021587,GO:0003682,GO:0006351,GO:0000122,GO:0005634,GO:0003714,GO:0048468,GO:0007474,GO:0021936,GO:0046332,GO:0045880,GO:0070410,GO:0030514,GO:0042826,GO:0030512,GO:0021702,GO:0048814	CG11093-PB				SM01046		PF08782,PF02437				G3DSA:3.10.260.20,G3DSA:3.10.390.10	SSF63763,SSF46955										
aly2188.10	Unknown		CG14115-PA				SM00718		PF07841														
aly2188.11	Unknown		CG14115-PA				SM00718		PF07841														
aly2188.12	Unknown		CG17780-PB																				
aly2188.13	Unknown		CG17782-PA				SM00718		PF07841														
aly2188.14	Unknown		CG17782-PA				SM00718		PF07841														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2188.15	Unknown		CG5768-PC				SM00718		PF07841														
aly2188.16	Unknown		CG5768-PC																				
aly2188.17	Acetylcholine receptor subunit alpha-like 1	GO:0006812,GO:0015464,GO:0005892,GO:0045211,GO:0004889,GO:0005887,GO:0017085,GO:0007271,GO:0098655,GO:0030054	CG5610-PB					TIGR00860	PF02932,PF02931		PR00252,PR00252,PR00252,PR00254,PR00254,PR00254	PS00236	G3DSA:1.20.120.370,G3DSA:1.20.120.370,G3DSA:2.70.170.10	SSF90112,SSF63712			REACT_13685						
aly2188.2	60S ribosomal protein L17	GO:0015934,GO:0051298,GO:0022625,GO:0003735,GO:0007052,GO:0000022,GO:0006412	CG3203-PB	MF_01331_A				TIGR01038	PF00237			PS00464	G3DSA:3.90.470.10	SSF54843									
aly2188.3	Heterogeneous nuclear ribonucleoprotein M	GO:0005737,GO:0003729,GO:0009952,GO:0030529,GO:0016363,GO:0005634,GO:0003998,GO:0000166,GO:0008595,GO:0008298,GO:0003730,GO:0003823,GO:0003723,GO:0007067,GO:0007277,GO:0035282,GO:0005681,GO:0045451	CG9373-PA				SM00360,SM00360,SM00360		PF14259,PF00076,PF00076	PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928	354~381								
aly2188.4	Unknown		n/a												52~72,10~44								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2188.5	Unknown		n/a																				
aly2188.6	Acetylcholine receptor subunit beta-like 2	GO:0006810,GO:0006812,GO:0005230,GO:0016020,GO:0005892,GO:0045211,GO:0004889,GO:0005887,GO:0017085,GO:0007271,GO:0098655,GO:0006811,GO:0030054	CG6798-PA					TIGR00860	PF02931,PF02932		PR00252,PR00252,PR00252,PR00252,PR00254,PR00254,PR00254,PR00254	PS00236	G3DSA:2.70.170.10,G3DSA:1.20.120.370,G3DSA:1.20.120.370	SSF90112,SSF63712			REACT_13685						
aly2188.7	Unknown	GO:0005575,GO:0008150,GO:0003674	CG30070-PA				SM00718		PF07841														
aly2188.8	Unknown		CG14115-PA				SM00718		PF07841														
aly2188.9	Unknown		CG42812-PA				SM00718		PF07841														
aly218921.1	Phospholipase D3	GO:0016021,GO:0016042,GO:0003824,GO:0070290,GO:0008152,GO:0004630,GO:0005789	CG9248-PB				SM00155		PF00614	PS50035			G3DSA:3.30.870.10	SSF56024									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2190.1	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG4302-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756										
aly2190.2	Glycerophosphodiester phosphodiesterase 1	GO:0005737,GO:0006629,GO:0008889,GO:0016021,GO:0008081,GO:0048812,GO:0006071,GO:0047395,GO:0046872	CG14883-PA						PF03009	PS51704			G3DSA:3.20.20.190	SSF51695										
aly2190.3	Unknown	GO:0016021,GO:0005272,GO:0006814	CG30181-PA						PF00858				G3DSA:1.10.287.820											
aly2195.1	Glucose-6-phosphatase 2	GO:0016787,GO:0004346,GO:0005783,GO:0016020,GO:0050796,GO:0005789,GO:0042593,GO:0030176,GO:0051156,GO:0006094	CG15400-PB			PIRSF000905	SM00014		PF01569				G3DSA:1.20.144.10	SSF48317		00010+3.1.3.9,00500+3.1.3.9,00052+3.1.3.9			UPA00138				
aly2195.2	Unknown		CG8736-PB																				
aly2195.3	Diacylglycerol kinase beta	GO:0005737,GO:0016310,GO:0007205,GO:0005509,GO:0005886,GO:0003951,GO:0006661,GO:0035556,GO:0042313,GO:0004143,GO:0005524	CG34361-PH				SM00054,SM00054,SM00045,SM00109,SM00109,SM00046		PF00781,PF00609,PF14513,PF13499,PF00130,PF00130	PS50222,PS50222,PS50081,PS50146,PS50081		PS00018,PS00479,PS00479,PS00018	G3DSA:1.10.238.10,G3DSA:3.30.60.20,G3DSA:3.30.60.20,G3DSA:1.10.238.110	SSF57889,SSF47473,SSF57889,SSF47473,SSF111331,SSF111331		00561+2.7.1.107,00564+2.7.1.107	REACT_14797,REACT_604	PWY-7039						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2195.4	Unknown		n/a																				
aly220.1	Unknown	GO:0016772	CG2004-PA				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly220.10	6-phosphogluconolactonase	GO:0005737,GO:0017057,GO:0005975,GO:0005575,GO:0006098,GO:0048029,GO:0009051	CG17333-PA					TIGR01198	PF01182				G3DSA:3.40.50.1360	SSF100950		00520+3.5.99.6,00030+3.1.1.31		PWY-5514,PWY-6906,PWY-6855	UPA00115				
aly220.11	La-related protein 6	GO:0005737,GO:0005634,GO:0000166,GO:0003723,GO:0006417,GO:0030529,GO:0006396	CG17386-PA				SM00715		PF05383	PS50961	PR00302,PR00302,PR00302		G3DSA:1.10.10.10,G3DSA:3.30.70.330	SSF46785									
aly220.12	Homer protein homolog 2	GO:0005783,GO:0048149,GO:0048148,GO:0030425,GO:0008277,GO:0030054,GO:0005737,GO:0045177,GO:0005730,GO:0005634,GO:0007216,GO:0005654,GO:0035584,GO:0043025,GO:0045938,GO:0035256,GO:0045471,GO:0005886,GO:0097481,GO:0030534,GO:0048875,GO:0040012,GO:0045211,GO:0005515,GO:2001256	CG11324-PE				SM00461		PF00568	PS50229			G3DSA:2.30.29.30	SSF50729	159~221,224~282								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly220.13	Patj homolog	GO:0016333,GO:0016332,GO:0016334,GO:0034332,GO:0034334,GO:0035003,GO:0007163,GO:0007043,GO:0005875,GO:0005737,GO:0002009,GO:0035088,GO:0045176,GO:0005635,GO:0045179,GO:0005080,GO:0032033,GO:0035509,GO:0016324,GO:0016327,GO:0008594,GO:0045186,GO:0005912,GO:0005886,GO:0001736,GO:0005918,GO:0035209,GO:0005515,GO:0045494	CG15803-PC				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156										
aly220.14	Inactivation-no after-potential D protein	GO:0050962,GO:0008104,GO:0071482,GO:0030159,GO:0016059,GO:0007605,GO:0007601,GO:0016027,GO:0017022,GO:0007602,GO:0016028,GO:0005516,GO:0005515,GO:0005886,GO:0009881,GO:0005198,GO:0031473	CG3504-PB				SM00228,SM00228,SM00228,SM00228,SM00228,SM00228,SM00228		PF00595,PF00595,PF00595,PF00595,PF00595,PF00595,PF00595	PS50106,PS50106,PS50106,PS50106,PS50106,PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156,SSF50156,SSF50156,SSF50156,SSF50156,SSF50156	783~814									
aly220.15	Unknown		CG17834-PA																				
aly220.16	Cuticle protein 19	GO:0040003,GO:0005214,GO:0008010,GO:0008012,GO:0031012,GO:0042302	CG9290-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly220.2	Unknown		n/a										G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly220.3	Mediator of RNA polymerase II transcription subunit 20	GO:0005634,GO:0003713,GO:0001104,GO:0006357,GO:0006351,GO:0006367,GO:0016592,GO:0003899	CG18780-PB																				
aly220.4	Mediator of RNA polymerase II transcription subunit 20	GO:0005634,GO:0003713,GO:0001104,GO:0006357,GO:0006351,GO:0006367,GO:0003899,GO:0016592	CG18780-PB						PF08612														
aly220.5	Homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 2 protein	GO:0006986,GO:0030968,GO:0006983,GO:0016021,GO:0007283,GO:0005515,GO:0005875,GO:0005783	CG14536-PA				SM00213		PF00240	PS50053			G3DSA:3.10.20.90	SSF54236									
aly220.6	Protein TIPIN homolog	GO:0005737,GO:0044770,GO:0000076,GO:0008284,GO:0005634,GO:0006974,GO:0000790,GO:0048478,GO:0003674,GO:0051301,GO:0007067,GO:0007049,GO:0031573	CG10336-PA						PF07962						9~29								
aly220.7	Protein lingerer	GO:0005737,GO:0060179,GO:0007620,GO:0007610,GO:0003674,GO:0005515	CG8715-PK						PF12478					SSF46934									
aly220.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly220.9	Protein lingerer	GO:0005737,GO:0060179,GO:0003674,GO:0007610,GO:0007620	CG8715-PK																				
aly2202.1	Murinoglobulin-2	GO:0006909,GO:0005615,GO:0004866,GO:0019731,GO:0030414,GO:0004867,GO:0050829	CG7052-PA						PF00207,PF01835,PF07678,PF07678,PF07703,PF10569			PS00477	G3DSA:1.50.10.20,G3DSA:1.50.10.20	SSF48239									
aly2202.10	3-ketoacyl-CoA thiolase, mitochondrial	GO:0006631,GO:0008152,GO:0006635,GO:0005743,GO:0044822,GO:0005811,GO:0005739,GO:0003824,GO:0006695,GO:0003988,GO:0071456,GO:1901029,GO:0005875,GO:1902109,GO:0070062	CG4600-PA			PIRSF000429		TIGR01930	PF00108,PF02803			PS00099,PS00098	G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10	SSF53901,SSF53901			REACT_22258						
aly2202.11	Methyltransferase-like protein 23	GO:0005737,GO:0008168,GO:0016021	CG5013-PA				SM00248,SM00248		PF13637,PF00887,PF10294	PS50088,PS50297,PS50088,PS51228	PR00689,PR00689,PR00689,PR00689		G3DSA:1.20.80.10,G3DSA:3.40.50.150,G3DSA:1.25.40.20	SSF47027,SSF48403,SSF53335									
aly2202.12	CCR4-NOT transcription complex subunit 11	GO:0000288,GO:0000289,GO:0008283,GO:0005829,GO:0010467,GO:0006355,GO:0030014,GO:0031047,GO:0017148,GO:0006417,GO:0006402,GO:0005634,GO:0006351	CG13567-PA						PF10155														
aly2202.13	E3 ubiquitin-protein ligase Nedd-4	GO:0005737,GO:0045746,GO:0007219,GO:0031623,GO:0005515,GO:0016874,GO:0005634,GO:0061630,GO:0016199,GO:0007528,GO:0016567,GO:0042787,GO:0017022,GO:0051965,GO:0005886,GO:0007411,GO:0045807,GO:0004842,GO:0005112,GO:0019904,GO:0002092	CG42279-PJ				SM00239,SM00119,SM00456,SM00456,SM00456		PF00632,PF00397,PF00397,PF00397,PF00168	PS50237,PS50020,PS50020,PS50020,PS50004	PR00360,PR00360	PS01159,PS01159,PS01159	G3DSA:2.20.70.10,G3DSA:3.30.2160.10,G3DSA:2.20.70.10,G3DSA:2.20.70.10,G3DSA:2.60.40.150	SSF51045,SSF56204,SSF51045,SSF51045,SSF49562	356~376				UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2202.14	Unknown	GO:0016772	CG1561-PB				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly2202.15	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG9447-PC																				
aly2202.16	Unknown	GO:0016772	CG1561-PB				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly2202.17	Unknown		n/a																				
aly2202.18	Unknown	GO:0040003,GO:0022600,GO:0007586,GO:0016021,GO:0016747,GO:0009651,GO:0048477,GO:0030421	CG32589-PA																				
aly2202.19	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2202.2	F-actin-capping protein subunit alpha	GO:0010591,GO:0007015,GO:0008290,GO:0006909,GO:0005869,GO:0030837,GO:0016324,GO:0046982,GO:0007018,GO:0051016,GO:0030036,GO:0051490,GO:0003779,GO:0051489,GO:0035220,GO:0007294,GO:0046329,GO:0071203,GO:0005875,GO:0000902	CG10540-PA						PF01267		PR00191,PR00191,PR00191	PS00749,PS00748		SSF90096									
aly2202.20	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG9447-PC						PF01757														
aly2202.21	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG9447-PC						PF01757														
aly2202.22	Unknown	GO:0016772	CG1561-PB				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly2202.23	Unknown	GO:0016772	CG1561-PB				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly2202.24	Epidermal growth factor receptor substrate 15-like 1	GO:0008021,GO:0016020,GO:0006897,GO:0016192,GO:0008582,GO:0005634,GO:0006898,GO:0042059,GO:0045746,GO:0007173,GO:0005509,GO:0007269,GO:0005886,GO:0030132,GO:0048488	CG16932-PA				SM00054,SM00054,SM00054,SM00027,SM00027,SM00027		PF13202,PF12763,PF12763	PS50222,PS50031,PS50031,PS50031,PS50222,PS50222		PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473,SSF47473,SSF47473	370~425,433~460,335~362,468~488									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2202.25	Glutathione S-transferase 1	GO:0005737,GO:0004364,GO:0006749,GO:0005515	CG17530-PA						PF13417,PF00043	PS50405,PS50404			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF52833,SSF47616									
aly2202.26	Glutathione S-transferase 1	GO:0005737,GO:0004364,GO:0006749,GO:0005515	CG17524-PA						PF02798	PS50404,PS50405			G3DSA:3.40.30.10,G3DSA:1.20.1050.10	SSF47616,SSF52833									
aly2202.27	Unknown		CG10283-PC						PF15295						169~212,131~158								
aly2202.28	DnaJ homolog subfamily C member 2	GO:0042393,GO:0006457,GO:0030308,GO:0005829,GO:0051082,GO:0043130,GO:0045893,GO:0003677,GO:0003682,GO:0005634,GO:0016568,GO:0006351	CG10565-PA				SM00271,SM00717,SM00717		PF00226,PF00249,PF16717	PS50090,PS51293,PS50076	PR00625,PR00625,PR00625		G3DSA:1.10.287.110,G3DSA:1.10.10.60	SSF46689,SSF46565	290~346,402~422								
aly2202.29	Pyroglutamyl-peptidase 1	GO:0006508,GO:0005829,GO:0008233,GO:0008234,GO:0016920	CG32147-PA			PIRSF015592			PF01470		PR00706,PR00706,PR00706		G3DSA:3.40.630.20	SSF53182									
aly2202.3	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 11	GO:0005743,GO:0016021,GO:0070469,GO:0055114	CG9350-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2202.30	40S ribosomal protein S9	GO:0005737,GO:0005840,GO:0005730,GO:0005829,GO:0045903,GO:0019843,GO:0003735,GO:0007052,GO:0003723,GO:0000228,GO:0006412,GO:0000022,GO:0022627	CG3395-PE				SM00363	TIGR01018	PF01479,PF00163	PS50889		PS00632	G3DSA:3.10.290.10	SSF55174									
aly2202.31	Protein KRI1 homolog	GO:0005575,GO:0008150,GO:0003674	CG5645-PA						PF12936,PF05178						280~306,417~444								
aly2202.32	Cleavage and polyadenylation specificity factor 73	GO:0016787,GO:0005847,GO:0046872,GO:0004519,GO:0006398,GO:0003723,GO:0003677,GO:0006378,GO:0006379,GO:0022008	CG7698-PA				SM00849,SM01027,SM01098		PF10996,PF07521,PF16661,PF11718				G3DSA:3.60.15.10	SSF56281									
aly2202.33	General transcription factor IIH subunit 4	GO:0001113,GO:0004003,GO:0005634,GO:0005675,GO:0006289,GO:0006355,GO:0004439,GO:0006367,GO:0006366,GO:0000990,GO:0008353,GO:0010224,GO:0001111,GO:0001671	CG7764-PA					TIGR00625	PF03849														
aly2202.34	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2202.35	Protein spitz	GO:0061331,GO:0016330,GO:0005783,GO:0048149,GO:0000086,GO:0035225,GO:0005789,GO:0046673,GO:0008317,GO:0003015,GO:0007298,GO:0008355,GO:0007432,GO:0048865,GO:0016021,GO:0007476,GO:0007438,GO:0050769,GO:0043066,GO:0045742,GO:0008284,GO:0005794,GO:0005154,GO:0045470,GO:0007173,GO:0035277,GO:0005886,GO:0022008,GO:0007424,GO:0007421,GO:0007422,GO:0000139,GO:0005576,GO:0046845	CG10334-PE									PS00022,PS01186	G3DSA:2.10.25.10										
aly2202.36	Protein espinas	GO:0005737,GO:0045184,GO:0008104,GO:0042067,GO:0016020,GO:0016348,GO:0045746,GO:0045185,GO:0007163,GO:0008270,GO:0005515,GO:0001737,GO:0001736,GO:0001738	CG11084-PC				SM00132,SM00132,SM00132		PF06297,PF00412,PF00412,PF00412	PS51303,PS50023,PS50023,PS50023		PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716										
aly2202.37	Retrovirus-related Pol polyprotein from type-2 retrotransposable element R2DM	GO:0003964,GO:0004519,GO:0046872,GO:0004190	n/a						PF00078	PS50878				SSF56672									
aly2202.38	Unknown		n/a				SM00409		PF00047	PS50835			G3DSA:2.60.40.10	SSF48726									
aly2202.39	Unknown		n/a							PS50835			G3DSA:2.60.40.10	SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2202.4	Unknown	GO:0022417,GO:0016021,GO:0051082,GO:0061077	CG30296-PC						PF15361														
aly2202.40	Delta(24)-sterol reductase	GO:0008104,GO:0008762,GO:0000246,GO:0008285,GO:0019899,GO:0005789,GO:0061024,GO:0044281,GO:0042987,GO:1901214,GO:0005783,GO:0005737,GO:0050660,GO:0016628,GO:0042605,GO:0016021,GO:0016020,GO:0031639,GO:0043066,GO:0043588,GO:0005856,GO:0006915,GO:0009888,GO:0007050,GO:0003824,GO:0007265,GO:0006979,GO:0055114,GO:0050614,GO:0016614,GO:0009725,GO:0005829,GO:0030539,GO:0000139,GO:0043154,GO:0006695,GO:0005634	n/a						PF01565	PS51387			G3DSA:3.30.465.10	SSF56176		00520+1.3.1.98,00550+1.3.1.98		PWY-6386,PWY-6387	UPA00219				
aly2202.41	Unknown		n/a				SM00355,SM00355			PS50157		PS00028	G3DSA:3.30.160.60	SSF57667									
aly2202.5	Uncharacterized protein C1orf43 homolog	GO:0016021	CG6665-PC						PF07406														
aly2202.6	Focadhesin	GO:0005575,GO:0003674,GO:0016021,GO:0005925,GO:0008150	CG3520-PA						PF12530					SSF48371,SSF48371,SSF48371,SSF48371,SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2202.7	Probable protein BRICK1-A	GO:0005737,GO:0005575,GO:0010592,GO:0008582,GO:0005856,GO:0051491,GO:0021551,GO:0008360,GO:0003674	CG30173-PA												48~68								
aly2202.8	3-ketoacyl-CoA thiolase, mitochondrial	GO:0006631,GO:0008152,GO:0006635,GO:0005743,GO:0044822,GO:0005811,GO:0005739,GO:0003824,GO:0006695,GO:0003988,GO:0071456,GO:1901029,GO:0005875,GO:1902109,GO:0070062	CG4600-PA			PIRSF000429		TIGR01930	PF02803,PF00108			PS00098	G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10	SSF53901,SSF53901			REACT_22258							
aly2202.9	3-ketoacyl-CoA thiolase, mitochondrial	GO:0006631,GO:0008152,GO:0006635,GO:0044822,GO:0005811,GO:0005739,GO:0005743,GO:0006695,GO:0016747,GO:0003988,GO:0071456,GO:1901029,GO:0005875,GO:1902109,GO:0070062	CG4600-PA			PIRSF000429		TIGR01930	PF00108,PF02803			PS00098,PS00099,PS00737	G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10	SSF53901,SSF53901	145~165		REACT_22258						
aly2204.1	Pickpocket protein 28	GO:0009415,GO:0005272,GO:0042756,GO:0015280,GO:0016021,GO:0016020,GO:0006814,GO:0035002,GO:0035725,GO:0071462,GO:0005886	CG8546-PC						PF00858				G3DSA:1.10.287.770										
aly2204.10	Group XIIB secretory phospholipase A2-like protein	GO:0006644,GO:0070328,GO:0016042,GO:0005576,GO:0005509,GO:0042632,GO:0004623	CG17035-PA						PF06951			PS00118	G3DSA:1.20.90.10	SSF48619		00564+3.1.1.4,00590+3.1.1.4,00592+3.1.1.4,00591+3.1.1.4,00565+3.1.1.4		PWY-7409,PWY-7417,PWY-6803,PWY-7416					
aly2204.11	Myotrophin	GO:0005634,GO:0005575,GO:0003674,GO:0005515,GO:0008150,GO:0048471	CG31715-PA				SM00248,SM00248		PF12796	PS50297,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20	SSF48403									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2204.12	Serendipity locus protein alpha	GO:0005737,GO:0007015,GO:0031941,GO:0000915,GO:0005829,GO:0016020,GO:0007349,GO:0032154,GO:0003779,GO:0005886	CG8247-PB						PF05482														
aly2204.13	Neuropeptide-like 1	GO:0007218,GO:0005184,GO:0005615,GO:0010753,GO:0048018,GO:0005576	CG3441-PC																				
aly2204.14	Unknown		n/a																				
aly2204.15	Unknown		n/a																				
aly2204.16	Protein gooseberry-neuro	GO:0043565,GO:0007367,GO:0003700,GO:0005634,GO:0006355,GO:0000977,GO:0005667,GO:0003677,GO:0022008,GO:0006351	CG2692-PA				SM00389,SM00351		PF00046,PF00292	PS51057,PS50071	PR00027,PR00027,PR00027,PR00027	PS00027,PS00034	G3DSA:1.10.10.10,G3DSA:1.10.10.10,G3DSA:1.10.10.60	SSF46689,SSF46689									
aly2204.17	Protein gooseberry	GO:0005737,GO:0007435,GO:0007367,GO:0006355,GO:0003700,GO:0005634,GO:0060025,GO:0007419,GO:0007268,GO:0000977,GO:0005667,GO:0003677,GO:0022008,GO:0006351	CG3388-PA				SM00351,SM00389		PF00292,PF00046	PS50071,PS51057	PR00027,PR00027,PR00027,PR00027	PS00034,PS00027	G3DSA:1.10.10.10,G3DSA:1.10.10.60,G3DSA:1.10.10.10	SSF46689,SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2204.18	Acidic juvenile hormone-suppressible protein 1	GO:0005615,GO:0005616,GO:0005811,GO:0046331,GO:0045735,GO:0005576	CG4178-PA						PF03722,PF03723,PF00372		PR00187,PR00187,PR00187		G3DSA:2.60.40.1520,G3DSA:1.10.1280.10,G3DSA:1.20.1370.10	SSF48056,SSF81296,SSF48050									
aly2204.19	Acidic juvenile hormone-suppressible protein 1	GO:0005615,GO:0005616,GO:0005811,GO:0046331,GO:0045735,GO:0005576	CG4178-PA						PF03722,PF00372,PF03723		PR00187,PR00187,PR00187,PR00187	PS00210	G3DSA:2.60.40.1520,G3DSA:1.10.1280.10,G3DSA:1.20.1370.10	SSF81296,SSF48050,SSF48056									
aly2204.2	Pickpocket protein 28	GO:0009415,GO:0005272,GO:0042756,GO:0015280,GO:0016021,GO:0016020,GO:0006814,GO:0035002,GO:0035725,GO:0071462,GO:0005886	CG8546-PC						PF00858				G3DSA:1.10.287.820										
aly2204.20	Arylphorin subunit alpha	GO:0005615,GO:0005811,GO:0005616,GO:0045735,GO:0005576	CG6821-PA						PF00372,PF03722,PF03723		PR00187,PR00187,PR00187,PR00187	PS00209,PS00210	G3DSA:1.10.1280.10,G3DSA:1.20.1370.10,G3DSA:2.60.40.1520	SSF81296,SSF48050,SSF48056									
aly2204.21	Arylphorin subunit alpha	GO:0005615,GO:0005811,GO:0005616,GO:0045735,GO:0005576	CG6821-PA						PF00372,PF03722,PF03723		PR00187,PR00187,PR00187,PR00187	PS00210,PS00209	G3DSA:1.20.1370.10,G3DSA:2.60.40.1520,G3DSA:1.10.1280.10	SSF81296,SSF48050,SSF48056									
aly2204.22	Sex-specific storage-protein 1	GO:0016201,GO:0005615,GO:0005616,GO:0005811,GO:0005576,GO:0045735,GO:0008045	CG6806-PA						PF03722,PF03723,PF00372		PR00187,PR00187,PR00187,PR00187	PS00210,PS00209	G3DSA:1.10.1280.10,G3DSA:2.60.40.1520,G3DSA:1.20.1370.10	SSF48056,SSF48050,SSF81296									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2204.23	Troponin C	GO:0005509	CG6514-PA				SM00054,SM00054,SM00054,SM00054		PF14658,PF13499	PS50222,PS50222,PS50222,PS50222		PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly2204.24	Arylphorin subunit alpha	GO:0005615,GO:0005811,GO:0005616,GO:0045735,GO:0005576	CG2559-PA						PF00372,PF03722,PF03723		PR00187,PR00187,PR00187	PS00210	G3DSA:2.60.40.1520,G3DSA:1.10.1280.10,G3DSA:1.20.1370.10	SSF81296,SSF48056,SSF48050									
aly2204.25	Basic juvenile hormone-suppressible protein 2	GO:0046331,GO:0005811,GO:0005616,GO:0045735,GO:0005576	CG4178-PA						PF03723,PF00372,PF03722		PR00187,PR00187,PR00187,PR00187	PS00209,PS00210	G3DSA:2.60.40.1520,G3DSA:1.10.1280.10,G3DSA:1.20.1370.10	SSF81296,SSF48056,SSF48050									
aly2204.3	Pickpocket protein 28	GO:0009415,GO:0005272,GO:0042756,GO:0015280,GO:0016021,GO:0016020,GO:0006814,GO:0035002,GO:0035725,GO:0071462,GO:0005886	CG8546-PC						PF00858														
aly2204.4	Pickpocket protein 28	GO:0005272,GO:0071462,GO:0015280,GO:0016021,GO:0009415,GO:0006814,GO:0035002,GO:0035725,GO:0042756,GO:0005886	CG8546-PC						PF00858		PR01078,PR01078,PR01078,PR01078,PR01078,PR01078,PR01078		G3DSA:1.10.287.770,G3DSA:2.60.470.10,G3DSA:2.60.470.10,G3DSA:2.60.470.10										
aly2204.5	Unknown	GO:0030071,GO:0031145,GO:0005680	n/a						PF10471						19~39				UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2204.6	Inhibitor of growth protein 3	GO:0005737,GO:0032777,GO:0006351,GO:0035064,GO:0016573,GO:0000123,GO:0043967,GO:0043968,GO:0005634,GO:0005730,GO:0004402,GO:0000812,GO:0043065,GO:0006355,GO:0008270,GO:0005515,GO:0040008,GO:0035267	CG6632-PA				SM00249		PF12998	PS50016		PS01359	G3DSA:3.30.40.10	SSF57903										
aly2204.7	Calcyclin-binding protein	GO:0007507,GO:0070062,GO:0005641,GO:0005654,GO:0030877,GO:0005875	CG3226-PA						PF09032,PF04969	PS51048,PS51203			G3DSA:2.60.40.790	SSF140106,SSF49764	6~26								
aly2204.8	Unknown		n/a												302~322								
aly2204.9	60S ribosomal protein L13a	GO:0007219,GO:0015934,GO:0005840,GO:0022625,GO:0008407,GO:0003735,GO:0006412,GO:0051298	CG1475-PB	MF_01366				TIGR01077	PF00572			PS00783	G3DSA:3.90.1180.10	SSF52161									
aly2206.1	Unknown		n/a																				
aly2206.2	Tryptase	GO:0004252,GO:0005576,GO:0006508	CG5390-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2206.3	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005576,GO:0005886,GO:0006508	CG5390-PA				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2206.4	Unknown		n/a												1~28								
aly221.1	Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	GO:0005737,GO:0051341,GO:0045087,GO:0005739,GO:0006952,GO:0007165,GO:0005515,GO:0008063,GO:0005634,GO:0055114,GO:0016651	CG10610-PA						PF14784,PF06239														
aly221.10	Unknown		CG16953-PB																				
aly221.11	Unknown		n/a																				
aly221.12	UDP-N-acetylglucosamine transferase subunit ALG14 homolog	GO:0016021,GO:0046331,GO:0005789	CG6308-PA						PF08660				G3DSA:3.40.50.2000	SSF53756									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly221.13	GPI inositol-deacylase	GO:0005783,GO:0004518,GO:0006886,GO:0005789,GO:0042578,GO:0090305,GO:0006505,GO:0015798,GO:0016021	CG3160-PA						PF07819				G3DSA:3.40.50.1820	SSF53474									
aly221.14	Signal peptidase complex subunit 1	GO:0005787,GO:0016021,GO:0045047,GO:0006465,GO:0030176,GO:0008233	CG11500-PA						PF06645														
aly221.15	Serine-threonine kinase receptor-associated protein	GO:0044822,GO:0010719,GO:0010633,GO:0032797,GO:0005829,GO:0000122,GO:0007476,GO:0050680,GO:0030512,GO:0005654,GO:0060394,GO:0030277,GO:0005515,GO:0005886,GO:0005102,GO:0000387,GO:0034719,GO:0005875	CG3957-PA				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50294,PS50082,PS50082,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978									
aly221.16	Peroxidasin homolog	GO:0005201,GO:0046872,GO:0070062,GO:0020037,GO:0005615,GO:0005578,GO:0006979,GO:0030198,GO:0042744,GO:0031012,GO:0004601,GO:0055114,GO:0005783	CG10211-PA						PF03098,PF03098,PF03098	PS50292,PS50292	PR00457,PR00457,PR00457,PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10,G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113,SSF48113	1341~1343								
aly221.17	Unknown	GO:0005575,GO:0005634,GO:0003674,GO:0035295	CG6611-PF																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly221.18	Sodium-independent sulfate anion transporter	GO:0045434,GO:0005794,GO:0005783,GO:0015301,GO:0016021,GO:0005886,GO:0015116,GO:0005765,GO:0008271,GO:0008272,GO:0008509,GO:0070062	CG7005-PA						PF00916														
aly221.19	Viral cathepsin	GO:0008234	n/a				SM00848		PF08246				G3DSA:3.90.70.10,G3DSA:3.90.70.10	SSF54001									
aly221.2	TM2 domain-containing protein CG10795	GO:0005575,GO:0003674,GO:0016021,GO:0008150	CG10795-PA						PF05154														
aly221.20	Unknown		n/a																				
aly221.21	Unknown		n/a																				
aly221.22	Actinidain	GO:0008234	n/a				SM00848		PF08246				G3DSA:3.90.70.10	SSF54001									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly221.3	Unknown		n/a				SM00692,SM00980		PF05485	PS50950				SSF57716									
aly221.4	Nuclear pore complex protein Nup214	GO:0006909,GO:0019221,GO:0006611,GO:0034605,GO:0019083,GO:0010827,GO:0015758,GO:0044281,GO:0005487,GO:0005925,GO:0044267,GO:0008645,GO:0005634,GO:0044613,GO:0005654,GO:0010467,GO:0019058,GO:0006406,GO:0000278,GO:0005215,GO:0043687,GO:0006606,GO:0007077,GO:0016925,GO:0055085,GO:0030718,GO:0005975,GO:0043231,GO:0051726,GO:0005643,GO:1900034,GO:0005829,GO:0007184,GO:0005515,GO:0016032	CG10198-PA										G3DSA:2.130.10.10	SSF117289	740~760								
aly221.5	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	GO:0005737,GO:0005739,GO:0005654,GO:0005743,GO:0003858,GO:0006697,GO:0005759	CG12068-PA						PF00106		PR00081,PR00081,PR00081,PR00080,PR00080,PR00080	PS00061	G3DSA:3.40.50.720	SSF51735	238~258								
aly221.6	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG4920-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly221.7	Brain-specific angiogenesis inhibitor 1-associated protein 2	GO:0005856,GO:0030175,GO:0008360,GO:0016020,GO:0004871,GO:0008093,GO:0005829,GO:0005543,GO:0051017,GO:0017124,GO:0001726,GO:0005575,GO:0061024,GO:0007009,GO:0070064,GO:0007165,GO:0005515,GO:0032956,GO:0051764,GO:0046847,GO:0009617	CG32082-PA				SM00326		PF08397,PF00018	PS50002,PS51338			G3DSA:1.20.1270.80,G3DSA:2.30.30.40	SSF50044,SSF103657	809~829								
aly221.8	Unknown		n/a																				
aly221.9	Cathepsin B	GO:0009897,GO:0004175,GO:0030984,GO:0071260,GO:0048102,GO:0009612,GO:0014075,GO:0014070,GO:0005737,GO:0042277,GO:0005615,GO:0007519,GO:0009611,GO:0005739,GO:0005576,GO:0032403,GO:0006508,GO:0009986,GO:0042383,GO:0034097,GO:0035071,GO:0051603,GO:0016324,GO:0060548,GO:0006914,GO:0050790,GO:0045471,GO:0007283,GO:0043434,GO:0043621,GO:0042470,GO:0009749,GO:0005764,GO:0070670,GO:0004197	CG10992-PA				SM00645		PF08127,PF00112		PR00705,PR00705,PR00705	PS00139,PS00640,PS00639	G3DSA:3.90.70.10	SSF54001									
aly2210.1	Multiple C2 and transmembrane domain-containing protein 2	GO:0019722,GO:0016021,GO:0016020,GO:0005622,GO:0008150,GO:0005509,GO:0005515	CG15078-PD						PF00168	PS50004	PR00360,PR00360		G3DSA:2.60.40.150	SSF49562									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2210.2	Uridine phosphorylase 1	GO:0005737,GO:0006139,GO:0043097,GO:0042332,GO:0005829,GO:0006206,GO:0044206,GO:0006218,GO:0009166,GO:0003824,GO:0009116,GO:0042149,GO:0046135,GO:0004850,GO:0055086,GO:0044281	CG6330-PA					TIGR01719	PF01048				G3DSA:3.40.50.1580	SSF53167		00983+2.4.2.3,00240+2.4.2.3			UPA00574				
aly222.1	Splicing factor 3B subunit 4	GO:0048026,GO:0005689,GO:0071011,GO:0044822,GO:0000398,GO:0000166,GO:0007052,GO:0003676,GO:0005686,GO:0022008,GO:0006397,GO:0008380,GO:0005681,GO:0003729	CG3780-PA				SM00360,SM00360		PF00076,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928									
aly222.2	F-box/LRR-repeat protein 4	GO:0005758,GO:0005634,GO:0016059	CG1839-PA				SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00256		PF12937	PS50181			G3DSA:3.80.10.10	SSF52047,SSF81383									
aly222.3	Alpha-amylase 4N	GO:0043169,GO:0005975,GO:0003824,GO:0004556,GO:0005576,GO:0046872	CG18730-PA				SM00642,SM00632		PF02806,PF00128		PR00110,PR00110,PR00110,PR00110,PR00110		G3DSA:3.20.20.80,G3DSA:2.60.40.1180	SSF51445,SSF51011		00500+2.4.1.18,00500+3.2.1.1	REACT_474	PWY-622,PWY-5067					
aly222.4	Alpha-amylase 2	GO:0043169,GO:0005975,GO:0003824,GO:0004556,GO:0005576,GO:0046872	CG18730-PA				SM00632,SM00642		PF00128,PF02806		PR00110,PR00110,PR00110,PR00110,PR00110		G3DSA:2.60.40.1180,G3DSA:3.20.20.80	SSF51011,SSF51445		00500+3.2.1.1,00500+2.4.1.18	REACT_474	PWY-622,PWY-5067					
aly222.5	Fibronectin type III domain-containing protein 5	GO:0005778,GO:0005783,GO:0016021,GO:0090336,GO:0005576,GO:0005515,GO:0005886,GO:0014850	CG33143-PF				SM00060		PF16066,PF00041	PS50853			G3DSA:2.60.40.10	SSF49265									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2221.1	Unknown	GO:0030718,GO:0006909,GO:0005643,GO:0044613,GO:0005515,GO:0005487,GO:0007184	CG10198-PA																				
aly2221.2	Nuclear pore complex protein Nup98-Nup96	GO:0006909,GO:0019221,GO:0034605,GO:0019083,GO:0010827,GO:0042405,GO:0051028,GO:0005487,GO:0034399,GO:0044267,GO:0007264,GO:0042277,GO:0008645,GO:0044615,GO:0005635,GO:0044613,GO:0015758,GO:0010467,GO:0019058,GO:0006260,GO:0007184,GO:0017056,GO:0000278,GO:0005215,GO:0043687,GO:0031965,GO:0006913,GO:0051292,GO:0007077,GO:0016925,GO:0055085,GO:0000059,GO:0030718,GO:0005975,GO:0031080,GO:0005643,GO:1900034,GO:0005829,GO:0006999,GO:0005515,GO:0005654,GO:0016032,GO:0044281	CG10198-PA																				
aly2221.3	Unknown		n/a																				
aly2221.4	Midasin	GO:0005634,GO:0016887,GO:0005524	n/a												371~391,570~597								
aly22264.1	Unknown		n/a												114~134								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly22279.1	Unknown	GO:0016012,GO:0016021,GO:0007517,GO:0008307	CG5657-PA						PF04790														
aly22303.1	Filamin-A	GO:0008104,GO:0035204,GO:0015629,GO:0048149,GO:0035324,GO:0007611,GO:0007301,GO:0007303,GO:0008045,GO:0007067,GO:0008355,GO:0035183,GO:0035182,GO:0030708,GO:0030725,GO:0005634,GO:0045179,GO:0003779,GO:0005886,GO:0048471,GO:0005884,GO:0008302,GO:0008340,GO:0005829,GO:0005515,G	CG3937-PM				SM00557		PF00630	PS50194			G3DSA:2.60.40.10	SSF81296										
aly223058.1	Nucleolar MIF4G domain-containing protein 1 homolog	GO:0022008,GO:0003723,GO:0005515,GO:0005730	CG9004-PA						PF02854				G3DSA:1.25.40.180	SSF48371									
aly2232.1	Transmembrane and TPR repeat-containing protein CG4341	GO:0005575,GO:0008150,GO:0016021,GO:0003674,GO:0005515	CG4341-PA				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF13176,PF13181,PF13181,PF13414,PF13414,PF08409	PS50293,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452	402~422								
aly22321.1	Unknown		n/a																				
aly22368.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2239.1	Ubiquitin carboxyl-terminal hydrolase 8	GO:0019897,GO:0090263,GO:0071108,GO:0008587,GO:0001669,GO:0045880,GO:0005737,GO:0043161,GO:0000281,GO:0005654,GO:0006511,GO:0016579,GO:0070536,GO:0005794,GO:0008283,GO:0061136,GO:0031313,GO:0007265,GO:0004843,GO:0007032,GO:0005829,GO:0030496,GO:0004197,GO:0005769	CG5798-PA						PF00443,PF08969	PS50235		PS00972	G3DSA:3.40.250.10	SSF54001,SSF52821,SSF140856	416~450,485~514								
aly2239.2	Synapse-associated protein of 47 kDa	GO:0003674,GO:0008306,GO:0048172,GO:0045202,GO:0007268	CG8884-PA				SM00751		PF03909	PS50858				SSF140383	314~348,350~370								
aly2239.3	Pancreatic triacylglycerol lipase	GO:0046872,GO:0005576,GO:0004806,GO:0006629,GO:0016042	CG17292-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly2239.4	Organic cation transporter protein	GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0008513,GO:0016021	CG8654-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473	251~271								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly22394.1	Serpin B9	GO:0009617,GO:0004867,GO:0010628,GO:0035009,GO:0005737,GO:0042270,GO:0005615,GO:0005634,GO:0016020,GO:0043066,GO:0002020,GO:0043027,GO:0071391,GO:0033668,GO:0006915,GO:0002448,GO:0006955,GO:0010951,GO:0070062,GO:0005829,GO:0005622,GO:0043154,GO:0045861	CG6680-PA				SM00093		PF00079				G3DSA:2.30.39.10,G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574										
aly22422.1	Unknown		n/a																				
aly224620.1	Unknown		n/a																				
aly225.1	Membrane-associated progesterone receptor component 2	GO:0035100,GO:0020037,GO:0016021,GO:0016020,GO:0003707,GO:0012505,GO:0043401,GO:0005886,GO:0005496	CG9066-PA										G3DSA:3.10.120.10	SSF55856									
aly225.2	Unknown	GO:0005549	n/a						PF01395				G3DSA:1.10.238.20	SSF47565									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly225.3	Unknown	GO:0005549	n/a						PF01395				G3DSA:1.10.238.20,G3DSA:1.10.238.20	SSF47565,SSF47565									
aly2250.1	Leucine-rich repeat-containing protein 47	GO:0004826,GO:0006432,GO:0009328,GO:0044822,GO:0000287,GO:0003723,GO:0005515,GO:0005524	CG5706-PA				SM00364,SM00364,SM00364,SM00364,SM00364,SM00369,SM00369,SM00369,SM00369,SM00873		PF03483,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10	SSF52058		00970+6.1.1.20							
aly2250.10	Coronin-6	GO:0003779,GO:0072686,GO:0015629,GO:0051015,GO:0050832,GO:0030036,GO:0007527	CG9446-PE				SM00320,SM00320,SM00320		PF16300,PF08953,PF00400	PS50082,PS50294,PS50082		PS00678	G3DSA:2.130.10.10	SSF101908	535~562								
aly2250.11	Probable ATP-dependent RNA helicase DDX55 homolog	GO:0004004,GO:0005575,GO:0008150,GO:0003723,GO:0003676,GO:0010501,GO:0005524	CG9630-PA				SM00487,SM00490		PF13959,PF00270,PF00271	PS51194,PS51195,PS51192		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	529~559								
aly2250.12	Transmembrane protein 134	GO:0016021	CG12025-PA						PF05915														
aly2250.13	Translation machinery-associated protein 16 homolog	GO:0005575,GO:0008150,GO:0003674	CG15027-PA						PF11176														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2250.14	Cell division control protein 45 homolog	GO:0000082,GO:0000083,GO:0031938,GO:0031261,GO:0005737,GO:0000727,GO:0005813,GO:0005634,GO:0005654,GO:0005656,GO:0006267,GO:0006260,GO:1902977,GO:1900087,GO:0000278,GO:0032508,GO:0031298,GO:0043138,GO:0000076,GO:0006271,GO:0006270,GO:0003697,GO:0003688,GO:0003682	CG32104-PB						PF08621,PF02724,PF02724,PF08620				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF64182,SSF48371,SSF48371									
aly2250.15	Venom serine carboxypeptidase	GO:0006508,GO:0033227,GO:0004185,GO:0005576	CG4572-PA						PF00450		PR00724,PR00724,PR00724,PR00724	PS00131,PS00560	G3DSA:3.40.50.1820	SSF53474									
aly2250.16	ATP-dependent RNA helicase WM6	GO:0016607,GO:0005700,GO:0000381,GO:0006338,GO:0005634,GO:0003724,GO:0004004,GO:0005681,GO:0006974,GO:0007052,GO:0005524,GO:0003676,GO:0000398,GO:0010501,GO:0005875,GO:0006406,GO:0003723	CG7269-PB				SM00490,SM00487		PF00270,PF00271	PS51194,PS51195,PS51192			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									
aly2250.17	Venom serine carboxypeptidase	GO:0006508,GO:0033227,GO:0004185,GO:0005576	CG4572-PA						PF00450		PR00724,PR00724,PR00724	PS00131	G3DSA:3.40.50.1820	SSF53474									
aly2250.18	Venom serine carboxypeptidase	GO:0006508,GO:0033227,GO:0004185,GO:0005576	CG4572-PA						PF00450		PR00724,PR00724,PR00724,PR00724	PS00560,PS00131	G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2250.19	Venom serine carboxypeptidase	GO:0006508,GO:0033227,GO:0004185,GO:0005576	CG4572-PA						PF00450		PR00724,PR00724,PR00724,PR00724	PS00560,PS00131	G3DSA:3.40.50.1820	SSF53474									
aly2250.2	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG1441-PA						PF07993				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly2250.20	Nucleoredoxin	GO:0047134,GO:0030154,GO:0005829,GO:0016055,GO:0072358,GO:0031397,GO:0005634,GO:0030178,GO:0004791	n/a						PF13905				G3DSA:3.40.30.10,G3DSA:3.40.30.10	SSF52833,SSF52833									
aly2250.21	Crossover junction endonuclease EME1	GO:0006310,GO:0005737,GO:0006281,GO:0004518,GO:0004519,GO:0005634,GO:0005730,GO:0072429,GO:0000790,GO:0003677,GO:0046872,GO:0005720	CG12936-PA																				
aly2250.22	Required for meiotic nuclear division protein 1 homolog	GO:0005575,GO:0003674,GO:0008150,GO:0006412,GO:0005739	CG11679-PA						PF02582														
aly2250.23	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2250.24	Unknown		n/a																				
aly2250.3	UPF0061 protein XOO2718		n/a						PF02696														
aly2250.4	UPF0061 protein XAC2392		n/a						PF02696														
aly2250.5	Unknown	GO:0005575,GO:0008150,GO:0003674	CG17778-PA						PF16740						1~28,47~81								
aly2250.6	Protein strawberry notch	GO:0007173,GO:0007219,GO:0048190,GO:0009790,GO:0007560,GO:0005634,GO:0008587,GO:0042676,GO:0030162,GO:0045944,GO:0048477	CG44436-PB						PF13871,PF13872				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									
aly2250.7	LIM domain kinase 1	GO:0048749,GO:0005737,GO:0006468,GO:0051124,GO:0050770,GO:0030496,GO:0007560,GO:0032154,GO:0030036,GO:0005524,GO:0004674,GO:0048812,GO:0008270,GO:0004672,GO:0001737,GO:0001736,GO:0007416	CG1848-PC				SM00132,SM00132		PF00412,PF00412,PF07714	PS50023,PS50023,PS50011		PS00478,PS00478,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF56112,SSF57716										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2250.8	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6457-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2250.9	Protein FAM57B	GO:0050291,GO:0005783,GO:0016021,GO:0005789,GO:0000139,GO:0046513,GO:0045599	CG17841-PA				SM00724		PF03798	PS50922													
aly22553.1	Probable sulfite oxidase, mitochondrial	GO:0020037,GO:0030151,GO:0042128,GO:0008482,GO:0006790,GO:0030163,GO:0005758,GO:0055114,GO:0009055	CG7280-PA										G3DSA:3.90.420.10	SSF56524									
aly2258.1	PR domain zinc finger protein 10	GO:0005634,GO:0006355,GO:0006351,GO:0003677,GO:0008168,GO:0046872	n/a				SM00355,SM00355			PS50157		PS00028,PS00028	G3DSA:2.170.270.10		402~409								
aly2258.10	Proton-coupled amino acid transporter 1	GO:0005280,GO:0016021,GO:0005783,GO:0055085,GO:0035524,GO:1902600,GO:0003333,GO:0006865,GO:0015816,GO:0015193,GO:0005765,GO:0015078,GO:0006811,GO:0005886,GO:0015180,GO:0015992,GO:0015187,GO:0015808,GO:0015171	CG13384-PC						PF01490														
aly2258.11	5'-AMP-activated protein kinase subunit beta-1	GO:0006633,GO:0031588,GO:0035090,GO:0005634,GO:0045859,GO:0070050,GO:0006974,GO:0010628,GO:0007165,GO:0005515,GO:0004672,GO:0004679	CG8057-PA				SM01010		PF04739,PF16561					SSF160219,SSF81296			REACT_11163,REACT_498						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2258.12	CMP-sialic acid transporter 3	GO:0005794,GO:0005797,GO:0015739,GO:0005351,GO:0016021,GO:0015136,GO:0000139,GO:0005459,GO:0008643	CG14040-PA						PF04142					SSF103481										
aly2258.13	TBC1 domain family member 23	GO:0032313,GO:0007298,GO:0006909,GO:0005097	CG4552-PA				SM00164,SM00450		PF00581,PF00566	PS50206,PS50086			G3DSA:3.40.250.10	SSF47923,SSF52821,SSF47923	70~90									
aly2258.14	Unknown	GO:0005515	n/a										G3DSA:2.60.40.10	SSF48726										
aly2258.15	Collagenase	GO:0006508,GO:0005576,GO:0030574,GO:0004252	CG6592-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494										
aly2258.16	Unknown	GO:0007157,GO:0005576,GO:0003674,GO:0005515	CG42242-PD				SM00409						G3DSA:2.60.40.10	SSF48726										
aly2258.17	Unknown		n/a																					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2258.18	Unknown	GO:0005887,GO:0055085,GO:0045433,GO:0007638,GO:0009987,GO:0042493,GO:0009612,GO:0006814,GO:0005509,GO:0005886,GO:0007268,GO:0005248,GO:0001666,GO:0046684,GO:0046680,GO:0001518	CG17800-PBX																				
aly2258.19	Unknown		n/a																				
aly2258.2	Galectin-8	GO:0005737,GO:0002317,GO:0070062,GO:0005829,GO:0016020,GO:0030246,GO:0008039,GO:0015143,GO:0016936,GO:0031295,GO:0005615	CG11372-PA				SM00276,SM00276,SM00908,SM00908		PF00337,PF00337	PS51304,PS51304			G3DSA:2.60.120.200,G3DSA:2.60.120.200	SSF49899,SSF49899										
aly2258.20	Unknown		n/a																				
aly2258.3	Glycogen phosphorylase	GO:0043234,GO:0005737,GO:0005975,GO:0005980,GO:0060361,GO:0045824,GO:0030170,GO:0045819,GO:0050829,GO:0008340,GO:0008184,GO:0042803	CG7254-PA			PIRSF000460		TIGR02093	PF00343			PS00102	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756		00500+2.4.1.1	REACT_474	PWY-6731,PWY-7238,PWY-6737,PWY-5941					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2258.4	Hemicentin-1	GO:0007638,GO:0005886,GO:0001666,GO:0030054,GO:0070062,GO:0009612,GO:0005509,GO:0046684,GO:0046680,GO:0009987,GO:0007601,GO:0006814,GO:0005938,GO:0005887,GO:0007268,GO:0055085,GO:0001518,GO:0005604,GO:0045433,GO:0050896,GO:0042493,GO:0005515,GO:0005248	CG17800-PBX				SM00060,SM00060,SM00060,SM00060,SM00060,SM00409,SM00408		PF13895,PF13895,PF13895,PF00047,PF00047,PF00047,PF13927,PF13927,PF13927,PF13927,PF13927,PF13927,PF13927,PF13927,PF12355,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679	PS50835,PS50835,PS50835,PS50835,PS50835,PS50853,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50853,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50853,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50853,PS50835,PS50853,PS50835,PS50835,PS50835,PS50835,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF49265,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726	5043~5043								
aly2258.5	ATP synthase subunit delta, mitochondrial	GO:0045261,GO:0015986,GO:0015992,GO:0046933,GO:0000275,GO:0005811,GO:0005753,GO:0005739,GO:0045259,GO:0005743,GO:0005740,GO:0046961,GO:0008553,GO:0015078	CG2968-PC	MF_00530				TIGR01216	PF02823				G3DSA:2.60.15.10,G3DSA:1.20.5.440	SSF51344,SSF46604	119~146								
aly2258.6	Breast cancer type 1 susceptibility protein homolog	GO:0006633,GO:0035066,GO:0035067,GO:0009048,GO:0008270,GO:0003677,GO:0007049,GO:0032355,GO:0031436,GO:0000724,GO:0033993,GO:0005634,GO:0071158,GO:0051865,GO:0005759,GO:0043009,GO:0005694,GO:0042127,GO:0007584,GO:0070531,GO:0004842,GO:0045893,GO:0005886,GO:0016874,GO:0010033,GO:0007420,GO:0085020,GO:0045944,GO:0006351,GO:0045717	n/a				SM00292,SM00292		PF00533	PS50172,PS50172			G3DSA:3.30.40.10,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190	SSF57850,SSF52113,SSF52113	709~736								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2258.7	Unknown		n/a																				
aly2258.8	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0060179,GO:0009744,GO:0016021,GO:0070328,GO:0005783,GO:0017105,GO:0019216,GO:0046872,GO:0031410,GO:0016717,GO:0005811,GO:0005789,GO:0042593,GO:0042811,GO:0048047,GO:0004768,GO:0010506,GO:0006723,GO:0055114	CG5887-PA						PF00487		PR00075,PR00075,PR00075,PR00075,PR00075,PR00075,PR00075	PS00476						PWY-5987,PWY-5996					
aly2258.9	ELAV-like protein 1	GO:0005737,GO:0005794,GO:0045727,GO:0018345,GO:0019901,GO:0003730,GO:0005634,GO:0016020,GO:0048255,GO:0017091,GO:0003725,GO:0008270,GO:0005515,GO:2000036,GO:0070935,GO:0019706,GO:0000166,GO:0035925,GO:0044822,GO:0003723	CG6618-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00360,SM00360,SM00360		PF12796,PF00076,PF00076,PF00076,PF01529,PF13857	PS50088,PS50297,PS50102,PS50088,PS50216,PS50088,PS50102,PS50088,PS50088,PS50102	PR00961,PR00961,PR00961,PR00961		G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:1.25.40.20	SSF48403,SSF54928,SSF54928									
aly22617.1	Unknown		n/a																				
aly22617.2	Unknown		n/a																				
aly22633.1	Unknown		n/a												78~119								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly226385.1	Unknown	GO:0016319,GO:0035147,GO:0030426,GO:0035149,GO:0030175,GO:0000226,GO:0030716,GO:0005874,GO:0005856,GO:0007517,GO:0007026,GO:0051491,GO:0007475,GO:0003779,GO:0005509,GO:0016203,GO:0016204,GO:0008017,GO:0044295,GO:0007050,GO:0000235,GO:0030036,GO:0007409,GO:0030516,GO:0007424,GO:0007017,GO:0007423,GO:0008092,GO:0001578,GO:0045773,GO:0016199,GO:0045169,GO:0048813,GO:0005515,GO:0005912	CG18076-PH				SM00150		PF00435				G3DSA:1.20.58.60	SSF46966	69~88								
aly2264.1	Unknown		n/a																				
aly22685.1	Intersectin-1	GO:0005089,GO:0008021,GO:0008104,GO:0019209,GO:0030139,GO:0051124,GO:0043524,GO:0005905,GO:0045202,GO:0051897,GO:0030054,GO:0005737,GO:0070064,GO:0045179,GO:0045746,GO:0005509,GO:0043005,GO:0030027,GO:0007269,GO:0005886,GO:0007264,GO:0042327,GO:0006897,GO:0042734,GO:0005829,GO:0002052,GO:0005515,GO:0045860,GO:0048488,GO:0032947	CG1099-PD				SM00326		PF14604	PS50002			G3DSA:2.30.30.40,G3DSA:2.30.30.40	SSF50044									
aly2272.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2272.2	G2/M phase-specific E3 ubiquitin-protein ligase	GO:0005737,GO:0042393,GO:0005730,GO:0019100,GO:0006915,GO:0005700,GO:0001824,GO:0008270,GO:0061630,GO:0016874,GO:0000209,GO:2001243	CG9576-PA						PF13771				G3DSA:3.30.40.10	SSF57903									
aly2272.3	Unknown	GO:0046872	n/a							PS50157		PS00028											
aly2272.4	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6467-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2272.5	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6467-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2272.6	Chymotrypsin BI	GO:0004252,GO:0005615,GO:0030574,GO:0006508	CG6467-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2272.7	Protein artemis	GO:0006310,GO:0016787,GO:0008409,GO:0010212,GO:0051276,GO:0030183,GO:0005634,GO:0000737,GO:0090305,GO:0000014,GO:0033151,GO:0000723,GO:0006281,GO:0006302	CG10018-PA						PF12706				G3DSA:3.60.15.10	SSF56281									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2272.8	Unknown		n/a																				
aly2273.1	Unknown		n/a																				
aly2273.2	Hemicentin-2	GO:0050896,GO:0007606,GO:0005575,GO:0003674,GO:0005509,GO:0005578	CG12191-PA				SM00406,SM00406,SM00409,SM00409,SM00408,SM00408		PF00047,PF07686	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly2273.3	Unknown		n/a																				
aly22733.1	Unknown		n/a												81~115								
aly22741.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly22741.2	Unknown		n/a										G3DSA:1.10.10.10										
aly22741.3	Unknown		n/a																				
aly2275.1	Unknown		n/a																				
aly2275.10	Transmembrane channel-like protein 3	GO:0016021,GO:0006811	CG3280-PC						PF07810						1172~1196								
aly2275.11	Laminin subunit gamma-1	GO:0048598,GO:0005605,GO:0005604,GO:0007494,GO:0070831,GO:0034446,GO:0009887,GO:0009888,GO:0007435,GO:0012505,GO:0061031,GO:0085029,GO:0031012,GO:0033627	CG3322-PA				SM00136,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00181,SM00181,SM00181,SM00181,SM00181,SM00281		PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00052,PF00055	PS50027,PS50027,PS50027,PS50027,PS50027,PS50027,PS50027,PS50027,PS50027,PS51115,PS50027,PS51117	PR00011,PR00011,PR00011,PR00011	PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.260,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF58104	1139~1166,1416~1457,1353~1373,1203~1223,1480~1500,1591~1611,1041~1068,1554~1574,1311~1338,1074~1094								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2275.12	Inhibitory POU protein	GO:0043565,GO:0003714,GO:0007636,GO:0003700,GO:0005634,GO:0070983,GO:0004722,GO:0008039,GO:1903507,GO:0050911,GO:0048813,GO:0045944,GO:0006351,GO:0003677,GO:0007411	CG9151-PA				SM00352,SM00389		PF00157,PF00046	PS51179,PS50071	PR00028,PR00028,PR00028,PR00028,PR00028	PS00035,PS00465,PS00027	G3DSA:1.10.260.40,G3DSA:1.10.10.60	SSF47413,SSF46689									
aly2275.13	Uncharacterized protein CG1161	GO:0016021,GO:0016020	CG1161-PA						PF05434						145~165								
aly2275.14	Transmembrane protein 9	GO:0016020,GO:0016021,GO:0005770,GO:0005764,GO:0005765,GO:0006810,GO:0031902	CG1161-PA						PF05434														
aly2275.15	Roquin-1	GO:0000932,GO:0008270,GO:0003723	CG16807-PA				SM00184			PS50089,PS50103		PS00518	G3DSA:4.10.1000.10,G3DSA:3.30.40.10	SSF57850,SSF90229	760~780								
aly2275.16	Nephrin	GO:0072015,GO:0007254,GO:0030838,GO:0070062,GO:0007588,GO:0032836,GO:0044062,GO:0005886,GO:0007519,GO:0017022,GO:0005622,GO:0007520,GO:0005887,GO:0008045,GO:0007155,GO:0042995,GO:0036057	CG31062-PC				SM00409,SM00409,SM00409,SM00409		PF07686,PF08205,PF13927,PF13927	PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726										
aly2275.17	Calpain-C	GO:0005737,GO:0006508,GO:0004198,GO:0005509,GO:0005622	CG3692-PA				SM00720,SM00230		PF01067,PF00648	PS50203,PS50222	PR00704,PR00704,PR00704,PR00704,PR00704,PR00704,PR00704,PR00704,PR00704,PR00704		G3DSA:1.10.238.10,G3DSA:2.60.120.380,G3DSA:3.90.70.10	SSF54001,SSF47473,SSF49758									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2275.18	Succinate dehydrogenase assembly factor 3, mitochondrial	GO:0050881,GO:0005739,GO:0006105,GO:0005759,GO:0055093,GO:0006979	CG14898-PA						PF13233														
aly2275.19	Serine/threonine-protein kinase PRP4 homolog	GO:0006468,GO:0071011,GO:0071013,GO:0044822,GO:0000398,GO:0005654,GO:0004674,GO:0008360,GO:0004672,GO:0007155,GO:0022008,GO:0005694,GO:0008380,GO:0005524,GO:0006397	CG7028-PC				SM00220		PF00069	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112	162~182,290~310								
aly2275.2	Protein RCC2 homolog	GO:0007032,GO:0000278,GO:0005730,GO:0005085,GO:0008150,GO:0007067,GO:0005875,GO:0051301	CG9135-PA						PF00415,PF00415,PF00415,PF00415,PF00415	PS50012,PS50012,PS50012,PS50012,PS50012	PR00633,PR00633,PR00633,PR00633,PR00633	PS00626,PS00626	G3DSA:2.130.10.30	SSF50985									
aly2275.20	Unknown		CG1927-PA																				
aly2275.21	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2275.22	Importin-7	GO:0016318,GO:0042393,GO:0042052,GO:0008586,GO:0000189,GO:0045465,GO:0043524,GO:0007169,GO:0035311,GO:0005737,GO:0030621,GO:0030620,GO:0006886,GO:0016020,GO:0007476,GO:0007474,GO:0005654,GO:0048471,GO:0016203,GO:0006608,GO:0048749,GO:0008283,GO:0045087,GO:0006606,GO:0008320,GO:0042675,GO:0046331,GO:0007173,GO:0005938,GO:0030619,GO:0005643,GO:0008536,GO:0030576,GO:0005515,GO:0015030,GO:0005634	CG7935-PA				SM00913		PF03810	PS50166			G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371										
aly2275.23	Type I inositol 3,4-bisphosphate 4 phosphatase	GO:0005515,GO:0016316,GO:0005575,GO:0034597,GO:0046856,GO:0036092,GO:0006798	CG42271-PC				SM00233		PF00169	PS50003			G3DSA:2.30.29.30,G3DSA:2.60.40.150	SSF49562,SSF50729									
aly2275.24	Probable NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 12	GO:0008137,GO:0005739,GO:0006120,GO:0005743,GO:0005747,GO:0070469,GO:0003954,GO:0009055	CG3214-PC						PF05071														
aly2275.25	Protein apterous	GO:0007559,GO:0007517,GO:0007479,GO:0048190,GO:0007481,GO:0007399,GO:0003700,GO:0007476,GO:0005634,GO:0007450,GO:0007451,GO:0036011,GO:0007472,GO:0045165,GO:0045944,GO:0008270,GO:0007411,GO:0000977,GO:0035218,GO:0007526,GO:0006351	CG8376-PA				SM00389,SM00132,SM00132		PF00046,PF00412,PF00412	PS50023,PS50023,PS50071		PS00478,PS00478,PS00027	G3DSA:2.10.110.10,G3DSA:1.10.10.60,G3DSA:2.10.110.10	SSF46689,SSF57716,SSF57716										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2275.26	Unknown		n/a												4~31								
aly2275.27	LIM/homeobox protein Lhx9	GO:0007450,GO:0008270,GO:0008045,GO:0007411,GO:0007559,GO:0043565,GO:0007517,GO:0007479,GO:0007472,GO:0005634,GO:0003714,GO:0007476,GO:0007451,GO:0006351,GO:0048190,GO:0007481,GO:0035218,GO:0045892,GO:0007526,GO:0045165,GO:0007399,GO:0003700,GO:0036011,GO:0045944,GO:0000977,GO:0021794	CG8376-PA				SM00132,SM00132,SM00389		PF00046,PF00412,PF00412	PS50023,PS50071,PS50023		PS00478,PS00478,PS00027	G3DSA:1.10.10.60,G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF46689,SSF57716										
aly2275.28	60S ribosomal protein L36	GO:0005737,GO:0005840,GO:0005730,GO:0022625,GO:0005622,GO:0003735,GO:0000228,GO:0006412	CG7622-PA						PF01158														
aly2275.29	Solute carrier family 22 member 24	GO:0006811,GO:0016021,GO:0008513,GO:0022857,GO:0055085	CG42269-PE						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly2275.3	Protein Jumonji	GO:0001889,GO:0035097,GO:0003677,GO:0048863,GO:0005719,GO:0000122,GO:0005634,GO:0048538,GO:0048536,GO:0000977,GO:0042127,GO:0008285,GO:0045892,GO:0031061,GO:0051574,GO:0035098,GO:0001227,GO:0005700,GO:0061085,GO:0006351,GO:0003682,GO:0016568	CG3654-PD				SM00558,SM00501,SM01014,SM00545		PF02375,PF02373,PF01388	PS51011,PS51183,PS51184			G3DSA:1.10.150.60	SSF46774,SSF51197										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2275.30	Unknown		n/a																				
aly2275.31	Unknown		n/a																				
aly2275.32	Unknown		n/a																				
aly2275.33	Otoferlin	GO:0008021,GO:0010996,GO:0030672,GO:0050885,GO:0030381,GO:0016079,GO:0016021,GO:0035045,GO:0009566,GO:0016323,GO:0009790,GO:0007283,GO:0005509,GO:0005789,GO:0030054	CG5747-PF																				
aly2275.34	Probable RNA directed DNA polymerase from transposon X-element	GO:0003964,GO:0006278,GO:0006313	n/a						PF14529				G3DSA:3.60.10.10	SSF56219	181~201								
aly2275.4	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	GO:0004047,GO:0006546,GO:0005759,GO:0019910,GO:0019909,GO:0055114,GO:0016491	CG3626-PA						PF01266,PF08669,PF01571,PF16350				G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.30.70.1400,G3DSA:2.40.30.110,G3DSA:3.30.1360.120,G3DSA:3.30.1360.120,G3DSA:3.30.9.10,G3DSA:3.30.9.10	SSF101790,SSF103025,SSF51905,SSF51905,SSF54373		00260+2.1.2.10,00670+2.1.2.10								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2275.5	Enkurin	GO:0031514	CG16984-PA						PF13864	PS51665					227~247								
aly2275.6	Unknown	GO:0005515	CG10508-PK				SM00546,SM00546			PS51140,PS51140				SSF46934									
aly2275.7	Deformed epidermal autoregulatory factor 1	GO:0043565,GO:0050776,GO:0003700,GO:0005634,GO:0008270,GO:0005700,GO:0006357,GO:0045893,GO:0003677,GO:0009792,GO:0006351	CG8567-PA				SM00258		PF01753,PF01342	PS50864,PS50865		PS01360	G3DSA:3.10.390.10	SSF63763,SSF144232	249~269								
aly2275.8	Laminin subunit alpha	GO:0008021,GO:0034446,GO:0007498,GO:0030155,GO:0030424,GO:0035001,GO:0007411,GO:0002121,GO:0030054,GO:0007417,GO:0031987,GO:0036062,GO:0007476,GO:0001964,GO:0033627,GO:0048598,GO:0009887,GO:0030334,GO:0007507,GO:0009888,GO:0016321,GO:0035011,GO:0045995,GO:0005606,GO:0005605,GO:0005604,GO:0007422,GO:0048854,GO:0045886,GO:0005102	CG10236-PA				SM00281,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00180,SM00136,SM00282,SM00282,SM00282,SM00282,SM00282		PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF00055,PF00052,PF06009,PF02210,PF02210,PF02210,PF02210,PF02210	PS50027,PS51115,PS50027,PS50027,PS50027,PS50025,PS50027,PS51257,PS50027,PS50027,PS50025,PS50025,PS50025,PS50027,PS51117,PS50027,PS50027,PS50027,PS50027,PS50027,PS50027,PS50027,PS50027,PS50025,PS50027,PS50027,PS50027,PS50027,PS50027	PR00011,PR00011,PR00011,PR00011	PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248,PS01248	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57196,SSF49899,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196,SSF49899,SSF57196,SSF49899,SSF57196,SSF57196,SSF57196,SSF49899,SSF57196,SSF49899,SSF57196,SSF57196,SSF57196,SSF57196,SSF57196	2327~2361,3629~3630,2572~2606,2369~2389								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2275.9	Unknown		n/a																				
aly2277.1	Dopamine D2-like receptor	GO:0004930,GO:0007212,GO:0007195,GO:0016021,GO:0007606,GO:0001591,GO:0007194,GO:0004952,GO:0005887,GO:0007268,GO:0007186,GO:0008227	CG33517-PH						PF00001	PS50262	PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly22776.1	Unknown	GO:0005575,GO:0008150,GO:0003674	CG43346-PA						PF05071														
aly228371.1	Unknown		n/a						PF14529				G3DSA:3.60.10.10	SSF56219									
aly228371.2	Unknown	GO:0005515	n/a				SM00249		PF00628	PS50016,PS50081		PS01359	G3DSA:3.30.40.10	SSF57903	126~153								
aly2284.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0046427,GO:0015771,GO:0016021,GO:0022857,GO:0005886,GO:0055085	CG10960-PB						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00217,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2284.10	GPI transamidase component PIG-T	GO:0005737,GO:0005783,GO:0030182,GO:0016023,GO:0016020,GO:0051402,GO:0042765,GO:0016255	CG11190-PA						PF04113										UPA00196				
aly2284.11	Unknown		n/a												465~485,504~541								
aly2284.12	Ras-related GTP-binding protein D	GO:0005737,GO:1990131,GO:0071230,GO:0034448,GO:0005634,GO:0034613,GO:0003924,GO:0010506,GO:0005575,GO:0005764,GO:0009267,GO:0032008,GO:0046982,GO:0008152,GO:0005525	CG8707-PA						PF04670				G3DSA:3.40.50.300	SSF52540									
aly2284.13	Phosphatidate phosphatase LPIN2	GO:0006656,GO:0016311,GO:0005789,GO:0009062,GO:0044281,GO:0042594,GO:0035183,GO:0005634,GO:0003713,GO:0010565,GO:0007474,GO:0019432,GO:0006646,GO:0005737,GO:0006644,GO:0006629,GO:0019217,GO:0055088,GO:0044255,GO:0030514,GO:0008195,GO:0005829,GO:0006357,GO:0045944,GO:0006351,GO:0046474	CG8709-PA				SM00775		PF04571,PF08235,PF16876				G3DSA:3.40.50.1000	SSF56784		00564+3.1.3.4,00561+3.1.3.4,00565+3.1.3.4,00600+3.1.3.4	REACT_22258	PWY-6453					
aly2284.14	mRNA turnover protein 4 homolog	GO:0005737,GO:0005654,GO:0022625,GO:0005634,GO:0005730,GO:0031965,GO:0042254,GO:0003735,GO:0044822,GO:0006412	CG1381-PA						PF00466					SSF160369									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2284.15	14-3-3 protein zeta	GO:0008103,GO:0007611,GO:0050821,GO:0045448,GO:0007294,GO:0006457,GO:0005875,GO:0040040,GO:0008355,GO:0005737,GO:0045172,GO:0008426,GO:0042803,GO:0006588,GO:0008283,GO:0019904,GO:0007059,GO:0007265,GO:0001751,GO:0016483,GO:0005515,GO:0046982,GO:0005634	CG17870-PD			PIRSF000868	SM00101		PF00244		PR00305,PR00305,PR00305,PR00305,PR00305,PR00305	PS00796,PS00797	G3DSA:1.20.190.20	SSF48445	191~211								
aly2284.16	Unknown		n/a						PF00001	PS50262			G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly2284.17	A disintegrin and metalloproteinase with thrombospondin motifs 14	GO:0004222,GO:0001541,GO:0030713,GO:0030574,GO:0030199,GO:0030198,GO:0008270,GO:0006508,GO:0048477,GO:0005578,GO:0005576	CG3622-PC						PF01562,PF13688	PS50215			G3DSA:3.40.390.10	SSF55486									
aly2284.18	Carbonic anhydrase 2	GO:0032849,GO:0038166,GO:0006730,GO:0030424,GO:0010043,GO:0005902,GO:0045780,GO:0008270,GO:0051453,GO:0044070,GO:0005737,GO:0002009,GO:0045177,GO:0070062,GO:0043209,GO:0006885,GO:0001822,GO:0004089,GO:0004064,GO:2001225,GO:0015670,GO:0032230,GO:0071498,GO:0016323,GO:0005886,G	CG7820-PA				SM01057		PF00194,PF00194	PS51144			G3DSA:3.10.200.10,G3DSA:3.10.200.10	SSF51069									
aly2284.19	Pleckstrin homology domain-containing family J member 1		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2284.2	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0005215,GO:0016021,GO:0005886,GO:0055085	CG1213-PA					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171	PS00216,PS00216,PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						
aly2284.20	Histone-lysine N-methyltransferase, H3 lysine-79 specific	GO:0006348,GO:0048096,GO:0006342,GO:0005634,GO:0051726,GO:0035097,GO:0005575,GO:0046331,GO:0016571,GO:0031151,GO:2000637	CG42803-PD						PF08123	PS51569			G3DSA:3.40.50.150	SSF53335	570~604,630~664,705~725	00310+2.1.1.43							
aly2284.21	Ankyrin repeat domain-containing protein 49	GO:0005575,GO:0008150,GO:0003674,GO:0045893	CG4140-PA				SM00248,SM00248,SM00248,SM00248		PF12796	PS50088,PS50088,PS50297			G3DSA:1.25.40.20	SSF48403									
aly2284.22	Kinetochore-associated protein 1	GO:0034501,GO:0007067,GO:0051301,GO:0015629,GO:0005737,GO:0005819,GO:0005634,GO:0000940,GO:0000922,GO:1990423,GO:0000278,GO:0006461,GO:0005886,GO:0007264,GO:0000776,GO:0000777,GO:0000070,GO:0005829,GO:0005828,GO:0007094,GO:0007096,GO:0007093	CG1569-PA						PF10493														
aly2284.23	Probable ATP-dependent RNA helicase Dbp73D	GO:0008026,GO:0005730,GO:0004004,GO:0003723,GO:0003676,GO:0022008,GO:0010501,GO:0005524,GO:0006364	CG9680-PA				SM00490,SM00487		PF00270,PF00271	PS51194,PS51192		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	19~39								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2284.24	Cullin-associated NEDD8-dissociated protein 1	GO:0005737,GO:0010265,GO:0008134,GO:0031647,GO:0016567,GO:0005488,GO:0005515,GO:2000435,GO:0031461,GO:0005634	CG5366-PA										G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371									
aly2284.25	Cullin-associated NEDD8-dissociated protein 1	GO:0005737,GO:0016020,GO:0030154,GO:0070062,GO:0010265,GO:0008134,GO:0031647,GO:0000151,GO:0005654,GO:0016567,GO:0005515,GO:2000435,GO:0031461,GO:0005634,GO:0043086,GO:0045899	CG5366-PA						PF08623				G3DSA:1.25.10.10	SSF48371									
aly2284.26	Protein SOGA3	GO:0016021,GO:0010506,GO:0005615	CG18304-PD						PF11365,PF11365,PF11365					SSF57997	1354~1374,1515~1573,1070~1104,720~761,833~867,885~919,663~704,294~328,1252~1328,1221~1241,388~486,780~830,1115~1174,1646~1666,1685~1705,1379~1459,1575~1630,503~537,572~616,972~992,1737~1821,997~1066,1182~1209,347~381,1464~1484								
aly2284.27	Sialic acid synthase	GO:0005737,GO:0044267,GO:0050462,GO:0070062,GO:0008781,GO:0018279,GO:0005829,GO:0070085,GO:0016051,GO:0006488,GO:0047444,GO:0043687,GO:0009103	CG5232-PA						PF03102				G3DSA:3.90.1210.10,G3DSA:3.20.20.70	SSF51569,SSF51269									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2284.28	Hydroxymethylglutaryl-CoA lyase, mitochondrial	GO:0004419,GO:0005743,GO:0000287,GO:0005777,GO:0030145,GO:0051262,GO:0006551,GO:0003824,GO:0005759,GO:0046872,GO:0005875,GO:0007005,GO:0046951	CG10399-PA						PF00682	PS50991			G3DSA:3.20.20.70	SSF51569									
aly2284.29	Protein KRTCAP2 homolog	GO:0005575,GO:0003674,GO:0016021,GO:0008150,GO:0005615	CG31460-PA						PF09775														
aly2284.3	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly2284.30	Rab11 family-interacting protein 2	GO:0005737,GO:0019901,GO:0042052,GO:0035773,GO:0017137,GO:0045055,GO:0005654,GO:0055038,GO:0005515,GO:0030010,GO:0005886,GO:0042803,GO:0005768,GO:0043231	CG6606-PA				SM00239		PF00168,PF09457	PS51511			G3DSA:2.60.40.150	SSF49562,SSF144270	433~453								
aly2284.31	Unknown		n/a																				
aly2284.32	Unknown		CG34351-PD						PF14523						65~85								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2284.33	Snurportin-1	GO:0008565,GO:0000387,GO:0030619,GO:0071254,GO:0030621,GO:0030620,GO:0005829,GO:0006606,GO:0061015,GO:0005643,GO:0010467,GO:0005515,GO:0000339,GO:0015030,GO:0034660,GO:0070062	CG42303-PA						PF11538					SSF56091									
aly2284.34	Integrator complex subunit 6-A	GO:0016180,GO:0005634,GO:0003674,GO:0034472,GO:0032039	CG3125-PA						PF13519,PF15300	PS50234			G3DSA:3.40.50.410	SSF53300									
aly2284.35	Unknown		n/a																				
aly2284.4	Sodium/hydrogen exchanger 6	GO:0048675,GO:0051386,GO:0050808,GO:0055038,GO:0030425,GO:0005789,GO:0045202,GO:0043679,GO:0006885,GO:0016021,GO:0005770,GO:0044308,GO:0035725,GO:0048471,GO:0060996,GO:0031901,GO:0006811,GO:0006810,GO:0006814,GO:0005886,GO:0031547,GO:0097484,GO:0055085,GO:0043231,GO:0048812,GO:0031410,GO:0015385	CG11328-PD					TIGR00840	PF00999		PR01088,PR01088,PR01088,PR01084,PR01084,PR01084,PR01084						REACT_15518						
aly2284.5	Metallo-beta-lactamase domain-containing protein 1	GO:0016787,GO:0046872	CG9117-PA				SM00849		PF00753				G3DSA:3.60.15.10	SSF56281									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2284.6	Aspartyl/asparaginyl beta-hydroxylase	GO:0035108,GO:0005783,GO:1901879,GO:0031585,GO:0060021,GO:0030176,GO:0060325,GO:0005737,GO:0007389,GO:0097202,GO:0032237,GO:0016021,GO:0018193,GO:0033017,GO:0005509,GO:0010524,GO:0032541,GO:0008285,GO:0090316,GO:0071277,GO:0045893,GO:0005886,GO:0042264,GO:0031647,GO:0070588,GO:0005515,GO:0045862,GO:0033198,GO:0004597	CG8421-PL						PF05118	PS50293			G3DSA:1.25.40.10,G3DSA:2.60.120.330	SSF48452,SSF51197	683~703,161~181,307~327								
aly2284.7	Sodium/potassium-transporting ATPase subunit beta-1-interacting protein	GO:0005575,GO:0016021,GO:0002028,GO:0005515,GO:0005886	CG34413-PK						PF05640														
aly2284.8	Ubiquitin carboxyl-terminal hydrolase	GO:0005737,GO:0004221,GO:0005875,GO:0006511,GO:0005622,GO:0016579,GO:0004843	CG4265-PB						PF01088		PR00707,PR00707,PR00707,PR00707,PR00707	PS00140	G3DSA:3.40.532.10	SSF54001									
aly2284.9	Major facilitator superfamily domain-containing protein 12	GO:0005765,GO:0016021,GO:0006810	n/a						PF13347				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly228609.1	Coatomer subunit alpha	GO:0006891,GO:0006890,GO:0006909,GO:0016192,GO:0005615,GO:0070062,GO:0006886,GO:0005198,GO:0030157,GO:0048812,GO:0030117,GO:0007112,GO:0010883,GO:0030126,GO:0000902	CG7961-PA						PF04053								REACT_11123						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2289.1	Unknown		n/a																				
aly22926.1	Unknown		n/a																				
aly22942.1	Unknown		n/a																				
aly22942.2	PiggyBac transposable element-derived protein 1	GO:0003700,GO:0005044,GO:0016020	n/a						PF13843														
aly2295.1	Ammonium transporter Rh type B-B	GO:0008519,GO:0016021,GO:0016020,GO:0016323,GO:0030659,GO:0015696	CG7499-PB						PF00909		PR00342,PR00342,PR00342,PR00342,PR00342,PR00342,PR00342,PR00342,PR00342,PR00342		G3DSA:1.10.3430.10	SSF111352									
aly2295.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly22970.1	Unknown		n/a																				
aly22970.2	G-protein coupled receptor Mth2	GO:0006950,GO:0004930,GO:0016021,GO:0005886	n/a																				
aly22970.3	G-protein coupled receptor Mth2	GO:0006950,GO:0004930,GO:0007186,GO:0016021,GO:0005886	CG31720-PC																				
aly22970.4	Unknown		n/a																				
aly22970.5	Unknown		n/a																				
aly229995.1	Unknown		n/a												84~104								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly230.1	Cilia- and flagella-associated protein 58	GO:0005615,GO:0005929	CG5882-PA											SSF57997	104~124,293~320,34~96,132~257								
aly230.10	Unknown		n/a						PF13384,PF01498					SSF46689									
aly230.2	Cilia- and flagella-associated protein 58	GO:0005615,GO:0005929	CG5882-PA												127~147,33~60,242~269								
aly230.3	C-terminal-binding protein	GO:0008022,GO:0051287,GO:0035220,GO:0030111,GO:0070491,GO:0001700,GO:0000122,GO:0005634,GO:0003714,GO:0003713,GO:0016360,GO:0042802,GO:0042803,GO:0046427,GO:0008134,GO:0022416,GO:0045892,GO:0055114,GO:0016616,GO:0016055,GO:0006355,GO:0006357,GO:0006351,GO:0005515	CG7583-PH						PF02826,PF00389			PS00065,PS00671	G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF52283,SSF51735										
aly230.4	Macrophage erythroblast attacher	GO:0005737,GO:0005856,GO:0043249,GO:0005575,GO:0008150,GO:0007049,GO:0005886,GO:0003674,GO:0016363,GO:0051301	CG31357-PA				SM00668,SM00757		PF10607	PS50897,PS50896			G3DSA:3.30.40.10	SSF57850	83~103								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly230.5	Zinc transporter ZIP13 homolog	GO:0005794,GO:0006829,GO:0005783,GO:0060586,GO:0016021,GO:0016020,GO:0016323,GO:0005381,GO:0030001,GO:0006826,GO:0046873,GO:0005622,GO:0034755,GO:0055085,GO:0000139	CG7816-PG						PF02535														
aly230.6	Zinc transporter ZIP13 homolog	GO:0005794,GO:0006829,GO:0005783,GO:0060586,GO:0016021,GO:0016020,GO:0016323,GO:0005381,GO:0030001,GO:0006826,GO:0046873,GO:0005622,GO:0034755,GO:0055085,GO:0000139	CG7816-PG						PF02535														
aly230.7	F-box/LRR-repeat protein 2	GO:0016567,GO:0004842,GO:0016020,GO:0031146,GO:0006513,GO:0019903,GO:0006511,GO:0019005,GO:0005515,GO:0014066,GO:0010506,GO:0036312	CG2010-PA				SM00256		PF12937	PS50181			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF81383,SSF52047,SSF52047									
aly230.8	Protein TRC8 homolog	GO:0045926,GO:0005783,GO:0016021,GO:0005789,GO:0007418,GO:0016567,GO:0008270,GO:0005515,GO:0004842	CG2304-PD				SM00184		PF13639,PF13705	PS50089			G3DSA:3.30.40.10	SSF57850									
aly230.9	Unknown		n/a																				
aly230056.1	Adrenodoxin, mitochondrial	GO:0042446,GO:0046872,GO:0051536,GO:0051537,GO:0006694,GO:0005759,GO:0009055,GO:0055114,GO:0008203	CG1319-PB						PF00111			PS00814	G3DSA:3.10.20.30	SSF54292									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2302.1	PR domain zinc finger protein 4	GO:0005737,GO:0071363,GO:0030308,GO:0031670,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0008168,GO:0046872	CG12605-PB				SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667									
aly2302.2	Unknown		n/a												821~855								
aly2302.3	Unknown		n/a												101~121								
aly2302.4	M-phase inducer phosphatase	GO:0008284,GO:0000086,GO:0000087,GO:0060305,GO:0035335,GO:0007067,GO:0051301,GO:0007346,GO:0005634,GO:0007369,GO:0007498,GO:0006470,GO:0045977,GO:0007088,GO:0005694,GO:0045931,GO:0045930,GO:0000278,GO:0008138,GO:0008283,GO:0009987,GO:0046331,GO:0007424,GO:0007030,GO:0045792,GO:0007422,GO:0004726,GO:0004725,GO:0005622,GO:0007099	CG1395-PA				SM00450		PF00581	PS50206	PR00716,PR00716,PR00716,PR00716,PR00716		G3DSA:3.40.250.10	SSF52821			REACT_152						
aly2302.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2302.6	Unknown		n/a												78~98								
aly2302.7	Catenin alpha	GO:0015629,GO:0034332,GO:0007293,GO:0060323,GO:0007163,GO:0030055,GO:0005737,GO:0030720,GO:0005198,GO:0003779,GO:0016342,GO:0060429,GO:0051015,GO:0005915,GO:0005914,GO:0005913,GO:0005912,GO:0005886,GO:0007155,GO:0007016,GO:0008092,GO:0045296,GO:0005515	CG17947-PA						PF01044		PR00805,PR00805		G3DSA:1.20.120.230	SSF47220	141~161								
aly2303.1	Unknown	GO:0005634,GO:0006511,GO:0008270,GO:0007275	CG6688-PA				SM00228			PS50106			G3DSA:3.30.40.10,G3DSA:2.30.42.10	SSF50156									
aly2303.2	Zinc finger protein 782	GO:0005737,GO:0005819,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0005876,GO:0006351	CG8474-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776,PF13894,PF12171,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	197~217								
aly2303.3	Zinc finger Y-chromosomal protein	GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG11696-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:2.20.25.10,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2303.4	Tubulin beta-1 chain	GO:0045298,GO:0051258,GO:0007017,GO:0003924,GO:0005737,GO:0007435,GO:0005200,GO:0006184,GO:0005874,GO:0005525	CG9359-PA				SM00865,SM00864		PF03953,PF00091		PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163	PS00227,PS00228	G3DSA:3.40.50.1440,G3DSA:1.10.287.600,G3DSA:3.30.1330.20	SSF52490,SSF55307	409~429		REACT_152						
aly2303.5	RNA-binding protein 48	GO:0005654,GO:0003723,GO:0000166	CG34231-PC										G3DSA:3.30.70.330	SSF54928									
aly2303.6	Zinc finger protein ZPR1	GO:0001833,GO:0045927,GO:0032797,GO:1990261,GO:0030426,GO:0035149,GO:0030424,GO:0010628,GO:0000226,GO:0008270,GO:0005737,GO:0043204,GO:0007430,GO:0005730,GO:0005634,GO:0005654,GO:0006360,GO:0048471,GO:0043025,GO:0008380,GO:0033120,GO:0061564,GO:0021510,GO:0042023,GO:0071931,GO:0042307,GO:0071364,GO:0097504,GO:0001834,GO:0031641,GO:0030576,GO:2000672,GO:0015030,GO:1902742,GO:0006397	CG9060-PA						PF03367														
aly23085.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2311.1	Leucine-rich repeat serine/threonine-protein kinase 1	GO:0050808,GO:0032418,GO:0018105,GO:0048489,GO:0005737,GO:0007264,GO:0048846,GO:1900242,GO:0004674,GO:0004672,GO:0046872,GO:0043025,GO:0031902,GO:0005524,GO:0005525,GO:0005794,GO:0034613,GO:0017137,GO:1901215,GO:0006979,GO:0005765,GO:0034976	CG5483-PD				SM00220		PF16095,PF00069	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF56112,SSF56112									
aly2311.10	Lipase member H	GO:0016020,GO:0052689,GO:0016042,GO:0005575,GO:0005576,GO:0016298	CG6472-PB						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly2311.2	Spectrin beta chain	GO:0032432,GO:0005811,GO:0050807,GO:0000281,GO:0031594,GO:0007009,GO:0005200,GO:0048790,GO:0007411,GO:0007274,GO:0030506,GO:0045170,GO:0007026,GO:0005543,GO:0030707,GO:0005546,GO:0003779,GO:0051693,GO:0032509,GO:0016328,GO:0016324,GO:0072499,GO:0008017,GO:0016327,GO:0042062,GO:0042060,GO:0010797,GO:0045186,GO:0005912,GO:0007409,GO:0005886,GO:0045478,GO:0006897,GO:0030424,GO:0008091,GO:0007399,GO:0008092,GO:0016199,GO:0045169,GO:0005515,GO:0030721	CG12008-PE				SM00326,SM00150,SM00033,SM00033,SM00233		PF00307,PF00307,PF15410,PF00435,PF00018	PS50003,PS50021,PS50002,PS50021	PR00683,PR00683,PR00683,PR00683	PS00020,PS00019	G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.10.418.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:2.30.29.30,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.10.418.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:2.30.30.40,G3DSA:1.20.58.60	SSF46966,SSF46966,SSF46966,SSF46966,SSF50044,SSF46966,SSF47576,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF50729,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966	613~654,2959~2993,1564~1591,793~820,3184~3218,41~68,1531~1558,1247~1267,1349~1379,1842~1862,2757~2784,2167~2177,2430~2450,3038~3058,1455~1485,2726~2746,3144~3171,1710~1730								
aly2311.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2311.4	E3 ubiquitin-protein ligase RNF38	GO:0005654,GO:0048149,GO:0007616,GO:0004842,GO:0005634,GO:0007611,GO:0005575,GO:0016567,GO:0008270,GO:0005515,GO:2001020,GO:0016874,GO:0008355	CG9381-PC						PF13639	PS50089			G3DSA:3.30.40.10	SSF57850									
aly2311.5	Unknown		n/a												136~156								
aly2311.6	Unknown		n/a																				
aly2311.7	Unknown		n/a																				
aly2311.8	Unknown		n/a																				
aly2311.9	Phospholipase A1 member A	GO:0008970,GO:0052689,GO:0016042,GO:0005575,GO:0005576,GO:0016298	CG17192-PA						PF00151,PF00151				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2312.1	Xaa-Pro aminopeptidase 1	GO:0005737,GO:0004177,GO:0005829,GO:0010815,GO:0030145,GO:0070006,GO:0006508	CG6291-PA						PF16189,PF16188,PF00557				G3DSA:3.90.230.10,G3DSA:3.40.350.10	SSF55920									
aly2313.1	Unknown		n/a																				
aly2314.1	Unknown		n/a																				
aly2314.2	Solute carrier family 22 member 21	GO:0015879,GO:0015226,GO:0016021,GO:1902603,GO:0005777,GO:0008513,GO:0031231,GO:0055085,GO:0005524	CG7458-PA						PF07690	PS50850		PS00216,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly2314.3	Organic cation transporter protein	GO:0005215,GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0008513,GO:0016021	CG7458-PA						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly2314.4	Serum response factor-binding protein 1	GO:0005634,GO:0016020,GO:0006355,GO:0008150,GO:0006351,GO:0003674,GO:0048471	CG8161-PA						PF09073						7~27,128~148								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2314.5	60S ribosomal protein L36	GO:0005737,GO:0005840,GO:0005730,GO:0022625,GO:0005622,GO:0003735,GO:0000228,GO:0006412	CG7622-PA						PF01158						93~113								
aly2314.6	Ribose-phosphate pyrophosphokinase 1	GO:0043234,GO:0002189,GO:0016208,GO:0043531,GO:0016301,GO:0031100,GO:0009156,GO:0000287,GO:0007476,GO:0030246,GO:0019693,GO:0004749,GO:0009165,GO:0006167,GO:0006015,GO:0019003,GO:0046101,GO:0007399,GO:0034418,GO:0005524,GO:0042803	CG6767-PB					TIGR01251	PF13793,PF14572			PS00114	G3DSA:3.40.50.2020,G3DSA:3.40.50.2020	SSF53271		00030+2.7.6.1,00230+2.7.6.1	REACT_474		UPA00087				
aly2314.7	Histone H4 transcription factor	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG17829-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13913	PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly2314.8	Unknown		n/a																				
aly2315.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly231799.1	Guanylate cyclase 32E	GO:0006468,GO:0016772,GO:0004383,GO:0004672,GO:0005525,GO:0006182,GO:0005622,GO:0004872,GO:0005887,GO:0005886,GO:0035556,GO:0009190,GO:0005524,GO:0007165	CG33114-PB											SSF53822									
aly231987.1	Unknown		n/a										G3DSA:3.40.50.1240										
aly2323.1	Unknown		CG12541-PD						PF16066														
aly2326.1	Unknown		n/a																				
aly2327.1	Zinc finger protein 208	GO:0045931,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178,GO:0008270	CG14938-PA				SM00355,SM00868,SM00868,SM00868			PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2327.10	Zinc finger and SCAN domain-containing protein 5B	GO:0009649,GO:0042051,GO:0003700,GO:0005634,GO:0003705,GO:0035271,GO:0006355,GO:0006357,GO:0045944,GO:0006351,GO:0043153,GO:0003677,GO:0007605,GO:0010114,GO:0046872,GO:0000981,GO:0001752	CG7672-PC				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12874,PF00096,PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										
aly2327.2	Unknown		n/a																				
aly2327.3	Codanin-1	GO:0042127,GO:0005737,GO:0008104,GO:0042048,GO:0016021,GO:0007560,GO:0008156,GO:0046331,GO:0003674,GO:0012505,GO:0031497,GO:0005886,GO:0046872,GO:0005634,GO:0001738	CG32315-PA				SM00355,SM00355,SM00355			PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly2327.4	Unknown		n/a																				
aly2327.5	Zinc finger and SCAN domain-containing protein 2	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0030154,GO:0007476,GO:0007275,GO:0007283,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF00096,PF00096,PF12874,PF12874,PF12874,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2327.6	Fasciclin-3	GO:0016339,GO:0007611,GO:0031594,GO:0007411,GO:0007413,GO:0005920,GO:0008355,GO:0005737,GO:0016021,GO:0007476,GO:0030707,GO:0016200,GO:0016328,GO:0031965,GO:0008039,GO:0016323,GO:0007409,GO:0005886,GO:0007156,GO:0005918,GO:0005829,GO:0005515	CG5803-PD						PF08205	PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726										
aly2327.7	Unknown		n/a																				
aly2327.8	Unknown		n/a																				
aly2327.9	Unknown		n/a												45~65,155~175								
aly233.1	Unknown	GO:0005515	n/a						PF02260	PS51190													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly233.10	Unknown		n/a																				
aly233.2	Serine protease 44	GO:0005737,GO:0004252,GO:0016021,GO:0005576,GO:0006508	CG5390-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly233.3	Trypsin-3 (Fragment)	GO:0004252,GO:0005615,GO:0007586,GO:0005576,GO:0006508,GO:0046872	CG5390-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly233.4	Serine protease 44	GO:0005737,GO:0004252,GO:0016021,GO:0005576,GO:0006508	CG5390-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly233.5	Unknown	GO:0001664,GO:0007186,GO:0005615	CG14871-PB							PS51257													
aly233.6	Cardioactive peptide	GO:0007218,GO:0005184,GO:0005615,GO:0008016,GO:0005576,GO:0045823,GO:0010460,GO:0071855	CG4910-PA						PF11105														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly233.7	Unknown		n/a												176~196								
aly233.8	DNA-dependent protein kinase catalytic subunit	GO:0005730,GO:0072431,GO:0050808,GO:0006303,GO:0006302,GO:0006281,GO:0016773,GO:0016310,GO:0004672,GO:0003677,GO:0005654,GO:0000724,GO:0004677,GO:0000184,GO:0035195,GO:0016246,GO:0070419,GO:0007274,GO:0005524,GO:0048489	CG32743-PA						PF00454	PS50290			G3DSA:1.10.1070.11	SSF56112										
aly233.9	Unknown		n/a																				
aly23313.1	Unknown		n/a										G3DSA:3.30.40.10	SSF57903									
aly23336.1	Unknown		n/a				SM00249		PF00628	PS50016,PS50089		PS01359	G3DSA:3.30.40.10	SSF57903	157~198								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2334.1	Unknown		n/a																				
aly2334.2	Unknown		n/a																				
aly2334.3	Unknown		n/a						PF00001	PS50262			G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly2334.4	Unknown		n/a				SM00595		PF10545	PS51029					193~213,53~73								
aly2334.5	Unknown		n/a																				
aly2334.6	Gamma-glutamyltranspeptidase 1	GO:0032355,GO:0007568,GO:0005615,GO:0048812,GO:0003810,GO:0034612,GO:0036374,GO:0005887,GO:0031638,GO:0006536,GO:0003840,GO:0006749,GO:0005886,GO:0006750,GO:0006751,GO:0034599,GO:0031179,GO:0032496	CG4829-PB						PF01019,PF01019		PR01210,PR01210,PR01210,PR01210,PR01210,PR01210,PR01210			SSF56235		00460+2.3.2.2,00430+2.3.2.2,00480+2.3.2.2+3.4.19.13		PWY-4041,PWY-5826					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2334.7	Sec1 family domain-containing protein 2	GO:0015031,GO:0006904,GO:0005623	n/a										G3DSA:3.40.50.1910										
aly2334.8	Cytochrome c oxidase subunit 6A1, mitochondrial	GO:0004129,GO:0030234,GO:0005811,GO:0006123,GO:0005751,GO:0005743,GO:0008340	CG17280-PA			PIRSF000277			PF02046			PS01329	G3DSA:4.10.95.10	SSF81411									
aly2334.9	Unknown		n/a										G3DSA:1.10.510.10										
aly23356.1	Collagen-like protein 1	GO:0007443,GO:0005201,GO:0005587,GO:0005581,GO:0005811,GO:0007519,GO:0019012,GO:0061327	CG16858-PA																				
aly2336.1	Leishmanolysin-like peptidase	GO:0045842,GO:0007155,GO:0019915,GO:0008233,GO:0051225,GO:0051301,GO:0005737,GO:0007100,GO:0016020,GO:0008406,GO:0022900,GO:0008354,GO:0006508,GO:0046872,GO:0004222,GO:0051298,GO:0031252,GO:0007052,GO:0007076,GO:0007420,GO:0006338,GO:0007444,GO:1902769	CG3953-PA						PF01457		PR00782,PR00782		G3DSA:3.90.132.10	SSF55486									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2336.10	Unknown		n/a																				
aly2336.2	Suppressor of lurcher protein 1	GO:0040012,GO:0008328,GO:0001966,GO:0045211,GO:0032589,GO:0045202,GO:0006972,GO:0005886,GO:0016247,GO:0051968,GO:0030054	CG34402-PC				SM00042,SM00042,SM00042		PF00431,PF00431,PF00431	PS01180,PS01180,PS01180			G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290	SSF49854,SSF49854,SSF49854									
aly2336.3	Unknown	GO:0000723,GO:0003678,GO:0006281	n/a						PF05970														
aly2336.4	Unknown	GO:0000723,GO:0003678,GO:0006281	n/a						PF05970														
aly2336.5	Unknown		n/a						PF01826,PF01826,PF01826				G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57567,SSF57567									
aly2336.6	Unknown		n/a						PF01826,PF01826				G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57567,SSF57567									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2336.7	Protocadherin-15	GO:0016339,GO:0060088,GO:0005902,GO:0048100,GO:0007304,GO:0007305,GO:0035264,GO:0060013,GO:0005737,GO:0002009,GO:0016021,GO:0016020,GO:0001964,GO:0005509,GO:0032420,GO:0050973,GO:0035058,GO:0016324,GO:0007601,GO:0032529,GO:0007628,GO:0050910,GO:0005887,GO:0005886,GO:0007155,GO:0007156,GO:0007015,GO:0007224,GO:0032533	CG31009-PA				SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112		PF00028,PF00028,PF00028,PF00028,PF00028,PF00028	PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00232,PS00232,PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313										
aly2336.8	Suppressor of lurcher protein 1	GO:0040012,GO:0008328,GO:0001966,GO:0045211,GO:0032589,GO:0045202,GO:0006972,GO:0005886,GO:0016247,GO:0051968,GO:0030054	CG34402-PC				SM00042,SM00042,SM00042		PF00431,PF00431,PF00431	PS01180,PS01180,PS01180			G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290	SSF49854,SSF49854,SSF49854									
aly2336.9	DNA ligase 3	GO:0051103,GO:0003910,GO:0003677,GO:0043504,GO:0007049,GO:0007005,GO:0005737,GO:0006303,GO:0006302,GO:0005634,GO:0005739,GO:0005654,GO:0006266,GO:0006260,GO:0051301,GO:0045910,GO:0005694,GO:0005524,GO:0006284,GO:0006281,GO:0006288,GO:0006289,GO:0000795,GO:0003909,GO:0006310,GO:0006273,GO:0070421,GO:0090298,GO:0097681,GO:0071897,GO:0008270	CG17227-PA					TIGR00574	PF00645,PF04679,PF16759,PF04675,PF01068	PS50172,PS50064,PS50160		PS00333,PS00697	G3DSA:3.30.1740.10,G3DSA:3.30.1490.70,G3DSA:3.30.1490.70,G3DSA:3.30.470.30,G3DSA:3.40.50.10190,G3DSA:1.10.3260.10,G3DSA:2.40.50.140	SSF52113,SSF57716,SSF117018,SSF56091,SSF50249			REACT_216						
aly234.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly234.10	Kelch-like protein diablo	GO:0005575,GO:0016049,GO:0050807,GO:0003779,GO:0016567,GO:0048812	CG6224-PA			PIRSF037037	SM00875,SM00225,SM00612,SM00612,SM00612,SM00612		PF07707,PF01344,PF01344,PF01344,PF01344,PF01344,PF01344,PF00651	PS50097			G3DSA:2.130.10.80,G3DSA:3.30.710.10	SSF50965,SSF54695									
aly234.11	Unknown		n/a						PF15928														
aly234.12	Thioredoxin domain-containing protein 3 homolog	GO:0006228,GO:0030154,GO:0005623,GO:0007275,GO:0007283,GO:0006241,GO:0004550,GO:0005524,GO:0006662,GO:0015035,GO:0045454,GO:0006183	CG14221-PC						PF00085	PS51352		PS00194	G3DSA:3.40.30.10	SSF52833	159~179,124~144								
aly234.13	Unknown		n/a																				
aly234.14	Maltase 1	GO:0032450,GO:0003824,GO:0005975,GO:0004558,GO:0043169	CG11669-PA				SM00642		PF00128				G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF51445									
aly234.15	Maltase A1	GO:0043169,GO:0005975,GO:0032450,GO:0003824,GO:0006006,GO:0004558	CG8696-PA				SM00642		PF00128				G3DSA:3.90.400.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF51445									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly234.16	Maltase 1	GO:0043169,GO:0005975,GO:0032450,GO:0003824,GO:0006006,GO:0004558	CG8696-PA				SM00642		PF00128				G3DSA:3.90.400.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF51445									
aly234.17	Unknown		n/a																				
aly234.18	Unknown		CG6024-PC				SM00192		PF00057	PS50068		PS01209	G3DSA:4.10.400.10,G3DSA:2.60.120.290	SSF57424,SSF49854									
aly234.19	Unknown		n/a																				
aly234.2	Beclin 1-associated autophagy-related key regulator	GO:0090207,GO:0008333,GO:0016236,GO:0098779,GO:0005737,GO:0097632,GO:0010608,GO:0005634,GO:0005776,GO:0000045,GO:0005654,GO:0010508,GO:0010506,GO:0035032,GO:0006914,GO:0045335,GO:0042149,GO:0061635,GO:0005930,GO:0034045,GO:0043552,GO:0000421,GO:0044233,GO:0097629,GO:0001933,GO:0001932,GO:0001934	CG11877-PA						PF10186						120~140								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly234.20	Laminin subunit alpha-2	GO:0005606,GO:0005605,GO:0030334,GO:0007502,GO:0070062,GO:0043197,GO:0008406,GO:0030155,GO:0007476,GO:0022011,GO:0005604,GO:0042383,GO:0045995,GO:0030198,GO:0007155,GO:0007411,GO:0005102,GO:0032224,GO:0005576	CG42677-PB				SM00180,SM00180,SM00180,SM00180		PF00053,PF00053,PF00053,PF00055	PS50027,PS50027,PS51117		PS01248,PS01248	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57196,SSF57196									
aly234.21	Laminin subunit alpha-1	GO:0061304,GO:0005201,GO:0045198,GO:0045995,GO:0007476,GO:0030155,GO:0031012,GO:0007155,GO:0060041,GO:0007166,GO:0031175,GO:0005615,GO:0043208,GO:0008406,GO:0060441,GO:0060445,GO:0006468,GO:0030334,GO:0009888,GO:0005911,GO:0043256,GO:0005606,GO:0005605,GO:0005604,GO:0007502,GO:0002011,GO:0005608,GO:0005576,GO:0005102,GO:0005578	CG42677-PB				SM00281,SM00180,SM00180,SM00180		PF00052,PF00053,PF00053,PF00053	PS51115,PS50027,PS50027		PS01248,PS01248	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57196,SSF57196									
aly234.22	Laminin subunit alpha-1	GO:0061304,GO:0005201,GO:0045198,GO:0045995,GO:0007476,GO:0030155,GO:0031012,GO:0007155,GO:0060041,GO:0007166,GO:0031175,GO:0005615,GO:0043208,GO:0008406,GO:0060441,GO:0060445,GO:0006468,GO:0030334,GO:0009888,GO:0005911,GO:0043256,GO:0005606,GO:0005605,GO:0005604,GO:0007502,GO:0002011,GO:0005608,GO:0005576,GO:0005102,GO:0005578	CG42677-PB				SM00181,SM00181,SM00181,SM00181,SM00181,SM00282,SM00282,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180		PF00053,PF00053,PF00053,PF00053,PF00053,PF00053,PF02210,PF02210,PF02210,PF00052	PS50027,PS51115,PS50027,PS50025,PS50027,PS50027,PS50027,PS50027,PS50027	PR00011,PR00011,PR00011,PR00011	PS01248,PS01248,PS01248,PS01248,PS01248,PS01248	G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.200	SSF49899,SSF57196,SSF57196,SSF49899,SSF49899,SSF49899	709~746,1063~1090,855~882								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly234.23	Laminin subunit alpha-1	GO:0061304,GO:0005201,GO:0045198,GO:0045995,GO:0007476,GO:0030155,GO:0031012,GO:0007155,GO:0060041,GO:0007166,GO:0031175,GO:0005615,GO:0043208,GO:0008406,GO:0060441,GO:0060445,GO:0006468,GO:0030334,GO:0009888,GO:0005911,GO:0043256,GO:0005606,GO:0005605,GO:0005604,GO:0007502,GO:0002011,GO:0005608,GO:0005576,GO:0005102,GO:0005578	CG42677-PB				SM00282		PF00054	PS50025			G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200	SSF49899,SSF49899										
aly234.24	Lysosome-associated membrane glycoprotein 1	GO:0016021,GO:0016020,GO:0005764,GO:0005765,GO:0048812,GO:0005886,GO:0010008	CG3305-PA						PF01299	PS51407	PR00336,PR00336,PR00336												
aly234.25	Sodium/potassium-transporting ATPase subunit beta-2	GO:0007424,GO:0008324,GO:0098655,GO:0035151,GO:0035158,GO:0006812,GO:0019991,GO:0035725,GO:0006814,GO:0005391,GO:0006813,GO:0005890,GO:0061343,GO:0060857,GO:0005886,GO:0007605,GO:0035159,GO:0030424,GO:0005918	CG9261-PC						PF00287				G3DSA:2.60.40.1660										
aly234.26	Sodium/potassium-transporting ATPase subunit beta-2	GO:0007424,GO:0098655,GO:0035151,GO:0006813,GO:0006812,GO:0019991,GO:0035725,GO:0006814,GO:0005391,GO:0007605,GO:0005890,GO:0061343,GO:0060857,GO:0005886,GO:0030424,GO:0035159,GO:0010996,GO:0035158,GO:0005918	CG8663-PE						PF00287			PS00390	G3DSA:2.60.40.1660,G3DSA:1.20.5.170										
aly234.27	Translation initiation factor IF-2	GO:0005737,GO:0003743,GO:0003924,GO:0005525	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly234.28	Sodium/potassium-transporting ATPase subunit beta-2	GO:0007424,GO:0008324,GO:0098655,GO:0035151,GO:0035158,GO:0006812,GO:0019991,GO:0035725,GO:0006814,GO:0005391,GO:0006813,GO:0005890,GO:0061343,GO:0060857,GO:0005886,GO:0007605,GO:0035159,GO:0030424,GO:0005918	CG9261-PC						PF00287				G3DSA:1.20.5.170,G3DSA:2.60.40.1660											
aly234.29	Sodium/potassium-transporting ATPase subunit beta-2	GO:0007424,GO:0008324,GO:0098655,GO:0035151,GO:0035158,GO:0006812,GO:0019991,GO:0035725,GO:0006814,GO:0005391,GO:0006813,GO:0005890,GO:0061343,GO:0060857,GO:0005886,GO:0007605,GO:0035159,GO:0030424,GO:0005918	CG9261-PC						PF00287				G3DSA:2.60.40.1660,G3DSA:1.20.5.170											
aly234.3	Unknown		n/a																				
aly234.30	Sodium/potassium-transporting ATPase subunit beta-1	GO:0006813,GO:0006812,GO:0008324,GO:0035725,GO:0006814,GO:0005391,GO:0005890,GO:0005515,GO:0005886,GO:0098655	CG9258-PA						PF00287,PF00287				G3DSA:2.60.40.1660,G3DSA:2.60.40.1660,G3DSA:1.20.5.170											
aly234.4	Brain mitochondrial carrier protein 1	GO:0015992,GO:0019222,GO:0007605,GO:0006810,GO:0022857,GO:0044237,GO:0005743,GO:0005740,GO:0009060,GO:0005739,GO:0005887,GO:0022904,GO:0006839,GO:0055085,GO:0044281	CG7314-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920	PR00926,PR00926,PR00926,PR00926		G3DSA:1.50.40.10	SSF103506									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly234.5	Unknown	GO:0016020	n/a							PS51225													
aly234.6	CKLF-like MARVEL transmembrane domain-containing protein 4	GO:0016021,GO:0016020,GO:0006935,GO:0005615	CG15211-PA						PF01284	PS51225													
aly234.7	CKLF-like MARVEL transmembrane domain-containing protein 4	GO:0016021,GO:0016020,GO:0006935,GO:0005615	CG15211-PA						PF01284	PS51225													
aly234.8	Conserved oligomeric Golgi complex subunit 4	GO:0015031,GO:0000139	CG7456-PA						PF08318														
aly234.9	Conserved oligomeric Golgi complex subunit 4	GO:0015031,GO:0000139	CG7456-PA						PF08318						15~42								
aly234412.1	HEAT repeat-containing protein 5B	GO:0022008,GO:0016020,GO:0070062	CG2747-PF																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2349.1	Unknown	GO:0046872	CG18265-PA				SM00355,SM00355,SM00355,SM00355					PS00028,PS00028,PS00028,PS00028,PS00028			193~213,152~172								
aly2349.2	Phospholipid scramblase 2	GO:0017128,GO:0017121,GO:0016021,GO:0005886,GO:0048812,GO:0007268,GO:0046872	CG32056-PA						PF03803														
aly2349.3	Transcription factor EB	GO:0005737,GO:0044212,GO:0006366,GO:0006959,GO:0046982,GO:0003700,GO:0006914,GO:0007040,GO:0005634,GO:0006355,GO:0010508,GO:0001077,GO:0045944,GO:0045893,GO:0005667,GO:0003677,GO:0046983,GO:0001745,GO:0001892,GO:0000978	CG43369-PC				SM00353		PF00010,PF15951	PS50888			G3DSA:4.10.280.10	SSF47459	305~339,69~89								
aly2349.4	Probable small nuclear ribonucleoprotein G	GO:0000245,GO:0030532,GO:0071011,GO:0005634,GO:0000398,GO:0007052,GO:0003723,GO:0071013,GO:0005681,GO:0005732	CG9742-PB			PIRSF037188	SM00651		PF01423				G3DSA:2.30.30.100	SSF50182									
aly2349.5	Transmembrane protein 234 homolog	GO:0005575,GO:0003674,GO:0016021,GO:0008150	CG12929-PA						PF10639					SSF103481									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2349.6	Three prime repair exonuclease 2	GO:0000738,GO:0006281,GO:0008853,GO:0000287,GO:0003676,GO:0006259,GO:0005634,GO:0008296,GO:0042803	CG3165-PA				SM00479		PF00929				G3DSA:3.30.420.10	SSF53098,SSF53098									
aly2349.7	Solute carrier family 12 member 9	GO:0005215,GO:0006811,GO:0016020,GO:0008511,GO:0055085,GO:0005886,GO:0016021	CG10413-PA						PF03522,PF00324								REACT_15518						
aly2349.8	Unknown		n/a																				
aly2349.9	Solute carrier family 12 member 9	GO:0005215,GO:0006811,GO:0016020,GO:0008511,GO:0055085,GO:0005886,GO:0016021	CG10413-PA						PF03522								REACT_15518						
aly235.1	Heparan sulfate glucosamine 3-O-sulfotransferase 5	GO:0016021,GO:0008146,GO:0006477,GO:0000139,GO:0046596,GO:0015015,GO:0050819,GO:0008467	CG33147-PA						PF00685				G3DSA:3.40.50.300	SSF52540									
aly235.10	Late secretory pathway protein AVL9 homolog	GO:0016021,GO:0016477,GO:0055037	CG11178-PB						PF09794														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly235.11	Unknown		n/a																				
aly235.12	Kinase D-interacting substrate of 220 kDa	GO:0043234,GO:0019901,GO:1990090,GO:0045859,GO:0019887,GO:0005829,GO:0005770,GO:0038180,GO:0005575,GO:0030165,GO:0003674,GO:0010976,GO:0008150,GO:0016021,GO:0016482	CG42672-PP				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF13637,PF13637,PF07693,PF12796,PF12796,PF12796	PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50297			G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403									
aly235.13	tRNA (guanine-N(7)-)-methyltransferase	GO:0006400,GO:0005575,GO:0005634,GO:0000049,GO:0008176	CG4045-PA					TIGR00091	PF02390	PS51625				SSF53335					UPA00989				
aly235.14	Tetratricopeptide repeat protein 37	GO:0005737,GO:0005634,GO:0005654,GO:0000956,GO:0035327,GO:0055087	CG8777-PA				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF13414,PF13176,PF13181,PF13181,PF13424	PS50005,PS50293,PS50005,PS50293,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452,SSF48452,SSF48452,SSF48452,SSF48452,SSF48452									
aly235.15	Rotatin	GO:0005737,GO:0036064,GO:0005813,GO:0007368,GO:0044782,GO:0016021	n/a						PF14726					SSF48371,SSF48371,SSF48371,SSF48371,SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly235.16	Cytochrome P450 6a2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0046680,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385		G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly235.17	Unknown		n/a						PF05004				G3DSA:1.25.10.10	SSF48371,SSF48371									
aly235.18	Unknown		n/a																				
aly235.19	Inositol-trisphosphate 3-kinase A	GO:0005737,GO:0097062,GO:0043197,GO:0008440,GO:0004683,GO:0061003,GO:0048167,GO:0030036,GO:0048365,GO:0005516,GO:0006020,GO:0006979,GO:0005524	CG4026-PA						PF03770					SSF56104									
aly235.2	INO80 complex subunit B	GO:0006310,GO:0005737,GO:0006338,GO:0006281,GO:0005634,GO:0005730,GO:0031011,GO:0005654,GO:0006355,GO:0006351,GO:0005886,GO:0046872	CG10395-PA						PF04438,PF04795														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly235.20	Protein claret segregational	GO:0008152,GO:0090306,GO:0090307,GO:0032888,GO:0005871,GO:0005872,GO:0000022,GO:0051301,GO:0007100,GO:0005819,GO:0005813,GO:0005634,GO:0008569,GO:0031534,GO:1990498,GO:0000212,GO:0051297,GO:0005524,GO:0042803,GO:0051298,GO:0032837,GO:0008017,GO:0072687,GO:0007051,GO:0007052,GO:0007056,GO:0007059,GO:0000070,GO:0051028,GO:0001578,GO:0005829,GO:1901673,GO:0007018,GO:0003777	CG7831-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380		G3DSA:3.40.850.10	SSF52540	103~220								
aly235.21	Probable RNA methyltransferase bin3	GO:0001085,GO:0032502,GO:0042048,GO:0005575,GO:0017069,GO:0017148,GO:0008168,GO:0032259	CG8276-PC						PF13847,PF06859	PS51515			G3DSA:3.40.50.150,G3DSA:3.40.50.150	SSF53335,SSF53335									
aly235.22	Unknown		n/a																				
aly235.23	Unknown		n/a																				
aly235.3	BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 3	GO:0005737,GO:0036038,GO:0043161,GO:0051260,GO:0005654,GO:0016567,GO:0005515,GO:0031463	CG10465-PA				SM00225		PF02214	PS50097			G3DSA:3.30.710.10	SSF54695									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly235.4	Protein phosphatase 1G	GO:0005737,GO:0005654,GO:0006470,GO:0005634,GO:0004722,GO:0007050,GO:0003824,GO:0035970,GO:0046872	CG10417-PA				SM00332		PF00481,PF00481	PS51746		PS01032	G3DSA:3.60.40.10,G3DSA:3.60.40.10	SSF81606,SSF81606									
aly235.5	Intraflagellar transport protein 20 homolog	GO:0030992,GO:0042384,GO:0005794,GO:0034067,GO:0005813,GO:0042073,GO:0061512,GO:0005929,GO:0036064,GO:0051642,GO:0005930	CG30441-PB						PF14931						50~70,89~109								
aly235.6	Spatacsin	GO:0005737,GO:0070062,GO:0005730,GO:0031410,GO:0005829,GO:0005765,GO:0005886,GO:0016021	CG13531-PB						PF14649						1759~1779								
aly235.7	Sn1-specific diacylglycerol lipase beta	GO:0005737,GO:0046872,GO:0006629,GO:0042136,GO:0005765,GO:0016021,GO:0007596,GO:0007602,GO:0004465,GO:0019369,GO:0005886,GO:0007405,GO:0016042,GO:0016298,GO:0030168	CG33174-PE						PF01764				G3DSA:3.40.50.1820	SSF53474			REACT_14797,REACT_604						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly235.8	Adenylate cyclase type 1	GO:0048675,GO:0007409,GO:0048149,GO:0007619,GO:0007616,GO:0007617,GO:0007614,GO:0005886,GO:0007591,GO:0007613,GO:0009408,GO:0007611,GO:0019933,GO:0035556,GO:0001661,GO:0090328,GO:0008355,GO:0005737,GO:0070062,GO:0007274,GO:0016021,GO:0016020,GO:0016849,GO:0009190,GO:0007186,GO:0006171,GO:0005524,GO:0007625,GO:0007623,GO:0007612,GO:0007528,GO:0042752,GO:0008306,GO:0030431,GO:0005887,GO:0007268,GO:0008340,GO:0004016,GO:0006979,GO:0046872,GO:0010226,GO:0042493,GO:0007190,GO:0005634,GO:0008294	CG9533-PA				SM00044,SM00044,SM00228		PF06327,PF00595,PF00595,PF16214,PF00211,PF00211,PF12053	PS50125,PS50125,PS50106,PS50106		PS00452,PS00452	G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:3.30.70.1230,G3DSA:3.30.70.1230	SSF50156,SSF50156,SSF55073,SSF55073	14~34	00230+4.6.1.1	REACT_14797,REACT_15295,REACT_11061,REACT_1505						
aly235.9	Serine/threonine-protein kinase tousled-like 2	GO:0006468,GO:0019730,GO:0051726,GO:0006325,GO:0005634,GO:0016572,GO:0004674,GO:0008360,GO:0045448,GO:0005515,GO:0004672,GO:0007155,GO:0007059,GO:0046777,GO:0005524	CG34412-PG				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112	331~358,421~455,241~268									
aly235040.1	Unknown	GO:0016021,GO:0005778	CG14778-PA																				
aly235051.1	Alpha-N-acetylgalactosaminidase	GO:0005737,GO:0008456,GO:0005975,GO:0016139,GO:0009311,GO:0005764,GO:0004557,GO:0004553,GO:0046477	CG7997-PB						PF16499			PS00512	G3DSA:3.20.20.70	SSF51445		00052+3.2.1.22,00600+3.2.1.22,00603+3.2.1.22,00561+3.2.1.22		PWY-6527					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2354.1	Dipeptidase 1	GO:0008239,GO:0035690,GO:0008270,GO:0034235,GO:0008235,GO:0031225,GO:0045177,GO:0050667,GO:0005615,GO:0016999,GO:0016805,GO:0043066,GO:0070573,GO:0006508,GO:0043027,GO:0030336,GO:0016324,GO:0071277,GO:0005886,GO:0031528,GO:0072341,GO:0071732,GO:0043154	CG42750-PB						PF01244	PS51365		PS00869	G3DSA:3.20.20.140	SSF51556				PWY-7533					
aly2354.2	Actin	GO:0005737,GO:0005856,GO:0005200,GO:0007010,GO:0005811,GO:0005884,GO:0005524	CG18290-PA				SM00268		PF00022		PR00190,PR00190,PR00190,PR00190,PR00190		G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.90.640.10	SSF53067,SSF53067									
aly2354.3	Actin	GO:0005737,GO:0007507,GO:0005200,GO:0007010,GO:0051297,GO:0005856,GO:0000281,GO:0051533,GO:0005884,GO:0005875,GO:0005524	CG10067-PA				SM00268		PF00022		PR00190,PR00190,PR00190,PR00190,PR00190,PR00190		G3DSA:3.30.420.40,G3DSA:3.90.640.10,G3DSA:3.30.420.40	SSF53067,SSF53067									
aly2354.4	Unknown		n/a																				
aly235578.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2357.1	Unknown	GO:0005267,GO:0016021,GO:0071805	CG1688-PA																				
aly2357.2	GTP-binding protein 128up	GO:0005525	CG8340-PA					TIGR00231	PF02824,PF16897,PF01926	PS51710	PR00326,PR00326		G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF81271	1~21	00970+6.1.1.3							
aly2357.3	Unknown		n/a																				
aly2357.4	POU domain, class 6, transcription factor 2	GO:0043565,GO:0007608,GO:0003700,GO:0005634,GO:0006366,GO:0007601,GO:0006355,GO:0007409,GO:0003677,GO:0007411,GO:0007412,GO:0007402,GO:0007417	CG42698-PF				SM00389,SM00352		PF00046,PF00157,PF00157	PS50071,PS51179	PR00028,PR00028,PR00028,PR00028,PR00028	PS00035	G3DSA:1.10.10.60,G3DSA:1.10.260.40	SSF47413,SSF46689									
aly2357.5	Tyrosine-protein phosphatase non-receptor type 4	GO:0005856,GO:0016319,GO:0035071,GO:0008092,GO:0048846,GO:0006470,GO:0004725,GO:0009898,GO:0005737,GO:0048102,GO:0048036,GO:0004726,GO:0035335,GO:0004040	CG1228-PG				SM00295,SM00194,SM00404		PF09379,PF00102,PF00373,PF09380	PS50055,PS50056,PS50057	PR00700,PR00700,PR00700,PR00700,PR00700,PR00700,PR00935,PR00935,PR00935	PS00660,PS00383,PS00661	G3DSA:3.90.190.10,G3DSA:3.10.20.90,G3DSA:2.30.29.30,G3DSA:2.30.42.10,G3DSA:1.20.80.10	SSF50156,SSF47031,SSF54236,SSF50729,SSF52799									
aly2357.6	Unknown	GO:0005214,GO:0040003,GO:0005578	CG14534-PA				SM00690		PF03103														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2357.7	Fibroblast growth factor receptor 2	GO:0008284,GO:0005794,GO:0006468,GO:0048701,GO:0016023,GO:0016021,GO:0006915,GO:0004714,GO:0004713,GO:0005007,GO:0005886,GO:0007169,GO:0005524	CG3277-PC			PIRSF000615	SM00219		PF07714	PS50011		PS00109,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112,SSF56112									
aly2357.8	Unknown		n/a																				
aly2357.9	Unknown		n/a																				
aly23582.1	Unknown		n/a						PF05380					SSF56672									
aly23583.1	Unknown		n/a												229~249								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly23605.1	Ankyrin-2	GO:0048675,GO:0005200,GO:0031647,GO:0010882,GO:0007614,GO:0060307,GO:0003283,GO:0098907,GO:0031594,GO:0036309,GO:0045887,GO:0010628,GO:0000226,GO:0007165,GO:0086066,GO:0042383,GO:0044325,GO:0060048,GO:0030018,GO:0043268,GO:0005737,GO:0086005,GO:0051924,GO:0031430,GO:0036062,GO:0031672,GO:0034394,GO:0086036,GO:0008104,GO:0030315,GO:0098904,GO:1901021,GO:0006874,GO:0048471,GO:0097481,GO:0072661,GO:0086004,GO:0098910,GO:0016324,GO:0005856,GO:0002027,GO:1901019,GO:0007605,GO:0051117,GO:0015459,GO:0034613,GO:0055117,GO:0030674,GO:0016323,GO:0007528,GO:0045211,GO:0072659,GO:0070972,GO:0005887,GO:0005886,GO:0033292,GO:0086070,GO:0086015,GO:0086014,GO:1901018,GO:0014704,GO:0007016,GO:0043195,GO:0042734,GO:0008092,GO:0036371,GO:0051928,GO:0070050,GO:0005622,GO:0086091,GO:1900074,GO:0010881,GO:2001259,GO:2001257,GO:0050821,GO:0043034	CG42734-PU				SM00218,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00005		PF00023,PF00023,PF00023,PF13637,PF00791,PF00531,PF12796,PF12796,PF12796,PF12796,PF12796	PS50088,PS50088,PS51145,PS50088,PS50088,PS50088,PS50088,PS50017,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50297,PS50088,PS50088	PR01415,PR01415	G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.10.533.10	SSF48403,SSF48403,SSF47986	4189~4216,1872~1892,2413~2433,5618~5624								
aly23605.10	Glycine receptor subunit alpha-2	GO:0007218,GO:0006810,GO:0016021,GO:0045211,GO:1902476,GO:0005230,GO:0016020,GO:0022824,GO:0006821,GO:0034707,GO:0019183,GO:0019182,GO:0030054,GO:0005887,GO:0006811,GO:0016934,GO:0043052,GO:0016933,GO:0016594	CG14723-PA						PF02931,PF02932		PR00253,PR00253,PR00253	PS00236	G3DSA:1.20.58.390,G3DSA:1.20.58.390,G3DSA:2.70.170.10	SSF63712,SSF90112									
aly23605.11	Growth/differentiation factor 8	GO:0016319,GO:0033673,GO:0071549,GO:0005615,GO:0014732,GO:0048632,GO:0007179,GO:0005623,GO:0046627,GO:0051898,GO:0046716,GO:0045893,GO:0045662,GO:0040007,GO:0008201,GO:1903146,GO:0008083	CG1838-PA				SM00204		PF00019	PS51362		PS00250	G3DSA:2.10.90.10	SSF57501									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly23605.12	Latrophilin Cirl	GO:0008021,GO:0004930,GO:0016192,GO:0016021,GO:0016020,GO:0007218,GO:0030246,GO:0007269,GO:0005886,GO:0007186,GO:0016524	CG8639-PI				SM00303		PF00002,PF01825,PF02140,PF16489	PS50221,PS50261,PS50228	PR00249,PR00249,PR00249,PR00249,PR00249												
aly23605.13	Catenin delta-2	GO:0050808,GO:0016337,GO:0007612,GO:0030425,GO:0034334,GO:0048167,GO:0001763,GO:0007165,GO:0001745,GO:0005737,GO:0043204,GO:0005813,GO:0005634,GO:0060997,GO:0008013,GO:0014069,GO:0005912,GO:0007155,GO:0016055,GO:0006355,GO:0006351,GO:0060828	CG17484-PA				SM00185,SM00185,SM00185,SM00185,SM00185		PF00514,PF00514,PF00514,PF00514	PS50176,PS50176,PS50176			G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371										
aly23605.14	Protein BCL9 homolog	GO:0007367,GO:0005634,GO:0016055,GO:0008587,GO:0030111,GO:0008013,GO:0001105,GO:0030177,GO:0045944,GO:0006351,GO:0005515	CG2041-PA						PF11502														
aly23605.15	CCR4-NOT transcription complex subunit 4	GO:0000288,GO:0003676,GO:0046425,GO:0004842,GO:0051297,GO:0044822,GO:0000166,GO:0010467,GO:0051865,GO:0045892,GO:0008270,GO:0005515,GO:0000289,GO:0005634,GO:0016874,GO:0005829,GO:0003729	CG31716-PK				SM00361		PF14570,PF00076	PS50089,PS50102,PS50103			G3DSA:3.30.40.10,G3DSA:3.30.70.330	SSF54928,SSF57850	753~797,460~480,806~826,77~104									
aly23605.16	Carbonyl reductase [NADPH] 3	GO:0005737,GO:0000253,GO:0005615,GO:0042376,GO:0005829,GO:0050890,GO:0005654,GO:0004090,GO:0008152,GO:0070402,GO:0016491	CG31549-PA						PF00106,PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly23605.17	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA			PIRSF036514			PF00011	PS01031	PR00299,PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly23605.18	Delta(24)-sterol reductase	GO:0008104,GO:0008762,GO:0000246,GO:0008285,GO:0019899,GO:0005789,GO:0061024,GO:0044281,GO:0042987,GO:1901214,GO:0005783,GO:0005737,GO:0050660,GO:0016628,GO:0042605,GO:0016021,GO:0016020,GO:0031639,GO:0043066,GO:0043588,GO:0005856,GO:0006915,GO:0009888,GO:0007050,GO:0003824,GO:0007265,GO:0006979,GO:0055114,GO:0050614,GO:0016614,GO:0009725,GO:0005829,GO:0030539,GO:0000139,GO:0043154,GO:0006695,GO:0005634	n/a						PF01565	PS51387			G3DSA:3.30.465.10	SSF56176		00520+1.3.1.98,00550+1.3.1.98		PWY-6386,PWY-6387	UPA00219				
aly23605.19	Unknown		n/a										G3DSA:3.90.20.10		59~79								
aly23605.2	63 kDa sperm flagellar membrane protein	GO:0031514,GO:0008407,GO:0007602,GO:0046331,GO:0005509,GO:0005515,GO:0005886,GO:0031225	CG11101-PB				SM00179,SM00181,SM00181,SM00181		PF07645	PS50026,PS50026		PS00010,PS01187,PS00022	G3DSA:2.10.25.10	SSF57184,SSF57184									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly23605.20	Fibrillin-1	GO:0005201,GO:0031012,GO:0001501,GO:0001527,GO:0009653,GO:0048048,GO:0090287,GO:0070062,GO:0005576,GO:0035583,GO:0005509,GO:0032403,GO:0022617,GO:0035582,GO:0005178,GO:0030023,GO:1990314,GO:0001656,GO:0007155,GO:0005615,GO:0007507,GO:0005604,GO:0071560,GO:0030198,GO:0005515,GO:0043010,GO:0005578,GO:0048050	CG31999-PA				SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181		PF12662,PF12662,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645,PF07645	PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026		PS01187,PS00010,PS01187,PS01187,PS01187,PS00010,PS00010,PS01186,PS01187,PS01186,PS00010,PS01186,PS01187,PS01186,PS00010,PS01187,PS01187,PS00010,PS01186,PS01187,PS01187,PS01187	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57184,SSF57184,SSF57184,SSF57184,SSF57184,SSF57184,SSF57184,SSF57184,SSF57184,SSF57184									
aly23605.21	Dual specificity protein phosphatase CDC14A	GO:0005737,GO:0005819,GO:0008138,GO:0008283,GO:0006470,GO:0004725,GO:0004721,GO:0005654,GO:0051301,GO:0005813,GO:0005634,GO:0007049	CG7134-PA				SM00404		PF00782,PF14671	PS50056		PS00383	G3DSA:3.90.190.10,G3DSA:3.90.190.10	SSF52799,SSF52799									
aly23605.22	Pyrroline-5-carboxylate reductase	GO:0005737,GO:0006561,GO:0005618,GO:0004735,GO:0009651,GO:0009408,GO:0055129,GO:0055114	CG5840-PA	MF_01925		PIRSF000193		TIGR00112	PF03807,PF14748				G3DSA:1.10.3730.10,G3DSA:3.40.50.720	SSF48179,SSF51735		00330+1.5.1.2		PWY-6344,PWY-4981,PWY-3341	UPA00098				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly23605.23	Ankyrin-2	GO:0048675,GO:0005200,GO:0031647,GO:0010882,GO:0007614,GO:0060307,GO:0003283,GO:0098907,GO:0031594,GO:0036309,GO:0045887,GO:0010628,GO:0000226,GO:0007165,GO:0086066,GO:0042383,GO:0044325,GO:0060048,GO:0030018,GO:0043268,GO:0005737,GO:0086005,GO:0051924,GO:0031430,GO:0036062,GO:0031672,GO:0034394,GO:0086036,GO:0008104,GO:0030315,GO:0098904,GO:1901021,GO:0006874,GO:0048471,GO:0097481,GO:0072661,GO:0086004,GO:0098910,GO:0016324,GO:0005856,GO:0002027,GO:1901019,GO:0007605,GO:0051117,GO:0015459,GO:0034613,GO:0055117,GO:0030674,GO:0016323,GO:0007528,GO:0045211,GO:0072659,GO:0070972,GO:0005887,GO:0005886,GO:0033292,GO:0086070,GO:0086015,GO:0086014,GO:1901018,GO:0014704,GO:0007016,GO:0043195,GO:0042734,GO:0008092,GO:0036371,GO:0051928,GO:0070050,GO:0005622,GO:0086091,GO:1900074,GO:0010881,GO:2001259,GO:2001257,GO:0050821,GO:0043034	CG42734-PU				SM00218,SM00248		PF13857,PF00023,PF12796,PF12796,PF12796,PF12796,PF12796,PF12796,PF13637,PF00791	PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS51145,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50297	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.20.120.20,G3DSA:1.25.40.20	SSF48403,SSF58113,SSF48403	2372~2372,2091~2118,1662~1722,1982~2013								
aly23605.24	Probable cation-transporting ATPase W08D2.5	GO:0042625,GO:0006457,GO:0016023,GO:0006812,GO:0016021,GO:0005774,GO:0000166,GO:0019829,GO:0016887,GO:0005886,GO:0046872,GO:0005524	CG32000-PH					TIGR01494	PF00122,PF12409,PF12710		PR00119,PR00119,PR00119	PS00154	G3DSA:3.40.1110.10,G3DSA:3.40.1110.10,G3DSA:3.40.50.1000,G3DSA:3.40.50.1000,G3DSA:2.70.150.10	SSF81665,SSF81665,SSF81653,SSF56784,SSF56784,SSF56784										
aly23605.3	Unknown	GO:0005575,GO:0003674,GO:0008150,GO:0005509	CG33978-PE						PF15950,PF15950,PF15950,PF15950						540~567								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly23605.4	Unknown		n/a																				
aly23605.5	Protein pangolin, isoforms A/H/I/S	GO:0030111,GO:0001077,GO:0010628,GO:0030178,GO:0070491,GO:0043565,GO:0007435,GO:0007367,GO:0005634,GO:0007476,GO:0005875,GO:0006366,GO:0072091,GO:0009880,GO:0044212,GO:0008013,GO:0019900,GO:0045892,GO:0045893,GO:0035277,GO:0007507,GO:0007500,GO:0060070,GO:0016055,GO:0003705,GO:0006355,GO:0006357,GO:0045944,GO:0005667,GO:0045610	CG34403-PR				SM00398		PF00505,PF08347	PS50118			G3DSA:1.10.30.10,G3DSA:1.10.30.10,G3DSA:4.10.900.10	SSF47095,SSF47095									
aly23605.6	Dihydropyrimidinase	GO:0051289,GO:0007613,GO:0044281,GO:0046135,GO:0016597,GO:0005737,GO:0070062,GO:0006208,GO:0006206,GO:0006207,GO:0008270,GO:0045747,GO:0019482,GO:0007265,GO:0051642,GO:0055086,GO:0016810,GO:0006210,GO:0006212,GO:0002059,GO:0002058,GO:0005829,GO:0004157	CG1411-PE					TIGR02033	PF01979				G3DSA:2.30.40.10,G3DSA:3.20.20.140,G3DSA:2.30.40.10	SSF51338,SSF51338,SSF51556			REACT_18266						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly23605.7	Endothelin-converting enzyme 1	GO:0009897,GO:0008217,GO:0042312,GO:0001666,GO:0008237,GO:0035994,GO:0031982,GO:0030819,GO:0031410,GO:0016021,GO:0016020,GO:0045745,GO:0046686,GO:0006508,GO:0001921,GO:0042803,GO:0004222,GO:0030141,GO:0006915,GO:0005886,GO:0016485,GO:0010613,GO:0046872,GO:0042493,GO:0005769,GO:0070372	CG9565-PA						PF05649,PF01431		PR00786,PR00786,PR00786,PR00786		G3DSA:3.40.390.10,G3DSA:3.40.390.10	SSF55486									
aly23605.8	Unknown		n/a				SM00717,SM00717		PF13837						769~789								
aly23605.9	Unknown	GO:0006810,GO:0016021,GO:0005230,GO:0016020,GO:0006821,GO:0019183,GO:0019182,GO:0043052,GO:0016933	CG14723-PA										G3DSA:2.70.170.10										
aly23611.1	Unknown		n/a																				
aly236122.1	Germinal-center associated nuclear protein	GO:0005737,GO:0005654,GO:0016973,GO:0016746,GO:0003676,GO:0005643,GO:0006606,GO:0005829,GO:0031965,GO:0000166,GO:0002376,GO:0009790,GO:0007283,GO:0045944,GO:0005515,GO:0003677,GO:0006260,GO:0051028,GO:0048477,GO:0005634,GO:0003729	CG32562-PA						PF03399														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly23615.1	Glucosylceramidase	GO:0006665,GO:0005765,GO:0005975,GO:0034620,GO:0004348	CG31414-PB						PF02055				G3DSA:3.20.20.80,G3DSA:2.60.40.1180	SSF51445									
aly2363.1	Metabotropic glutamate receptor 8	GO:0004930,GO:0042734,GO:0030818,GO:0007200,GO:0016021,GO:0005886,GO:0007608,GO:0030425,GO:0007601,GO:0008066,GO:0051966,GO:0001642,GO:0005887,GO:0017085,GO:0008343,GO:0007186,GO:0016595,GO:0007196	CG30361-PG						PF00003,PF01094,PF07562	PS50259	PR00248,PR00248,PR00248,PR00248,PR00248,PR00248,PR00248,PR00248,PR00593,PR00593,PR00593,PR00593,PR00593	PS00981	G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300	SSF53822	781~801		REACT_14797							
aly2363.2	Transmembrane and coiled-coil domain-containing protein 6	GO:0005737,GO:0008565,GO:0005634,GO:0006606,GO:0046331,GO:0005488,GO:0016021	CG15443-PA				SM00185,SM00185,SM00185						G3DSA:1.25.10.10	SSF48371									
aly2363.3	Coiled-coil domain-containing protein 74B		n/a						PF14916						173~207,258~78,109~157								
aly2363.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2363.5	Unknown		n/a																				
aly2363.6	Cationic amino acid transporter 2	GO:1903352,GO:0042116,GO:0006865,GO:0015189,GO:0050829,GO:0015181,GO:0006809,GO:0002537,GO:0040007,GO:0097639,GO:0097638,GO:0016020,GO:0050727,GO:0005292,GO:1903401,GO:0015297,GO:0006629,GO:0097640,GO:0005887,GO:0005886,GO:0015809,GO:0005289,GO:0097626,GO:0097627,GO:0003333,GO:0015326,GO:0000064,GO:0045824,GO:0043030	CG11128-PA						PF13906,PF13520						582~602,671~691								
aly2363.7	Cationic amino acid transporter 2	GO:1903352,GO:0042116,GO:0006865,GO:0015189,GO:0050829,GO:0015181,GO:0006809,GO:0002537,GO:0040007,GO:0097639,GO:0097638,GO:0016020,GO:0050727,GO:0055085,GO:0005292,GO:1903401,GO:0015297,GO:0006629,GO:0006811,GO:0006810,GO:0097640,GO:0005887,GO:0005886,GO:0006520,GO:0005289,GO:0097626,GO:0097627,GO:0003333,GO:0015326,GO:0000064,GO:0045824,GO:0015174,GO:0043030,GO:0015171	CG11128-PA						PF13520,PF13906														
aly2363.8	Transforming growth factor beta-1-induced transcript 1 protein	GO:0005737,GO:0005856,GO:0016331,GO:0045165,GO:0016363,GO:0010718,GO:0016055,GO:0003713,GO:0030579,GO:0031012,GO:0008270,GO:0030855,GO:0005925,GO:0030511,GO:0030512,GO:0045599,GO:0045893	CG34325-PA				SM00132,SM00132,SM00132		PF00412,PF00412,PF00412	PS50023,PS50023,PS50023		PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716										
aly2370.1	E3 ubiquitin-protein ligase RNF115	GO:0061630,GO:0005829,GO:0042059,GO:0051865,GO:0004842,GO:0008270,GO:0005515,GO:0043162,GO:0070936,GO:0016874,GO:0070534	CG11982-PA				SM00184		PF13639	PS50089			G3DSA:3.30.40.10	SSF57850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2370.10	Heterogeneous nuclear ribonucleoprotein 27C	GO:0048024,GO:0007411,GO:0007298,GO:0000166,GO:0005737,GO:0048027,GO:0043186,GO:0005730,GO:0005634,GO:0030529,GO:0005654,GO:0003730,GO:0045727,GO:0003697,GO:0007317,GO:0046331,GO:0007319,GO:0045451,GO:0043234,GO:0005515,GO:0003729,GO:0006397	CG10377-PA				SM00360,SM00360		PF00076,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									
aly2370.11	Unknown	GO:0006909	CG2993-PC				SM01017		PF02752					SSF81296									
aly2370.12	Importin-11	GO:0005737,GO:0008565,GO:0006610,GO:0006886,GO:0008536,GO:0005634	CG33139-PA				SM00913		PF03810	PS50166			G3DSA:1.25.10.10	SSF48371,SSF48371									
aly2370.13	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG4927-PC						PF00089	PS50240			G3DSA:2.40.10.10	SSF50494									
aly2370.14	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2370.15	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG14642-PB				SM00020		PF00089,PF00089	PS50240		PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2370.16	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2370.17	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2370.18	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089,PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494,SSF50494									
aly2370.19	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2370.2	RNA-binding protein MEX3B	GO:0000932,GO:0005634,GO:0000381,GO:0003723,GO:0008270	CG11360-PA				SM00184,SM00322,SM00322		PF13920,PF00013,PF00013	PS50084,PS50084,PS50089			G3DSA:3.30.40.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10	SSF57850,SSF54791,SSF54791									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2370.20	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2370.21	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2370.3	Coatomer subunit epsilon	GO:0006891,GO:0006890,GO:0006888,GO:0005198,GO:0005654,GO:0015031,GO:0030126,GO:0005875	CG9543-PA			PIRSF016478			PF04733				G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452									
aly2370.4	Collagen and calcium-binding EGF domain-containing protein 1	GO:0060855,GO:0005581,GO:0048845,GO:0001946,GO:0005576,GO:0048514,GO:0005509,GO:0005515,GO:0007412,GO:0002040	CG7526-PD				SM00181,SM00181,SM00179		PF14670			PS00010,PS01187	G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57196									
aly2370.5	Neuroendocrine convertase 1	GO:0004252,GO:0004175,GO:0005615,GO:0034774,GO:0043043,GO:0005788,GO:0005886,GO:0016485,GO:0006508,GO:0030133,GO:0016486	CG18734-PB						PF16470,PF01483,PF00082		PR00723,PR00723,PR00723	PS00138,PS00137	G3DSA:2.60.120.260,G3DSA:3.30.70.850,G3DSA:3.40.50.200	SSF52743,SSF49785									
aly2370.6	Clavesin-2	GO:0008431,GO:0005802,GO:0080025,GO:0005215,GO:0006810,GO:0005622,GO:0007040,GO:0030136,GO:0005768,GO:0031901,GO:0016918	CG10026-PB				SM01100,SM00516		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF46938,SSF52087									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2370.7	Clavesin-2	GO:0008431,GO:0005802,GO:0080025,GO:0005215,GO:0006810,GO:0005622,GO:0007040,GO:0030136,GO:0005768,GO:0031901,GO:0016918	CG10026-PB				SM00516,SM01100		PF00650,PF03765	PS50191	PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087,SSF46938									
aly2370.8	Clavesin-2	GO:0008431,GO:0005802,GO:0080025,GO:0005215,GO:0006810,GO:0005622,GO:0007040,GO:0030136,GO:0005768,GO:0031901,GO:0016918	CG10026-PB				SM01100,SM00516		PF00650,PF03765	PS50191			G3DSA:3.40.525.10	SSF46938,SSF52087									
aly2370.9	Ankyrin-3	GO:0048675,GO:0005200,GO:0005783,GO:0007614,GO:0072660,GO:0019228,GO:0045211,GO:0031594,GO:1900827,GO:0045887,GO:0010628,GO:0000226,GO:0007165,GO:0043266,GO:0007411,GO:0044325,GO:0010960,GO:0071286,GO:0030507,GO:0036062,GO:0000281,GO:0014731,GO:0030315,GO:0043001,GO:0042383,GO:0050808,GO:0033270,GO:0045838,GO:0071709,GO:0072661,GO:0010765,GO:0005794,GO:0014704,GO:0016328,GO:1902260,GO:0007605,GO:0009986,GO:0030674,GO:0016323,GO:0007528,GO:0045296,GO:0007409,GO:0005886,GO:0072659,GO:0045184,GO:0007016,GO:0043195,GO:0043194,GO:0042734,GO:0008092,GO:0007009,GO:0070050,GO:0005764,GO:1900074,GO:0005515,GO:0033268,GO:2000651,GO:0043034	CG42734-PU				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796,PF13637	PS50088,PS50088,PS50297,PS50088,PS50088,PS50088,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403									
aly23726.1	Unknown		CG3655-PC						PF01697														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly23726.2	Apolipophorin 3	GO:0048598,GO:0005605,GO:0009887,GO:0005604,GO:0045089,GO:0006869,GO:0008406,GO:0070831,GO:0009888,GO:0031012,GO:0048513,GO:0008289,GO:0050829,GO:0016477,GO:0005576	CG7123-PA						PF07464				G3DSA:1.20.120.20	SSF47857	219~286,295~315								
aly23726.3	Unknown		n/a																				
aly23726.4	Unknown		n/a																				
aly23726.5	Unknown		n/a																				
aly2375.1	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155		PS00233											
aly2375.10	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2375.11	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2375.12	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2375.13	Pupal cuticle protein Edg-84A	GO:0040003,GO:0005214,GO:0008011,GO:0008010,GO:0031012,GO:0042302	CG2345-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2375.14	Larval/pupal rigid cuticle protein 66	GO:0040003,GO:0005214,GO:0008011,GO:0008010,GO:0031012,GO:0042302	CG2345-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2375.15	Longitudinals lacking protein like	GO:0016319,GO:0035167,GO:0031208,GO:0003677,GO:0001700,GO:0007435,GO:0031519,GO:0006342,GO:0005634,GO:0007476,GO:0016458,GO:0046872,GO:0042803,GO:0045892,GO:0045893,GO:0000794,GO:0007426,GO:0003700,GO:0005700,GO:0048813,GO:0006357,GO:0006351,GO:0016568	CG31666-PE				SM00355,SM00355,SM00225		PF13894,PF00651	PS50157,PS50097,PS50157		PS00028,PS00028	G3DSA:3.30.710.10	SSF54695,SSF57667										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2375.16	Cytochrome b-c1 complex subunit Rieske, mitochondrial	GO:0005743,GO:0016021,GO:0051537,GO:0008121,GO:0006122,GO:0005739,GO:0005750,GO:0070469,GO:0046872,GO:0005875,GO:0055114,GO:0016491	CG7361-PB					TIGR01416	PF02921,PF09165,PF00355	PS51296	PR00162,PR00162,PR00162		G3DSA:1.20.5.270,G3DSA:2.102.10.10	SSF81502,SSF50022		00190+1.10.2.2		PWY-7279,PWY-6692,PWY-7082,PWY-3781					
aly2375.17	Protein spire	GO:0030036,GO:0051639,GO:0007304,GO:0005737,GO:0045010,GO:0051493,GO:0003779,GO:0048471,GO:0048477,GO:0005856,GO:0030029,GO:0008017,GO:0030659,GO:0007315,GO:0005938,GO:0005886,GO:0045451,GO:0007015,GO:0016192,GO:0007316,GO:0030717,GO:0005515,GO:0015031	CG10076-PA										G3DSA:3.30.40.10	SSF57903									
aly2375.2	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG34461-PA						PF00379	PS51155		PS00233											
aly2375.3	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG1919-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2375.4	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG34461-PA						PF00379	PS51155		PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2375.5	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155		PS00233											
aly2375.6	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2375.7	Unknown		n/a																				
aly2375.8	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2375.9	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2379.1	Protein max	GO:0005737,GO:0000122,GO:0003700,GO:0005634,GO:0030425,GO:0005654,GO:0006355,GO:0003677,GO:0046982,GO:0071339	CG9648-PA				SM00353		PF00010	PS50888	PR00044,PR00044,PR00044		G3DSA:4.10.280.10	SSF47459	88~122								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2379.10	Unknown	GO:0070822,GO:0006909,GO:0003677	CG34422-PD						PF11717				G3DSA:2.30.30.270	SSF54160									
aly2379.11	Pre-mRNA-processing factor 39	GO:0000381,GO:0005634,GO:0000398,GO:0005685,GO:0008380,GO:0006397	CG1646-PB				SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386						G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452	261~281								
aly2379.12	39S ribosomal protein L9, mitochondrial	GO:0003735,GO:0044822,GO:0005739,GO:0006412,GO:0005762	CG31478-PA						PF01281				G3DSA:3.40.5.10	SSF55658									
aly2379.13	Unknown		n/a												80~100								
aly2379.14	Unknown		CG13365-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2379.15	Scaffold protein salvador	GO:0042127,GO:0008285,GO:0048863,GO:0010212,GO:0040014,GO:0007444,GO:0046621,GO:0006915,GO:0005737,GO:0043065,GO:0045464,GO:0005912,GO:0005515,GO:0045570,GO:0048814,GO:0072002,GO:0046666,GO:0035329,GO:0072089,GO:0007165	CG33193-PA				SM00456,SM00456		PF00397	PS50020,PS50020,PS50951		PS01159	G3DSA:2.20.70.10,G3DSA:2.20.70.10	SSF51045,SSF51045									
aly2379.16	Diphthine methyl ester synthase	GO:0017183,GO:0008168,GO:0008152,GO:0004164	CG31289-PA			PIRSF036432		TIGR00522	PF00590				G3DSA:3.40.1010.10,G3DSA:3.30.950.10	SSF53790				PWY-6482	UPA00559				
aly2379.17	Rap guanine nucleotide exchange factor 2	GO:0031697,GO:0006930,GO:1990090,GO:0005770,GO:2001214,GO:0005088,GO:0034333,GO:0007476,GO:0030155,GO:0021884,GO:0005085,GO:0043950,GO:0030552,GO:0043234,GO:0043025,GO:0001764,GO:0045202,GO:0019933,GO:0050774,GO:0007412,GO:0061028,GO:0048022,GO:0048471,GO:0005737,GO:0007218,GO:0021591,GO:0043547,GO:0038180,GO:0001568,GO:0050699,GO:0000165,GO:0043005,GO:0016476,GO:0016477,GO:0048477,GO:2001224,GO:0048749,GO:0008285,GO:0007485,GO:0035211,GO:0017034,GO:0017132,GO:2000481,GO:0016327,GO:0005096,GO:0032092,GO:0017016,GO:0032854,GO:0031175,GO:0030165,GO:0005912,GO:0005911,GO:0005886,GO:0031547,GO:0045314,GO:0071880,GO:0035099,GO:0030718,GO:0045860,GO:0007186,GO:0071321,GO:0071320,GO:0048167,GO:0007391,GO:0005622,GO:0010976,GO:2000670,GO:1901888,GO:0070374,GO:0019901,GO:0032486	CG9491-PA				SM00229,SM00314,SM00147,SM00228,SM00100		PF00618,PF00595,PF00617,PF00788	PS50212,PS50009,PS50106,PS50042,PS50200			G3DSA:2.60.120.10,G3DSA:2.30.42.10,G3DSA:3.10.20.90,G3DSA:1.10.840.10,G3DSA:1.20.870.10,G3DSA:1.20.870.10	SSF48366,SSF48366,SSF48366,SSF54236,SSF51206,SSF50156									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2379.18	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	GO:0008601,GO:0005737,GO:0005829,GO:0031430,GO:0000159,GO:0051726,GO:0006914,GO:0016020,GO:0004722,GO:0090219,GO:0000775,GO:0035307,GO:0019900,GO:0007165,GO:0007059,GO:0008340,GO:0090005,GO:0005634,GO:0051225,GO:0030018	CG5643-PB			PIRSF028043			PF01603					SSF48371	457~458		REACT_69000,REACT_152,REACT_11045,REACT_383						
aly2379.19	Unknown	GO:0005515	n/a				SM00015,SM00015		PF00612,PF00612	PS50096			G3DSA:1.20.890.10	SSF47391	62~97								
aly2379.2	Unknown		n/a																				
aly2379.20	Polyglutamine binding protein 1	GO:0016607,GO:0006351,GO:0008022,GO:0072372,GO:0000380,GO:0060271,GO:0071011,GO:0005813,GO:0071013,GO:0000398,GO:0006355,GO:0097546,GO:0005515,GO:0031175,GO:0005634,GO:0008355	CG11820-PA				SM00456		PF00397	PS50020			G3DSA:2.20.70.10	SSF51045									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2379.21	Cystathionine beta-synthase	GO:0001958,GO:0019899,GO:0030170,GO:0043506,GO:0060135,GO:0005737,GO:0050880,GO:0050667,GO:0006535,GO:0005634,GO:0070026,GO:0070025,GO:0043066,GO:0071456,GO:0046872,GO:0042802,GO:0042803,GO:0060351,GO:0020037,GO:0005730,GO:0004122,GO:0051593,GO:0031625,GO:0008340,GO:0050421,GO:0055114,GO:0072341,GO:0021587,GO:0019825,GO:0030823,GO:0043231,GO:0030554,GO:0005829,GO:1904047,GO:0070814,GO:0001974,GO:0019344,GO:0019343,GO:0019346,GO:0006801	CG1753-PA					TIGR01137	PF00291	PS51371,PS51371		PS00901	G3DSA:3.40.50.1100,G3DSA:3.40.50.1100,G3DSA:3.10.580.10,G3DSA:3.40.50.1100	SSF54631,SSF53686		00270+4.2.1.22,00260+4.2.1.22		PWY-801					
aly2379.22	Venom carboxylesterase-6	GO:0016787,GO:0052689,GO:0005575,GO:0005576,GO:0008150,GO:0008152	CG10175-PD						PF00135			PS01173,PS00122,PS00941	G3DSA:3.40.50.1820	SSF53474									
aly2379.23	Lipopolysaccharide-induced tumor necrosis factor-alpha factor homolog	GO:0005737,GO:0006355,GO:0006351	CG13516-PA				SM00714		PF10601														
aly2379.24	Lipopolysaccharide-induced tumor necrosis factor-alpha factor	GO:0005737,GO:0005794,GO:0006351,GO:0007568,GO:0043231,GO:0050699,GO:0071222,GO:0006915,GO:0001817,GO:0005575,GO:0005765,GO:0006357,GO:0003674,GO:0007165,GO:0004871,GO:0005886,GO:0008150,GO:0005654,GO:0042347,GO:0043123	CG30273-PA				SM00714		PF10601														
aly2379.25	NTF2-related export protein	GO:0005737,GO:0006408,GO:0016973,GO:0006611,GO:0005634,GO:0005635,GO:0005654,GO:0006409,GO:0045824,GO:0015031,GO:0009267,GO:0050829,GO:0006406	CG12752-PA						PF02136	PS50177			G3DSA:3.10.450.50	SSF54427									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2379.26	Probable ATP-dependent RNA helicase spindle-E	GO:0003676,GO:0009994,GO:0030423,GO:0030154,GO:0007294,GO:0008186,GO:0007275,GO:0005737,GO:0043186,GO:0009949,GO:0005634,GO:0030720,GO:0010529,GO:0016246,GO:0046872,GO:0048477,GO:0005524,GO:0004004,GO:0004386,GO:0007317,GO:0007315,GO:0031047,GO:0007076,GO:0051321,GO:0001556,GO:0045451,GO:0006403,GO:0007283,GO:0009951,GO:0060213,GO:0030717,GO:0003724,GO:0008298,GO:0006342,GO:0046843	CG3158-PA				SM00847,SM00490,SM00333,SM00487		PF00567,PF04408,PF00270,PF00271	PS51194,PS51192			G3DSA:2.40.50.90,G3DSA:3.40.50.300,G3DSA:2.30.30.140,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF63748										
aly2379.27	C-1-tetrahydrofolate synthase, cytoplasmic	GO:0005737,GO:0004329,GO:0009396,GO:0006730,GO:0005811,GO:0004477,GO:0035999,GO:0004488,GO:0055114,GO:0006164,GO:0000105,GO:0009086,GO:0005829,GO:0005524	CG4067-PB	MF_01576,MF_01543					PF02882,PF01268,PF00763		PR00085,PR00085,PR00085,PR00085,PR00085,PR00085	PS00721,PS00767,PS00722,PS00766	G3DSA:3.10.410.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.192.10,G3DSA:3.40.50.720,G3DSA:3.30.1510.10,G3DSA:3.30.1510.10	SSF51735,SSF53223,SSF52540,SSF52540		00720+6.3.4.3,00720+1.5.1.5+3.5.4.9,00670+1.5.1.5+3.5.4.9,00670+6.3.4.3		PWY-1722,PWY-3841,PWY-2161,PWY-5030,PWY-5497,PWY-2201,PWY-6613	UPA00193				
aly2379.28	G-protein coupled receptor Mth2	GO:0004930,GO:0016021,GO:0016020,GO:0006950,GO:0004888,GO:0007166,GO:0005886,GO:0008340,GO:0007186	CG17061-PB						PF00002	PS50261													
aly2379.29	Intron-binding protein aquarius	GO:0097157,GO:0071011,GO:0071013,GO:0016020,GO:0044822,GO:0000398,GO:0005654,GO:0005634	CG31368-PD						PF16399,PF13087,PF13086				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									
aly2379.3	Testis-specific serine/threonine-protein kinase 2	GO:0005737,GO:0006468,GO:0007286,GO:0005634,GO:0000287,GO:0005814,GO:0046777,GO:0004674,GO:0001669,GO:0004672,GO:0035556,GO:0007275,GO:0005524	CG14305-PA				SM00220		PF00069	PS50011	PR00109,PR00109,PR00109	PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2379.30	Unknown		n/a																				
aly2379.31	Unknown		n/a																				
aly2379.4	Exocyst complex component 5	GO:0005737,GO:0016192,GO:0000145,GO:0016081,GO:0016080,GO:0090522,GO:0006887,GO:0008013,GO:0048278,GO:0007269,GO:0015031	CG6159-PA						PF07393						51~78								
aly2379.5	ATP synthase subunit d, mitochondrial	GO:0000276,GO:0015992,GO:0051881,GO:0046034,GO:0005811,GO:0005739,GO:0005875,GO:0015986,GO:0006979,GO:0032007,GO:0008340,GO:0008553,GO:0070373,GO:0015078	CG6030-PB			PIRSF005514			PF05873					SSF161065	104~124								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2379.6	Protein C-ets-1	GO:2001234,GO:0061331,GO:0061320,GO:0048870,GO:0009997,GO:0008285,GO:0060439,GO:0060438,GO:0035225,GO:0007428,GO:0045467,GO:0001077,GO:0046677,GO:0009612,GO:0003677,GO:0034616,GO:0006909,GO:0001666,GO:0042981,GO:0007265,GO:0070491,GO:0007362,GO:0043565,GO:0050728,GO:0045171,GO:0045648,GO:0007455,GO:0005634,GO:0007476,GO:0030707,GO:0045766,GO:0005654,GO:0021854,GO:0006366,GO:0045765,GO:0000981,GO:0008284,GO:0005737,GO:0030154,GO:0048190,GO:0005667,GO:0007507,GO:0008134,GO:0070301,GO:0032355,GO:0048747,GO:0044849,GO:0007173,GO:0060055,GO:0006955,GO:0045786,GO:0007157,GO:0021983,GO:0007424,GO:0007427,GO:0007426,GO:0010595,GO:0007422,GO:0003700,GO:0007565,GO:0010715,GO:0030578,GO:0007429,GO:0007464,GO:0070555,GO:0006355,GO:0051272,GO:0045944,GO:0006351,GO:0005515,GO:0008293,GO:0045610,GO:0050767,GO:0045893	CG17077-PB				SM00251,SM00413		PF02198,PF00178	PS50061,PS51433	PR00454,PR00454,PR00454,PR00454	PS00346,PS00345	G3DSA:1.10.150.50,G3DSA:1.10.10.10	SSF46785,SSF47769									
aly2379.7	39S ribosomal protein L37, mitochondrial	GO:0003735,GO:0005739,GO:0006412,GO:0005762,GO:0005840	CG42632-PB																				
aly2379.8	E3 ubiquitin-protein ligase HRD1	GO:0005783,GO:0030968,GO:0016874,GO:0016021,GO:0061630,GO:0005789,GO:0016881,GO:0016567,GO:0008270,GO:0005515,GO:0030433,GO:0002039,GO:0004842	CG1937-PA				SM00184		PF13639	PS50089			G3DSA:3.30.40.10	SSF57850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2379.9	AT-rich interactive domain-containing protein 4B	GO:0070822,GO:0006909,GO:0044212,GO:0005634,GO:0006357,GO:0006351,GO:0003677	CG34422-PD				SM01014,SM00501		PF01388,PF08169	PS51011			G3DSA:1.10.150.60	SSF46774,SSF63748									
aly2383.1	Endocuticle structural glycoprotein SgAbd-1	GO:0040003,GO:0005214,GO:0008010,GO:0031012,GO:0022008,GO:0042302	CG8515-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2385.1	Nuclear pore complex protein Nup98-Nup96	GO:0006909,GO:0019221,GO:0034605,GO:0019083,GO:0010827,GO:0042405,GO:0051028,GO:0005487,GO:0034399,GO:0044267,GO:0007264,GO:0042277,GO:0008645,GO:0044615,GO:0005635,GO:0044613,GO:0015758,GO:0010467,GO:0019058,GO:0006260,GO:0007184,GO:0017056,GO:0000278,GO:0005215,GO:0043687,GO:0006810,GO:0031965,GO:0006913,GO:0051292,GO:0007077,GO:0016925,GO:0055085,GO:0000059,GO:0030718,GO:0005975,GO:0031080,GO:0005643,GO:1900034,GO:0005829,GO:0006999,GO:0005515,GO:0005654,GO:0016032,GO:0044281	CG10198-PA						PF04096	PS51434			G3DSA:3.30.1610.10,G3DSA:3.30.1610.10	SSF82215									
aly2386.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2388.1	Unknown		n/a																				
aly2388.2	Telomere-associated protein RIF1	GO:0005720,GO:0035392,GO:0005819,GO:0000077,GO:0001939,GO:0000781,GO:0019827,GO:0001940,GO:0005634,GO:0005737,GO:0006974,GO:0008150,GO:2001034,GO:0005886,GO:0007049	CG30085-PA												840~860								
aly2388.3	Patched domain-containing protein 3	GO:0016328,GO:0016324,GO:0016021,GO:0097225,GO:0010004,GO:0004872,GO:0005886,GO:0008158	CG11212-PA						PF02460	PS50156			G3DSA:1.20.1640.10,G3DSA:1.20.1640.10	SSF82866,SSF82866									
aly2388.4	Unknown		n/a																				
aly239.1	Bromodomain adjacent to zinc finger domain protein 2B	GO:0007399,GO:0006338,GO:0005634,GO:0006355,GO:0045944,GO:0008270,GO:0005515,GO:0003677,GO:0003682,GO:0008134,GO:0006351	CG10897-PE				SM00571,SM00249,SM00297		PF15614,PF02791,PF00628,PF00439	PS50827,PS50014,PS50016	PR00503,PR00503,PR00503,PR00503	PS00633	G3DSA:3.30.40.10,G3DSA:1.20.920.10	SSF47370,SSF57903	902~922,1041~1068,1246~1307,629~656								
aly239.2	Unknown	GO:0003676	n/a				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly239.3	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005886,GO:0006508	CG34350-PB								PR01217,PR01217,PR01217,PR01217,PR01217												
aly239.4	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005886,GO:0006508	CG34350-PB						PF00089	PS50240		PS00134	G3DSA:2.40.10.10	SSF50494									
aly239.5	Bromodomain adjacent to zinc finger domain protein 2B	GO:0007399,GO:0006338,GO:0005634,GO:0006355,GO:0045944,GO:0008270,GO:0005515,GO:0003677,GO:0003682,GO:0008134,GO:0006351	CG10897-PE							PS50982			G3DSA:3.30.890.10	SSF54171	404~437								
aly2394.1	Unknown	GO:0003674,GO:0005576,GO:0008150,GO:0005515	CG13532-PA										G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly2394.2	Unknown		n/a																				
aly2394.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2394.4	Unknown		n/a																				
aly2394.5	Unknown		n/a																				
aly2394.6	Unknown		n/a																				
aly2394.7	Unknown		n/a												94~149								
aly2394.8	Unknown		n/a												21~55								
aly2396.1	Unknown	GO:0016810,GO:0005975	CG15918-PA						PF01522				G3DSA:3.20.20.370	SSF88713									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2396.2	Unknown	GO:0016810,GO:0005975	CG15918-PA						PF01522,PF01522				G3DSA:3.20.20.370,G3DSA:3.20.20.370	SSF88713,SSF88713									
aly2396.3	Unknown	GO:0003824,GO:0016810,GO:0005975	CG15918-PA											SSF88713									
aly2396.4	Unknown		n/a							PS51257													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2396.5	Protein Wnt-4	GO:2001234,GO:0005783,GO:0050840,GO:0007616,GO:0005788,GO:0008584,GO:0022407,GO:0035263,GO:0030501,GO:0001745,GO:0090002,GO:0061382,GO:0051894,GO:0007367,GO:0060914,GO:0016023,GO:0051496,GO:0005771,GO:0005770,GO:0030917,GO:0001822,GO:0033080,GO:0010894,GO:0045836,GO:0045669,GO:0042127,GO:0005796,GO:0048076,GO:0035170,GO:0008585,GO:0035277,GO:0007523,GO:0040037,GO:0007442,GO:0042326,GO:0007447,GO:0007446,GO:0007444,GO:0007448,GO:0048599,GO:0042691,GO:0046847,GO:0061331,GO:0016055,GO:0030336,GO:0090263,GO:0035167,GO:0010629,GO:0035311,GO:0002168,GO:0072033,GO:0007346,GO:0043547,GO:0072034,GO:0071560,GO:0014019,GO:0035217,GO:0035153,GO:0060070,GO:0035017,GO:0035019,GO:0072273,GO:0061184,GO:0007223,GO:0045165,GO:0007423,GO:0048018,GO:2000026,GO:0005539,GO:0006355,GO:0061180,GO:0061369,GO:0035147,GO:0016318,GO:0003714,GO:0009267,GO:0007498,GO:0007450,GO:0035224,GO:0035225,GO:0035220,GO:0007418,GO:0046672,GO:0032967,GO:0010002,GO:0009798,GO:0008544,GO:0030325,GO:0005737,GO:0000122,GO:2000225,GO:0030707,GO:0072091,GO:0008284,GO:0048332,GO:0009986,GO:0051017,GO:0045596,GO:0072162,GO:0032876,GO:0045893,GO:0001658,GO:0060748,GO:0045599,GO:0030139,GO:0035289,GO:0032349,GO:0005578,GO:0005109,GO:0045944,GO:0005515,GO:0016015,GO:0048542,GO:0005102,GO:0045611,GO:0030032,GO:0038030,GO:0061320,GO:0007394,GO:0009996,GO:0061328,GO:0048754,GO:0035288,GO:0003136,GO:0072174,GO:0001889,GO:0061045,GO:0007479,GO:0005615,GO:0007476,GO:0043066,GO:0048728,GO:0005112,GO:0005110,GO:0048749,GO:0006	CG4889-PA				SM00097		PF00110		PR01349,PR01349,PR01349,PR01349	PS00246				REACT_14797							
aly239636.1	Unknown		n/a																				
aly23996.1	Unknown		n/a												72~99,34~61								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly24.1	Facilitated trehalose transporter Tret1	GO:0022891,GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171		G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						
aly24.2	Chymotrypsin-2	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG5255-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly24.3	Vanin-like protein 3	GO:0016787,GO:0016810,GO:0016811,GO:0019898,GO:0017159,GO:0006807	CG32750-PA										G3DSA:3.60.110.10	SSF56317									
aly24.4	Probable 39S ribosomal protein L24, mitochondrial	GO:0005840,GO:0005739,GO:0005622,GO:0003735,GO:0005762,GO:0006412	CG8849-PA				SM00739	TIGR01079	PF00467				G3DSA:2.30.30.30	SSF50104									
aly24.5	V-type proton ATPase subunit C	GO:0016820,GO:0015992,GO:0015991,GO:0007557,GO:0033181,GO:0033180,GO:0000221,GO:0046961,GO:0005886,GO:0015078	CG8048-PC						PF03223				G3DSA:3.30.70.100,G3DSA:1.20.1460.10,G3DSA:1.20.1460.10	SSF118203,SSF118203	135~155								
aly24.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly24.7	ATP synthase subunit gamma, mitochondrial	GO:0045261,GO:0015986,GO:0015992,GO:0046933,GO:0000275,GO:0005811,GO:0005739,GO:0005743,GO:0046961,GO:0006909,GO:0008553	CG7610-PC			PIRSF039089		TIGR01146	PF00231		PR00126,PR00126,PR00126,PR00126	PS00153	G3DSA:3.40.1380.10,G3DSA:1.10.287.80	SSF52943									
aly24.8	Unknown		n/a												521~542,547~585								
aly24.9	Unknown		n/a																				
aly240.1	Unknown	GO:0005515	CG34113-PO				SM00409		PF07686	PS50835			G3DSA:2.60.40.10	SSF48726									
aly240.10	Unknown		n/a																				
aly240.11	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly240.12	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	GO:0008104,GO:0005783,GO:0007295,GO:0042311,GO:0001886,GO:0031418,GO:0001701,GO:0070062,GO:0016705,GO:0048471,GO:0021915,GO:0060425,GO:0032870,GO:0008475,GO:0005506,GO:0055114,GO:0005615,GO:0033823,GO:0030867,GO:0070831,GO:0030199,GO:0048730	CG6199-PA				SM00702			PS51471				SSF53448										
aly240.13	Guanine nucleotide-binding protein subunit beta-2	GO:0005737,GO:0016028,GO:0004871,GO:0016059,GO:0016056,GO:0007601,GO:0007202,GO:0003924,GO:0007602,GO:0005834,GO:0008152,GO:0005886,GO:0046982,GO:0007186	CG8770-PA			PIRSF002394	SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50294,PS50082,PS50082,PS50082	PR00319,PR00319,PR00319,PR00319,PR00319,PR00320,PR00320,PR00320	PS00678,PS00678,PS00678	G3DSA:2.130.10.10	SSF50978										
aly240.14	Alpha-(1,3)-fucosyltransferase C	GO:0036065,GO:0006486,GO:0016021,GO:0016020,GO:0008417,GO:0005886,GO:0032580,GO:0046920	CG40305-PB						PF17039,PF00852					SSF53756					UPA00378				
aly240.15	Unknown		n/a																				
aly240.16	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly240.17	Unknown		n/a																				
aly240.18	Eukaryotic translation initiation factor 4 gamma 1	GO:0000184,GO:0019221,GO:0000082,GO:0000340,GO:0000022,GO:0007067,GO:0001662,GO:0005737,GO:0044267,GO:0000288,GO:0000289,GO:0016281,GO:0016020,GO:0010467,GO:0045666,GO:0006446,GO:0008286,GO:0016032,GO:0044822,GO:0008135,GO:0007052,GO:0008190,GO:0005829,GO:0003723,GO:0005515,GO:0007095,GO:0006413,GO:0006412,GO:0003743	CG10811-PB				SM00543,SM00544		PF02854,PF02847	PS51363,PS51366			G3DSA:1.25.40.180,G3DSA:1.25.40.180,G3DSA:1.25.40.180	SSF48371,SSF48371,SSF48371	1319~1339,1222~1256,1925~1929								
aly240.19	Facilitated trehalose transporter Tret1	GO:0015574,GO:0015771,GO:0016021,GO:0022857,GO:0015749,GO:0005886,GO:0015145,GO:0055085	CG31100-PA						PF00083	PS50850		PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	252~272								
aly240.2	Ras-associated and pleckstrin homology domains-containing protein 1	GO:0048639,GO:0007015,GO:0045927,GO:0032433,GO:0030027,GO:0048675,GO:0030175,GO:0007444,GO:0051781,GO:0005737,GO:0007160,GO:0005856,GO:0008361,GO:0046331,GO:0007165,GO:0008157,GO:0005886	CG11940-PA				SM00314,SM00233		PF00788,PF00169	PS50003,PS50200			G3DSA:2.30.29.30,G3DSA:3.10.20.90	SSF50729,SSF54236									
aly240.20	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly240.21	Zinc finger protein 214	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG11902-PB				SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF13912,PF00096,PF00096,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										
aly240.22	Unknown	GO:0005634,GO:0008150,GO:0008270,GO:0003676,GO:0003677	CG44002-PA				SM00868		PF07776	PS50157		PS00028		SSF57716,SSF57667									
aly240.23	Unknown		n/a																				
aly240.24	Tetratricopeptide repeat protein 39A		n/a						PF10300														
aly240.25	Tetratricopeptide repeat protein 39B		n/a						PF10300														
aly240.26	Insulin-like growth factor 2 mRNA-binding protein 2	GO:0005737,GO:0005856,GO:0048027,GO:0045182,GO:0005829,GO:0044822,GO:0000166,GO:0010467,GO:0042035,GO:0003730,GO:0003676,GO:0017148,GO:0051028,GO:0009653,GO:0005634	n/a				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly240.27	Insulin-like growth factor 2 mRNA-binding protein 1	GO:0051124,GO:0030426,GO:0030175,GO:0022013,GO:0070934,GO:0070937,GO:0048027,GO:0051028,GO:0005634,GO:0000166,GO:0030027,GO:0003730,GO:0048471,GO:0097150,GO:0071011,GO:0071013,GO:0007283,GO:0010976,GO:0045182,GO:0010494,GO:0010610,GO:0007399,GO:0000398,GO:0003723,GO:0017148,GO:0003729	CG1691-PL				SM00322,SM00322,SM00322,SM00322,SM00360		PF00013,PF00013,PF00013,PF00013,PF00076	PS50084,PS50084,PS50102,PS50084,PS50084			G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.70.330,G3DSA:3.30.1370.10	SSF54791,SSF54791,SSF54928,SSF54791,SSF54791										
aly240.28	Unknown		n/a										G3DSA:3.30.40.10	SSF57903	174~201								
aly240.29	Unknown		n/a																				
aly240.3	Venom carboxylesterase-6	GO:0005576,GO:0052689	CG6414-PA						PF00135			PS00122,PS00941,PS01173	G3DSA:3.40.50.1820	SSF53474									
aly240.30	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly240.31	Muscle M-line assembly protein unc-89	GO:0005089,GO:0019902,GO:0031034,GO:0043547,GO:0032041,GO:0031672,GO:0017048,GO:0031430,GO:0004672,GO:0005524	CG14141-PA				SM00408		PF07679	PS50835			G3DSA:2.60.40.10	SSF48726									
aly240.32	Unknown		n/a																				
aly240.4	Catalase	GO:0007568,GO:0035206,GO:0020037,GO:0042542,GO:0038001,GO:0016209,GO:0005886,GO:0005777,GO:0016339,GO:0003007,GO:0045471,GO:0042744,GO:0072593,GO:0004096,GO:0008340,GO:0046872,GO:0006979,GO:0055114	CG6871-PA			PIRSF038928	SM01060		PF06628,PF00199	PS51402	PR00067,PR00067,PR00067,PR00067,PR00067,PR00067	PS00437,PS00438	G3DSA:2.40.180.10	SSF56634		00630+1.11.1.6,00380+1.11.1.6		PWY-5506					
aly240.5	Nuclease-sensitive element-binding protein 1	GO:0051020,GO:0001077,GO:0044822,GO:0003676,GO:0003677,GO:0070934,GO:0070937,GO:0005737,GO:0001701,GO:0070062,GO:0000122,GO:0005634,GO:0030529,GO:0005654,GO:0010467,GO:0006366,GO:0003690,GO:0048477,GO:0008380,GO:0071011,GO:0071013,GO:0031965,GO:0051154,GO:0010494,GO:0043231,GO:0003700,GO:0000398,GO:0003697,GO:0006355,GO:0051781,GO:0045944,GO:0003723,GO:0005689,GO:0000978,GO:0003682,GO:0071204,GO:0003729	CG5654-PA						PF00313		PR00050,PR00050		G3DSA:2.40.50.140	SSF50249									
aly240.6	Potassium channel subfamily T member 1	GO:0005267,GO:0006813,GO:0016021,GO:0016020,GO:0048812,GO:0005886,GO:0022008,GO:0015269	CG42732-PD						PF03493,PF07885				G3DSA:3.40.50.720,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly240.7	Unknown		n/a																				
aly240.8	Unknown		n/a																				
aly240.9	Unknown		n/a																				
aly24045.1	Unknown		n/a																				
aly2406.1	Unknown		n/a																				
aly2406.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2406.3	Unknown	GO:0008270,GO:0003676	n/a				SM00343,SM00343			PS50158			G3DSA:4.10.60.10	SSF57756									
aly2417.1	Troponin I	GO:0007507,GO:0007517,GO:0007399,GO:0030239,GO:0007519,GO:0005634,GO:0000280,GO:0046716,GO:0003779,GO:0048738,GO:0060047,GO:0045214,GO:0005523,GO:0046872,GO:0005861	CG7178-PG						PF00992				G3DSA:1.20.5.350	SSF90250	64~88,103~133		REACT_17044						
aly2417.10	Histone deacetylase complex subunit SAP30 homolog	GO:0005634,GO:0003714,GO:0006355,GO:0006351,GO:0003677,GO:0046872	CG4756-PA						PF13866,PF13867														
aly2417.11	High mobility group protein DSP1	GO:0017055,GO:0032502,GO:0006338,GO:0000122,GO:0007379,GO:0017025,GO:0005634,GO:0005700,GO:0035218,GO:0008348,GO:0008301,GO:0003697,GO:0003677,GO:0043388,GO:0045892,GO:0006268,GO:0008134	CG12223-PF				SM00398,SM00398		PF00505,PF09011	PS50118,PS50118	PR00886,PR00886,PR00886,PR00886		G3DSA:1.10.30.10,G3DSA:1.10.30.10	SSF47095,SSF47095	321~340,108~135								
aly2417.12	Transmembrane and TPR repeat-containing protein CG4050	GO:0016021,GO:0017122,GO:0008150,GO:0005515,GO:0016262	CG4050-PA				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF08409,PF13181,PF13424,PF13424,PF13414	PS50005,PS50005,PS50293,PS50005,PS50005,PS50005,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452									
aly2417.2	Tetratricopeptide repeat protein 17	GO:0005737,GO:0015629,GO:0005575,GO:0008150,GO:0005515,GO:0005886,GO:0030041,GO:0003674,GO:0044782	CG11436-PA				SM00028,SM00028,SM00028		PF13181,PF13181	PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452	320~347								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2417.3	Post-GPI attachment to proteins factor 2-like	GO:0005575,GO:0003674,GO:0016021,GO:0008150	CG7990-PA						PF10277														
aly2417.4	Protein scalloped	GO:0055013,GO:0035220,GO:0007293,GO:0001745,GO:0035331,GO:0007049,GO:0005634,GO:0007476,GO:0046872,GO:0000980,GO:0007480,GO:0008134,GO:0060429,GO:0019904,GO:0007525,GO:0044212,GO:0007423,GO:0007399,GO:0003700,GO:0003705,GO:0006355,GO:0006357,GO:0045944,GO:0006351,GO:0072089	CG8544-PQ				SM00426		PF01285	PS51088	PR00065,PR00065,PR00065	PS00554												
aly2417.5	Glucosylceramidase	GO:0034620,GO:0005765,GO:0005975,GO:0004348,GO:0006665	CG31414-PB						PF02055		PR00843,PR00843,PR00843,PR00843		G3DSA:2.60.40.1180,G3DSA:3.20.20.80	SSF51445									
aly2417.6	Mitochondrial inner membrane protease subunit 1	GO:0042720,GO:0016021,GO:0006627,GO:0005739,GO:0005743,GO:0005740,GO:0006508,GO:0008236	CG9240-PA					TIGR02227	PF00717		PR00727,PR00727,PR00727		G3DSA:2.10.109.10	SSF51306									
aly2417.7	Zinc/cadmium resistance protein	GO:0000324,GO:0016324,GO:0006812,GO:0016021,GO:0005886,GO:0006882,GO:0016323,GO:0071577,GO:0005385,GO:0046686,GO:0031966,GO:0055069,GO:0055085	CG17723-PF					TIGR01297	PF01545				G3DSA:1.20.1510.10,G3DSA:1.20.1510.10	SSF160240,SSF161111,SSF161111									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2417.8	Glutamate receptor ionotropic, delta-1	GO:0045211,GO:0009593,GO:0035199,GO:0008328,GO:0035235,GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0034220,GO:0030054,GO:0004970,GO:0005886,GO:0035176,GO:0030425,GO:0035249,GO:1902075,GO:0070062	CG7385-PA						PF00060				G3DSA:3.40.190.10,G3DSA:1.10.287.70	SSF53850,SSF53850										
aly2417.9	Exosome complex component RRP45	GO:0005737,GO:0005654,GO:0000178,GO:0071028,GO:0070062,GO:0071035,GO:0045111,GO:0030307,GO:0044822,GO:0005730,GO:0000176,GO:0000177,GO:0000175,GO:0017091,GO:0006364,GO:0000228,GO:0043928,GO:0006397	CG9606-PA						PF01138				G3DSA:3.30.230.70	SSF55666,SSF54211,SSF54211			REACT_21257						
aly2420.1	40S ribosomal protein S17	GO:0000028,GO:0005840,GO:0005622,GO:0003735,GO:0006414,GO:0006412,GO:0022627	CG3922-PB						PF00833														
aly242142.1	Unknown		n/a																				
aly242289.1	Muscle M-line assembly protein unc-89	GO:0005089,GO:0006468,GO:0031430,GO:0043547,GO:0030241,GO:0035023,GO:0017048,GO:0031034,GO:0045214,GO:0031672,GO:0004672,GO:0019902,GO:0005524,GO:0007527	CG33519-PC				SM00409,SM00408		PF07679	PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly2423.1	Alpha-2-macroglobulin receptor-associated protein	GO:0032091,GO:0031982,GO:0005783,GO:0009986,GO:0010916,GO:0008201,GO:0048019,GO:0048237,GO:0005576,GO:1900222,GO:0005886,GO:0070326,GO:1900116,GO:0005875,GO:0050750	CG8507-PA						PF06401				G3DSA:1.20.81.10	SSF47045,SSF47045	162~182								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2423.10	Soluble guanylate cyclase 89Da	GO:0046982,GO:0020037,GO:0008074,GO:0004383,GO:0005525,GO:0000302,GO:0046872,GO:0006184,GO:0035556,GO:0001666,GO:0006182	CG14885-PB				SM00044		PF07700,PF07700,PF07701,PF00211	PS50125			G3DSA:3.30.70.1230,G3DSA:3.90.1520.10,G3DSA:3.90.1520.10	SSF111126,SSF55073	541~561	00230+4.6.1.2							
aly2423.2	Unknown		n/a																				
aly2423.3	Ankyrin repeat domain-containing protein 17	GO:0007492,GO:0005200,GO:0019730,GO:0000785,GO:0042742,GO:0007169,GO:0051298,GO:0005737,GO:0045787,GO:1900246,GO:0005634,GO:0016020,GO:0043066,GO:1900245,GO:0045087,GO:1900087,GO:0046427,GO:0008283,GO:0043123,GO:0044822,GO:0051151,GO:0001751,GO:0007016,GO:0001955,GO:0005811,GO:0006275,GO:0003723,GO:0003682	CG33106-PC				SM00248,SM00322		PF13637,PF12796,PF12796,PF12796,PF12796,PF12796,PF12796,PF12796,PF00013,PF00023	PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50297,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50084,PS50088,PS50088,PS50088,PS50088	PR01415,PR01415	G3DSA:3.30.1370.10,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF54791,SSF48403,SSF48403	997~1017,1548~1573								
aly2423.4	Solute carrier family 35 member F4	GO:0016021,GO:0006810	CG42322-PN											SSF103481									
aly2423.5	Polycomb protein EED	GO:0005737,GO:0035098,GO:0006349,GO:0070734,GO:0005730,GO:0045120,GO:0061087,GO:0006355,GO:0001739,GO:0042054,GO:0006351,GO:0005515,GO:0003682	CG5202-PA				SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50294,PS50082,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2423.6	Transmembrane protease serine 6	GO:0004252,GO:0042730,GO:0006879,GO:0005615,GO:0016021,GO:0033619,GO:0045944,GO:0055072,GO:0045892,GO:0097264,GO:0005886,GO:0006508,GO:0030514	CG11836-PI				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2423.7	Trypsin-1	GO:0007586,GO:0006508,GO:0046872,GO:0005615,GO:0004252	CG4386-PA				SM00020		PF00089,PF00089	PS51257,PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2423.8	Unknown		n/a																				
aly2423.9	Glucose transporter type 1	GO:0022891,GO:0005355,GO:0016021,GO:0016020,GO:0008643,GO:0055085	CG43946-PP					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171,PR00171,PR00171	PS00217,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						
aly24262.1	Organic cation transporter protein	GO:0055085,GO:0006811,GO:0006915,GO:0008513,GO:0022857,GO:0016021	CG7442-PA						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly24356.1	Unknown		n/a												51~71								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2437.1	Unknown	GO:0016198,GO:0005576,GO:0003674,GO:0001746,GO:0007411,GO:0007415	CG4846-PB						PF08205				G3DSA:2.60.40.10,G3DSA:2.60.40.10										
aly24380.1	Facilitated trehalose transporter Tret1-2 homolog	GO:0005355,GO:0022891,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473	236~256								
aly2448.1	Unknown		n/a																				
aly2448.2	Uncharacterized 50 kDa protein in type I retrotransposable element R1DM	GO:0008270,GO:0003676	n/a				SM00343,SM00343			PS50158			G3DSA:4.10.60.10	SSF57756									
aly2448.3	Unknown		n/a											SSF50630									
aly2452.1	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0003851,GO:0008152	CG4739-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly24583.1	Esterase FE4	GO:0005737,GO:0005811,GO:0052689,GO:0019915,GO:0008340,GO:0046683	CG1112-PA						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly24589.1	Unknown		n/a																				
aly24589.2	Unknown		n/a																				
aly2462.1	Chaoptin	GO:0004930,GO:0016028,GO:0042052,GO:0050896,GO:0007601,GO:0035996,GO:0046658,GO:0005515,GO:0005886,GO:0007156	CG4168-PC				SM00082,SM00369,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365		PF00560,PF13855,PF13855,PF13855,PF13855,PF13855	PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047,SSF52058,SSF52058,SSF52058,SSF52058									
aly2462.2	Aldo-keto reductase AKR2E4	GO:0004032,GO:0008202,GO:0055114,GO:0016491	CG12766-PA						PF00248		PR00069,PR00069,PR00069	PS00062	G3DSA:3.20.20.100	SSF51430									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly24621.1	Unknown		n/a																				
aly246277.1	DnaJ protein homolog	GO:0006457,GO:0031072,GO:0051082,GO:0005886,GO:0009408,GO:0022008,GO:0046872,GO:0005524	CG8863-PA										G3DSA:2.60.260.20										
aly2468.1	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG6475-PD						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									
aly2468.2	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0005515,GO:0048812,GO:0005887,GO:0005886,GO:0007155,GO:0007156,GO:0042802	CG31190-PE				SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00060,SM00060		PF13927,PF13927,PF07679,PF07679,PF07679,PF07679,PF13895,PF00041	PS50835,PS50835,PS50853,PS50835,PS50853,PS50853,PS50835,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF49265,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF48726									
aly2468.3	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0007156,GO:0005887,GO:0055085,GO:0045433,GO:0007638,GO:0048812,GO:0009987,GO:0042493,GO:0009612,GO:0006814,GO:0005248,GO:0042802,GO:0005509,GO:0005515,GO:0007268,GO:0005886,GO:0001666,GO:0046684,GO:0046680,GO:0001518	CG17800-PBX							PS50835			G3DSA:2.60.40.10										
aly2468.4	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0007156,GO:0005887,GO:0042802,GO:0048812	CG42256-PP							PS50835,PS50835			G3DSA:2.60.40.10	SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2468.5	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0005515,GO:0048812,GO:0005887,GO:0005886,GO:0007155,GO:0007156,GO:0042802	CG31190-PE				SM00409,SM00408		PF13895	PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726									
aly2468.6	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0005887,GO:0007156,GO:0042802,GO:0005515,GO:0048812	CG42256-PP				SM00408,SM00408,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409,SM00409,SM00060,SM00060,SM00060,SM00060,SM00060		PF13927,PF00041,PF00041,PF00041,PF00041,PF07679,PF07679,PF07679	PS50853,PS50853,PS50835,PS50835,PS50853,PS50835,PS50853,PS50835,PS50853,PS50853,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF49265,SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265									
aly2468.7	Odorant receptor 85b	GO:0005549,GO:0007608,GO:0016021,GO:0005886,GO:0050911,GO:0004984,GO:0032590	CG11735-PA						PF02949						13~33								
aly2468.8	Unknown		n/a						PF12272														
aly24754.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly24800.1	Unknown		n/a																				
aly24816.1	Unknown		n/a																				
aly2484.1	Unknown	GO:0033109,GO:0006468,GO:0032879,GO:0000132,GO:0000902,GO:0008283,GO:0000281,GO:0032154,GO:1990023,GO:0004674,GO:0007052,GO:0005938,GO:0004702,GO:0042801,GO:0010800,GO:0007091,GO:0005524	CG4527-PD																				
aly24842.1	Glandular kallikrein	GO:0004252,GO:0005576,GO:0006508	CG12386-PA						PF00089			PS00135	G3DSA:2.40.10.10	SSF50494									
aly24842.2	Unknown		CG7381-PA						PF01683,PF01683														
aly24842.3	Unknown		n/a						PF01683														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly24847.1	ATP-binding cassette sub-family A member 2	GO:0043190,GO:0042626,GO:0008152,GO:0006869,GO:0016023,GO:0005215,GO:0016021,GO:0006810,GO:0005815,GO:0005764,GO:0005765,GO:0006357,GO:0048545,GO:0016887,GO:0042632,GO:0032383,GO:0005768,GO:0055085,GO:0005524,GO:0010008	CG1718-PB						PF00005				G3DSA:3.40.50.300	SSF52540										
aly2485.1	Unknown		n/a																				
aly2485.2	Chymotrypsin-like elastase family member 2A	GO:0004252,GO:0005576,GO:0061436,GO:0006508	CG31326-PA				SM00020,SM00020		PF00089,PF00089	PS50240,PS50240	PR00722,PR00722,PR00722	PS00134,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494,SSF50494										
aly2485.3	Unknown		n/a																				
aly2485.4	Proclotting enzyme	GO:0004252,GO:0005576,GO:0042381	n/a										G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2485.5	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG9447-PC						PF01757														
aly2485.6	Unknown		n/a																				
aly2485.7	Odorant receptor Or2	GO:0005549,GO:0007608,GO:0042048,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984	CG15377-PA						PF02949														
aly2485.8	Unknown		n/a																				
aly248669.1	Unknown		n/a																				
aly2487.1	Transmembrane protein 245	GO:0016021	CG2698-PD																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2487.10	L-threonine ammonia-lyase	GO:0006567,GO:0030170,GO:0008152,GO:0009097,GO:0004794,GO:0003941,GO:0016597	CG8129-PB						PF00291				G3DSA:3.40.50.1100	SSF53686									
aly2487.11	DNA-directed RNA polymerase II subunit RPB3	GO:0034605,GO:0003677,GO:0050434,GO:0034587,GO:0005875,GO:0005737,GO:0005634,GO:0005654,GO:0010467,GO:0006367,GO:0006366,GO:0006368,GO:0008380,GO:0015630,GO:0006283,GO:0006281,GO:0006289,GO:0035019,GO:0005703,GO:0000398,GO:0006370,GO:0005665,GO:0006351,GO:0016032,GO:0003899,GO:0046983	CG7885-PA				SM00662		PF01000,PF01193			PS00446	G3DSA:3.30.1360.10,G3DSA:3.30.1360.10,G3DSA:2.170.120.12	SSF56553,SSF55257,SSF55257		00240+2.7.7.6,00230+2.7.7.6	REACT_1788						
aly2487.12	L-threonine ammonia-lyase	GO:0006567,GO:0030170,GO:0008152,GO:0009097,GO:0004794,GO:0003941,GO:0016597	CG8129-PB					TIGR01127	PF00291				G3DSA:3.30.70.260,G3DSA:3.40.50.1100	SSF53686		00290+4.3.1.19,00260+4.3.1.19			UPA00052				
aly2487.13	L-threonine ammonia-lyase	GO:0006567,GO:0030170,GO:0008152,GO:0009097,GO:0004794,GO:0003941,GO:0016597	CG8129-PB						PF00291,PF00291				G3DSA:3.40.50.1100,G3DSA:3.40.50.1100,G3DSA:3.40.50.1100	SSF53686,SSF53686									
aly2487.14	Pterin-4-alpha-carbinolamine dehydratase	GO:0006729,GO:0008124	CG1963-PA	MF_00434					PF01329				G3DSA:3.30.1360.20	SSF55248				PWY-7158					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2487.15	DNA repair protein XRCC3	GO:0009994,GO:0090267,GO:0030261,GO:0010824,GO:0007294,GO:0003677,GO:0005737,GO:0007126,GO:0006302,GO:0000724,GO:0009949,GO:0005634,GO:0033065,GO:0005739,GO:0005657,GO:0048471,GO:0048477,GO:0005524,GO:0006281,GO:0006974,GO:0007131,GO:0010033,GO:0006310,GO:0008094,GO:0009951,GO:0000150,GO:0030717,GO:0008298,GO:0006417,GO:0071140	CG3325-PA			PIRSF005856	SM00382		PF08423	PS50162			G3DSA:3.40.50.300	SSF52540									
aly2487.16	CCA tRNA nucleotidyltransferase 1, mitochondrial	GO:0052927,GO:0005739,GO:0005622,GO:0001680,GO:0004810,GO:0006626,GO:0009022,GO:0052928,GO:0004652,GO:0042780,GO:0003723,GO:0000049,GO:0022008,GO:0052929,GO:0005524	CG2100-PA						PF12627,PF01743				G3DSA:1.10.3090.10,G3DSA:3.30.460.10	SSF81891,SSF81301	450~458								
aly2487.17	Signal recognition particle 54 kDa protein	GO:0005786,GO:0016607,GO:0030942,GO:0005048,GO:0042493,GO:0005634,GO:0003924,GO:0006614,GO:0006617,GO:0008144,GO:0019003,GO:0008312,GO:0045047,GO:0008152,GO:0005525	CG4659-PA	MF_00306			SM00962,SM00382,SM00963	TIGR01425	PF02881,PF00448,PF02978			PS00300	G3DSA:1.20.120.140,G3DSA:3.30.40.10,G3DSA:1.10.260.30,G3DSA:3.40.50.300	SSF57845,SSF47446,SSF52540,SSF47364,SSF57903			REACT_15380					
aly2487.18	26S protease regulatory subunit 4	GO:0004175,GO:0036402,GO:0017025,GO:0031595,GO:0031597,GO:0016887,GO:0000022,GO:0008540,GO:0005737,GO:0005838,GO:0043161,GO:0006511,GO:1901800,GO:0006508,GO:0005524,GO:0008283,GO:0009987,GO:0017111,GO:0006974,GO:0007052,GO:0030163,GO:0030433,GO:0000502,GO:0045899,GO:0090307	CG5289-PA				SM00382	TIGR01242	PF00004			PS00674	G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2487.19	Presenilin homolog	GO:0004175,GO:0016337,GO:0055037,GO:0030426,GO:0030424,GO:0031594,GO:0042987,GO:0050435,GO:0030018,GO:0005737,GO:0007219,GO:0005765,GO:0005634,GO:0005770,GO:0070765,GO:0043066,GO:0006509,GO:0048471,GO:0043025,GO:0042803,GO:0016324,GO:0048190,GO:0035253,GO:0009986,GO:0006915,GO:0006816,GO:0015677,GO:0046331,GO:0005938,GO:0005887,GO:0008593,GO:0005789,GO:0002027,GO:0007220,GO:0007010,GO:0043198,GO:0045121,GO:0000139,GO:0005743,GO:0048812,GO:0004190,GO:0016021,GO:0007338	CG18803-PA				SM00730		PF01080		PR01072,PR01072,PR01072,PR01072						REACT_29,REACT_11061							
aly2487.2	Beta-mannosidase	GO:0005764,GO:0046355,GO:0004567	CG12582-PA						PF00703				G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:2.60.40.320,G3DSA:2.60.120.260,G3DSA:2.60.120.260	SSF49785,SSF49303,SSF49303,SSF51445										
aly2487.20	Adipocyte plasma membrane-associated protein	GO:0004252,GO:0070062,GO:0016844,GO:0009986,GO:0005811,GO:0009058,GO:0004872,GO:0004064,GO:0016021,GO:0003729	CG3373-PA						PF03088				G3DSA:2.120.10.30	SSF63829,SSF63829										
aly2487.21	Unknown		CG31142-PA						PF09811														
aly2487.22	Mediator of RNA polymerase II transcription subunit 6	GO:0005737,GO:0045824,GO:0005515,GO:0006357,GO:0005634,GO:0003713,GO:0001104,GO:0046331,GO:0006351,GO:0006367,GO:0006366,GO:0050829,GO:0016592	CG9473-PB						PF04934														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2487.23	Cysteine protease ATG4D	GO:0005737,GO:0006995,GO:0016485,GO:0000422,GO:0035071,GO:0006914,GO:0006915,GO:0000045,GO:0006501,GO:0048102,GO:0044804,GO:0004197,GO:0006612,GO:0005759,GO:0006508,GO:0005829,GO:0051697	CG6194-PA						PF03416					SSF54001,SSF54001										
aly2487.24	Protein farnesyltransferase subunit beta	GO:0048146,GO:0008144,GO:0008270,GO:0022400,GO:0005875,GO:0014070,GO:0042277,GO:0045787,GO:0005965,GO:0005968,GO:0051770,GO:0042127,GO:0008285,GO:0034097,GO:0007603,GO:0042060,GO:0010035,GO:0018343,GO:0016056,GO:0005829,GO:0019840,GO:0004311,GO:0004663,GO:0004660	CG17565-PA						PF00432,PF00432,PF00432,PF00432,PF00432				G3DSA:1.50.10.20	SSF48239										
aly2487.25	Digestive organ expansion factor homolog	GO:0032040,GO:0005730,GO:0005634,GO:0044822,GO:0007275,GO:0000462,GO:0034511,GO:0019843,GO:0022008	CG3735-PA						PF06862,PF06862				G3DSA:3.40.50.300		43~66								
aly2487.26	Unknown		n/a						PF15018														
aly2487.27	Luciferin 4-monooxygenase	GO:0046872,GO:0006637,GO:0045289,GO:0004321,GO:0005777,GO:0004467,GO:0046949,GO:0001676,GO:0008218,GO:0047077,GO:0005524	CG6178-PA						PF13193,PF00501			PS00455	G3DSA:3.40.50.980,G3DSA:3.30.300.30,G3DSA:3.40.50.980,G3DSA:2.30.38.10	SSF56801										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2487.28	Luciferin 4-monooxygenase	GO:0046872,GO:0006637,GO:0045289,GO:0004321,GO:0005777,GO:0004467,GO:0046949,GO:0001676,GO:0008218,GO:0047077,GO:0005524	CG6178-PA						PF13193,PF00501			PS00455	G3DSA:3.30.300.30,G3DSA:3.40.50.980,G3DSA:3.40.50.980	SSF56801										
aly2487.29	3'(2'),5'-bisphosphate nucleotidase 1	GO:0006139,GO:0070062,GO:0007399,GO:0008441,GO:0016311,GO:0005829,GO:0006805,GO:0044281,GO:0046854,GO:0050427,GO:0046872	CG7789-PA						PF00459			PS00629,PS00630	G3DSA:3.40.190.80,G3DSA:3.30.540.10	SSF56655									
aly2487.3	Unknown		CG14253-PB												519~523								
aly2487.30	Zinc finger protein 333	GO:0031936,GO:0043565,GO:0005515,GO:0005634,GO:0005700,GO:0006355,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0000785,GO:0046872,GO:0043035	CG8573-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667	405~425									
aly2487.31	TRAF3-interacting protein 1	GO:0005737,GO:0030992,GO:0042384,GO:0005813,GO:0008017,GO:0048793,GO:0042073,GO:0030990,GO:0005929	CG3259-PA						PF10243						538~558,584~604								
aly2487.32	Unknown	GO:0005634,GO:0008270	CG31109-PA				SM00868		PF07776					SSF57716									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2487.33	DNA-directed RNA polymerases I and III subunit RPAC1	GO:0005736,GO:0000183,GO:0003677,GO:0005654,GO:0006360,GO:0006351,GO:0005666,GO:0003899,GO:0046983,GO:0006383,GO:0005875	CG3756-PA				SM00662		PF01193,PF01000			PS00446	G3DSA:3.30.1360.10,G3DSA:3.30.1360.10,G3DSA:2.170.120.12	SSF56553,SSF55257,SSF55257	316~334	00240+2.7.7.6,00230+2.7.7.6	REACT_1788						
aly2487.34	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 8	GO:0008137,GO:0006120,GO:0005747,GO:0005758,GO:0003954,GO:0055114	CG3683-PA						PF06747														
aly2487.35	Unknown		CG12947-PC																				
aly2487.36	Uncharacterized protein C15orf41 homolog	GO:0005575,GO:0003674,GO:0008150	CG12713-PA						PF14811														
aly2487.37	Putative OPA3-like protein CG13603	GO:0005575,GO:0003674,GO:0008150	CG13601-PB						PF07047														
aly2487.38	DNA-directed RNA polymerase III subunit RPC6	GO:0045089,GO:0051607,GO:0005634,GO:0005666,GO:0006351,GO:0032728,GO:0003677,GO:0003899,GO:0022008,GO:0006383,GO:0045087	CG5380-PA			PIRSF028763			PF05158					SSF46785,SSF46785									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2487.39	Glucoside xylosyltransferase 1	GO:0035252,GO:0016021,GO:0016266,GO:0016757	CG9996-PB						PF01501				G3DSA:3.90.550.10	SSF53448									
aly2487.4	Probable cytochrome P450 6a14	GO:0004497,GO:0043231,GO:0020037,GO:0016705,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG8687-PD						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly2487.40	Epididymal secretory protein E1	GO:0032934,GO:0032504,GO:0015485,GO:0015918,GO:0032366,GO:0070062,GO:0019899,GO:0030301,GO:0005764,GO:0009615,GO:0033344,GO:0032367,GO:0045456,GO:0042632,GO:0008203,GO:0005783,GO:0005615	CG3153-PB				SM00737		PF02221				G3DSA:2.60.40.770	SSF81296									
aly2487.41	Ecdysteroid-regulated 16 kDa protein	GO:0032934,GO:0032504,GO:0015918,GO:0005576,GO:0045456,GO:0005615	CG3153-PB				SM00737		PF02221				G3DSA:2.60.40.770	SSF81296									
aly2487.42	Dimethyladenosine transferase 2, mitochondrial	GO:0000179,GO:0003712,GO:0005739,GO:0006355,GO:0005759,GO:0003723,GO:0031167,GO:0006390,GO:0006391	CG3910-PA			PIRSF027833			PF00398	PS51689			G3DSA:3.40.50.150	SSF53335									
aly2487.43	Unknown	GO:0008565,GO:0048749,GO:0042051,GO:0046907,GO:0032588,GO:0035650	CG8538-PC						PF15045														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2487.44	Unknown	GO:0005811	CG18212-PG						PF05104						47~81,473~535,431~465,582~666,697~742,382~402,744~764								
aly2487.45	WD repeat-containing protein 37	GO:0046331,GO:0005515	CG12333-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50082,PS50294	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978									
aly2487.46	Transcriptional adapter 2B	GO:0000124,GO:0006351,GO:0035066,GO:0006338,GO:2000331,GO:0004402,GO:0005634,GO:0035222,GO:0035079,GO:0006355,GO:0006357,GO:0008270,GO:0005515,GO:0003677,GO:0007412,GO:0003682,GO:0005700,GO:0043966	CG9638-PB			PIRSF025024	SM00291,SM00717		PF00569,PF00249	PS50135,PS51293		PS01357	G3DSA:1.10.10.60	SSF57850,SSF46689,SSF46689									
aly2487.47	Cyclin-dependent kinase 20	GO:0005737,GO:0006468,GO:0060271,GO:0005634,GO:0005929,GO:0004674,GO:0005524,GO:0051301,GO:0004672,GO:0004693,GO:0007275,GO:0007049	CG6800-PA				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly2487.48	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG31002-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly2487.49	JNK1/MAPK8-associated membrane protein	GO:0031625,GO:0006986,GO:0016021,GO:0005789,GO:0030433	CG2126-PB						PF05571														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2487.5	Kinesin-like protein KIF16B	GO:0007492,GO:0032801,GO:0005871,GO:0008543,GO:0080025,GO:0001704,GO:0005874,GO:0005547,GO:0043325,GO:0031901,GO:0008017,GO:0003777,GO:0007173,GO:0045022,GO:0008574,GO:0006895,GO:0035091,GO:0007018,GO:0032266,GO:0005524,GO:0001919,GO:0005768,GO:0005769	CG5658-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380		G3DSA:3.40.850.10	SSF52540	1064~1084								
aly2487.50	Unknown		n/a																				
aly2487.51	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0005515,GO:0048812,GO:0005887,GO:0005886,GO:0007155,GO:0007156,GO:0042802	CG31190-PE				SM00060,SM00060,SM00060,SM00060,SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408,SM00408		PF13895,PF13927,PF00041,PF00041,PF00041,PF00041,PF07679,PF07679,PF07679	PS50853,PS50853,PS50835,PS50835,PS50853,PS50835,PS50853,PS50835,PS50853,PS50835,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF48726,SSF48726,SSF49265,SSF48726,SSF49265,SSF48726,SSF48726,SSF48726									
aly2487.52	Protein NDRG3	GO:0005737,GO:0070062,GO:0046579,GO:0005575,GO:0003674,GO:0007165	CG15669-PI						PF03096				G3DSA:3.40.50.1820	SSF53474									
aly2487.53	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2487.54	Unknown		n/a																				
aly2487.55	Unknown		n/a										G3DSA:3.80.10.10	SSF51126									
aly2487.56	Transmembrane emp24 domain-containing protein 1	GO:0005794,GO:0005783,GO:0048193,GO:0090263,GO:0005215,GO:0016021,GO:0006810,GO:0033116,GO:0005789,GO:0061357,GO:0048042,GO:0005886,GO:0015031,GO:0022008,GO:0000003	CG9053-PC						PF01105	PS50866				SSF101576									
aly2487.57	Putative transmembrane protein INAFM2	GO:0042391,GO:0016058,GO:0016056,GO:0016021,GO:0016020,GO:0009416,GO:0016247,GO:0005246	CG42563-PB						PF15018														
aly2487.6	Isopentenyl-diphosphate Delta-isomerase 1	GO:0016787,GO:0050992,GO:0005777,GO:0008299,GO:0004452,GO:0006695,GO:0046872	CG5919-PB					TIGR02150	PF00293	PS51462			G3DSA:3.90.79.10	SSF55811		00900+5.3.3.2	REACT_22258	PWY-6174,PWY-922,PWY-6859,PWY-6383,PWY-7391,PWY-5123,PWY-7560,PWY-7102,PWY-7524	UPA00059				
aly2487.7	Photoreceptor outer segment membrane glycoprotein 2	GO:0016021,GO:0007601	n/a								PR00218,PR00218												

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2487.8	Peroxisomal biogenesis factor 6	GO:0005778,GO:0007031,GO:0005777,GO:0017111,GO:0005524	CG11919-PD						PF00004				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540,SSF52540										
aly2487.9	40S ribosomal protein S25	GO:0003735,GO:0006412,GO:0005840,GO:0022627	CG6684-PA						PF03297				G3DSA:1.10.10.10										
aly24881.1	Unknown		n/a						PF08574														
aly24907.1	Pregnancy-specific beta-1 glycoprotein 5	GO:0007565,GO:0005576	CG14372-PD						PF13927				G3DSA:2.60.40.10	SSF48726									
aly2492.1	Geranylgeranyl transferase type-1 subunit beta	GO:0018344,GO:0035050,GO:0004662,GO:0008270,GO:0004661,GO:0005953,GO:0022008,GO:0007265	CG3469-PA						PF00432,PF00432,PF00432,PF00432				G3DSA:1.50.10.20	SSF48239									
aly2492.10	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0030672,GO:0016021,GO:0007268,GO:0022857,GO:0001669,GO:0006836,GO:0055085,GO:0030054	CG3168-PC						PF07690,PF07690	PS50850		PS00216,PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2492.11	Unknown	GO:0016021,GO:0009593,GO:0015276	CG13576-PA										G3DSA:1.10.287.70,G3DSA:3.40.190.10	SSF53850,SSF53850	621~641								
aly2492.2	40S ribosomal protein S6	GO:0005840,GO:0042274,GO:0005622,GO:0003735,GO:0007052,GO:0006364,GO:0006955,GO:0000022,GO:0022627,GO:0006412,GO:0051298	CG10944-PA			PIRSF002129			PF01092			PS00578											
aly2492.3	Unknown		n/a												341~361								
aly2492.4	Ubiquitin-like modifier-activating enzyme ATG7	GO:0019778,GO:0016239,GO:0055013,GO:0050688,GO:2000619,GO:0016236,GO:0034727,GO:0061025,GO:0004839,GO:0019779,GO:0001889,GO:0021987,GO:0005737,GO:0039689,GO:0016567,GO:0006520,GO:0031396,GO:0006501,GO:0032446,GO:0010508,GO:0043066,GO:0071455,GO:0021955,GO:0021860,GO:0048477,GO:0042803,GO:0039521,GO:0050877,GO:0008134,GO:0006464,GO:0007628,GO:0003824,GO:0044805,GO:0030163,GO:0009267,GO:0008340,GO:0005930,GO:0000407,GO:0006497,GO:0009791,GO:0006995,GO:0051607,GO:0000422,GO:0010506,GO:0005829,GO:0031401,GO:0035096,GO:0045732,GO:0043065,GO:0015031,GO:0021680,GO:1903146,GO:0070257	CG5489-PA					TIGR01381	PF16420,PF00899				G3DSA:3.40.50.720	SSF69572									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2492.5	39S ribosomal protein L2, mitochondrial	GO:0005840,GO:0044822,GO:0005739,GO:0003735,GO:0005762,GO:0006412	CG7636-PA						PF00181,PF03947				G3DSA:2.40.50.140,G3DSA:2.30.30.30	SSF50249,SSF50104									
aly2492.6	Protein pygopus	GO:0007223,GO:0007367,GO:0035214,GO:0009880,GO:0007472,GO:0060232,GO:0005634,GO:0016055,GO:0030177,GO:0001105,GO:0048813,GO:0045944,GO:0006351,GO:0005515,GO:0022008,GO:0048526,GO:0008270	CG11518-PA				SM00249		PF00628	PS50016		PS01359	G3DSA:3.30.40.10	SSF57903									
aly2492.7	Unknown		n/a																				
aly2492.8	Putative odorant-binding protein A10	GO:0005576	CG30172-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly2492.9	Unknown		CG14200-PA						PF00855				G3DSA:2.30.30.160	SSF63748	1005~1025								
aly2498.1	Arginine/serine-rich protein PNISR	GO:0005737,GO:0016607,GO:0005634,GO:0005654,GO:0044822	CG31211-PB						PF15996						232~278								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2498.2	Unknown	GO:0005575,GO:0003674,GO:0008150	CG32816-PB																				
aly2498.3	Unknown		n/a																				
aly2498.4	Unknown		n/a																				
aly2498.5	Gustatory and odorant receptor 22	GO:0007608,GO:0016021,GO:0005886,GO:0008527,GO:0050911,GO:0050912,GO:0030425,GO:0004984,GO:0010037,GO:0007610,GO:0050909,GO:0043025,GO:0003031	CG13948-PA						PF08395														
aly25.1	Centrosomal protein of 97 kDa	GO:0005737,GO:0043234,GO:0000242,GO:0030030,GO:0005813,GO:0005815,GO:0007099,GO:0008599	CG3980-PB				SM00365,SM00365,SM00365,SM00365,SM00365		PF12799,PF00612	PS51450,PS51450,PS50096,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058	617~637								
aly25.10	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly25.11	Unknown	GO:0005549	n/a				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly25.12	Unknown		n/a																				
aly25.13	Unknown		n/a																				
aly25.14	Unknown		n/a																				
aly25.15	Unknown		n/a																				
aly25.16	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly25.2	GPI mannosyltransferase 3	GO:0016021,GO:0097502,GO:0005789,GO:0016757,GO:0006506,GO:0000030	CG12006-PA						PF03901														
aly25.3	Hemicentin-2	GO:0005887,GO:0030425,GO:0030424,GO:0004872,GO:0008045,GO:0007411,GO:0030054,GO:0022409,GO:0003151,GO:0007432,GO:0031982,GO:0008406,GO:0071666,GO:0001964,GO:0005509,GO:0043025,GO:0031987,GO:0035385,GO:2000274,GO:0072499,GO:0035050,GO:0044295,GO:0008038,GO:0046716,GO:0009649,GO:0005886,GO:0008201,GO:0043234,GO:0007427,GO:0005604,GO:0050773,GO:0048854,GO:0050896,GO:0070983,GO:0016199,GO:0048813,GO:0005576,GO:0005515,GO:0005938	CG13521-PA				SM00408,SM00408,SM00409,SM00409		PF07679,PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly25.4	Hemicentin-1	GO:0005604,GO:0005515,GO:0070062,GO:0030054,GO:0007601,GO:0048812,GO:0005509,GO:0005887,GO:0007156,GO:0050896,GO:0042802,GO:0005938	CG42256-PP				SM00209,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409		PF00090,PF07679,PF07679,PF13927,PF13895,PF13895	PS50835,PS50835,PS50835,PS50835,PS50092,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.20.100.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF82895,SSF48726									
aly25.5	Unknown		n/a						PF15372						54~81								
aly25.6	Centromere/kinetochore protein zw10 homolog	GO:0005737,GO:0006461,GO:0007030,GO:0016020,GO:0006888,GO:0005783,GO:0034501,GO:0000922,GO:0005634,GO:0005828,GO:0005789,GO:0000070,GO:0007080,GO:0000776,GO:0015031,GO:0000132,GO:0007096,GO:0007093,GO:0051301,GO:0000777	CG30101-PA						PF06248						63~90								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly25.7	UPF0587 protein GA18326	GO:0005575,GO:0008150,GO:0003674	CG4646-PA						PF05907					SSF141678	160~161								
aly25.8	Ataxin-10	GO:0005737,GO:0070207,GO:0005615,GO:0007399,GO:0005829,GO:0016020,GO:0030425,GO:0008150,GO:0005886,GO:0031175,GO:0003674,GO:0048471,GO:0043025	CG4975-PC						PF09759				G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371									
aly25.9	E3 ubiquitin-protein ligase SH3RF1	GO:0005794,GO:0008104,GO:0008103,GO:0042052,GO:0030159,GO:0008258,GO:0030027,GO:0060548,GO:0006915,GO:0007391,GO:0007390,GO:0022407,GO:0016874,GO:0008270,GO:0005515,GO:0016567,GO:0008340,GO:0048471,GO:0004842,GO:0046328,GO:0045451	CG4909-PA				SM00184,SM00326,SM00326,SM00326,SM00326		PF00097,PF14604,PF14604,PF07653,PF00018	PS50002,PS50002,PS50089,PS50002,PS50002	PR00452,PR00452,PR00452,PR00499,PR00499,PR00499	PS00518	G3DSA:2.30.30.40,G3DSA:2.30.30.40,G3DSA:3.30.40.10,G3DSA:2.30.30.40,G3DSA:2.30.30.40	SSF50044,SSF57850,SSF50044,SSF50044,SSF50044									
aly250.1	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005886,GO:0006508	CG13744-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly250.2	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005886,GO:0006508	CG8170-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494	305~325								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly250.3	Angiotensin-converting enzyme	GO:0005737,GO:0007507,GO:0004180,GO:0004222,GO:0005615,GO:0008241,GO:0016021,GO:0016020,GO:0005576,GO:0008270,GO:0005886,GO:0045938,GO:0006508,GO:0046872,GO:0008237,GO:0030431	CG10593-PA						PF01401,PF01401		PR00791,PR00791,PR00791,PR00791,PR00791			SSF55486,SSF55486									
aly250.4	Bone morphogenetic protein receptor type-2	GO:0042127,GO:0045906,GO:0005887,GO:0030308,GO:0060173,GO:0006366,GO:0030425,GO:0014916,GO:0030509,GO:0045887,GO:0007165,GO:0048010,GO:0030501,GO:0010862,GO:0007274,GO:1902731,GO:0005737,GO:0005615,GO:0001938,GO:0060841,GO:0097481,GO:0016020,GO:0048842,GO:0036122,GO:0004675,GO:0060836,GO:0009925,GO:0002063,GO:0046872,GO:0043025,GO:2000279,GO:0005524,GO:0060350,GO:0006468,GO:0001946,GO:0001707,GO:0016324,GO:0009986,GO:0004672,GO:0045669,GO:0007528,GO:0046331,GO:0009267,GO:0005886,GO:0030166,GO:0010595,GO:0030513,GO:0001893,GO:0061298,GO:0007420,GO:0010634,GO:0061036,GO:0072577,GO:0009952,GO:0005901,GO:0001935,GO:0003085,GO:0005026,GO:0005024,GO:0001974,GO:0048813,GO:0048286,GO:0004702,GO:0007178,GO:0060840,GO:0005769	CG10776-PB						PF01064,PF00069	PS50011	PR00653,PR00653	PS00107	G3DSA:3.30.200.20,G3DSA:2.10.60.10,G3DSA:1.10.510.10	SSF57302,SSF56112									
aly250.5	Carnosine N-methyltransferase	GO:0005575,GO:0003674,GO:0008150	CG11596-PC																				
aly250.6	Carnosine N-methyltransferase	GO:0005575,GO:0003674,GO:0008150	CG11596-PC						PF07942				G3DSA:3.40.50.150,G3DSA:3.40.50.150	SSF53335									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly250.7	Protein KTI12 homolog	GO:0005524	CG3587-PA						PF08433				G3DSA:3.40.50.300	SSF52540									
aly250.8	Acyl-CoA-binding domain-containing protein 5	GO:0050809,GO:0005778,GO:0042049,GO:0006914,GO:0006810,GO:0008289,GO:0000062,GO:0004857,GO:0016021	CG8814-PA						PF00887	PS51228	PR00689,PR00689,PR00689	PS00880	G3DSA:1.20.80.10	SSF47027									
aly250.9	Ceropsin	GO:0008020,GO:0004930,GO:0016028,GO:0009881,GO:0000122,GO:0007605,GO:0016021,GO:0007601,GO:0018298,GO:0007602,GO:0007186	CG5192-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00578,PR00578,PR00578,PR00578	PS00238,PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly250170.1	Unknown	GO:0005575,GO:0007606,GO:0003674	CG33512-PB						PF07679	PS50835			G3DSA:2.60.40.10	SSF48726									
aly2507.1	Pogo transposable element with KRAB domain	GO:0006355,GO:0005634,GO:0007275,GO:0003677	n/a						PF03184					SSF46689									
aly25076.1	Tachykinin-like peptides receptor 99D	GO:0004930,GO:0042048,GO:0016021,GO:0008188,GO:0007218,GO:0050805,GO:0007217,GO:0050911,GO:0005887,GO:0005886,GO:0004995,GO:0007186	CG7887-PC						PF00001	PS50262	PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2508.1	Riboflavin transporter 2	GO:0016021,GO:0006810,GO:0005886	CG11576-PA						PF06237														
aly2508.10	WD repeat-containing protein on Y chromosome	GO:0005575,GO:0003674,GO:0008150,GO:0005509,GO:0005515	CG40583-PB				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400	PS50082,PS50294,PS50082,PS50082,PS50222		PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:1.10.238.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF69322,SSF69322,SSF47473,SSF50978,SSF50978,SSF50978,SSF50978									
aly2508.11	Leucine-rich repeat-containing protein 71		n/a				SM00368,SM00368,SM00368,SM00368			PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047,SSF52047									
aly2508.12	U4/U6.U5 tri-snRNP-associated protein 1	GO:0005737,GO:0046540,GO:0000387,GO:0005794,GO:0071011,GO:0071013,GO:0005654,GO:0044822,GO:0045292,GO:0000398,GO:0097193,GO:0007050,GO:0045585,GO:0015030,GO:0022008,GO:0000481,GO:0005829	CG6686-PA						PF03343						215~235								
aly2508.13	Unknown		n/a												23~43								
aly2508.14	Lysosomal-trafficking regulator	GO:0005737,GO:0032510,GO:0015630,GO:0006909,GO:0043473,GO:0042267,GO:0045771,GO:0007041,GO:0007040,GO:0015031	CG42863-PB				SM01026		PF14844,PF02138	PS50197			G3DSA:2.30.29.40,G3DSA:1.10.1540.10	SSF50729,SSF81837									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2508.15	Unknown		n/a												155~155								
aly2508.16	Unknown		n/a																				
aly2508.17	Unknown		n/a																				
aly2508.18	Sphingosine-1-phosphate phosphatase 1	GO:0042392,GO:0005783,GO:0016311,GO:0016021,GO:0016020,GO:0097191,GO:0097193,GO:0006668,GO:0005789,GO:0006665,GO:0006670	n/a				SM00014		PF01569				G3DSA:1.20.144.10	SSF48317									
aly2508.19	NF-kappa-B inhibitor cactus	GO:0005737,GO:0006952,GO:0019732,GO:0007399,GO:0019730,GO:0009950,GO:0009620,GO:0008134,GO:0008063,GO:0006967,GO:0030097,GO:0031594,GO:0006974,GO:0005515,GO:0006955,GO:0006909,GO:0042994,GO:0048477,GO:0045087,GO:0042308,GO:0046843	CG5848-PA				SM00248,SM00248,SM00248,SM00248		PF12796	PS50297,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20	SSF48403									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2508.2	Glutamate receptor ionotropic, kainate 4	GO:0006810,GO:0032983,GO:0042734,GO:0045211,GO:0035235,GO:0016021,GO:0016020,GO:0015277,GO:0015276,GO:0005234,GO:0007215,GO:0034220,GO:0007268,GO:0030054,GO:0050907,GO:0005887,GO:0005886,GO:0030425,GO:0035249,GO:0004970	CG14076-PC						PF00060				G3DSA:3.40.190.10,G3DSA:1.10.287.70	SSF53850,SSF53850										
aly2508.20	DNA replication complex GINS protein PSF1	GO:0005737,GO:0005634,GO:0001833,GO:0000811,GO:0046331,GO:0006260,GO:0022008,GO:0043138,GO:1900087	CG9187-PA						PF05916					SSF158573	6~26								
aly2508.3	Acetylcholine receptor subunit alpha-L1	GO:0006810,GO:0006812,GO:0005230,GO:0016020,GO:0015464,GO:0005892,GO:0045211,GO:0004889,GO:0005887,GO:0007271,GO:0016021,GO:0030054	CG6844-PA						PF02931				G3DSA:2.70.170.10	SSF63712									
aly2508.4	DNA-binding protein D-ETS 6	GO:0043565,GO:0003700,GO:0005634,GO:0030154,GO:0006355,GO:0048813,GO:0006357,GO:0042742,GO:0003677,GO:0000981	CG2914-PA				SM00413		PF00178	PS50061	PR00454,PR00454,PR00454,PR00454	PS00346	G3DSA:1.10.10.10	SSF46785									
aly2508.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2508.6	Trafficking protein particle complex subunit 4	GO:0005795,GO:0043547,GO:0006888,GO:0016192,GO:0008021,GO:0005801,GO:0006810,GO:0016358,GO:0017112,GO:0045211,GO:0045212,GO:0030425,GO:0005886,GO:0045202,GO:0030008,GO:0030054,GO:0005783	CG9298-PA						PF04099				G3DSA:3.30.450.70,G3DSA:3.30.450.70	SSF64356,SSF64356										
aly2508.7	WD repeat-containing protein 26 homolog	GO:0005737,GO:0008150,GO:0003674,GO:0005515	CG7611-PE				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00668,SM00667		PF00400,PF00400,PF00400	PS50896,PS50082,PS50082,PS50897,PS50082,PS50082,PS50294	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10	SSF50978									
aly2508.8	Out at first protein	GO:0007275,GO:0007562,GO:0007399,GO:0016321	CG9884-PD						PF14941														
aly2508.9	28S ribosomal protein S21, mitochondrial	GO:0070126,GO:0006996,GO:0070124,GO:0070125,GO:0005840,GO:0044822,GO:0006412,GO:0003735,GO:0005743,GO:0005763,GO:0032543	CG32854-PA					TIGR00030	PF01165														
aly250871.1	Neuropathy target esterase sws	GO:0007420,GO:0006643,GO:0007399,GO:0034349,GO:0016021,GO:0005789,GO:0061024,GO:0051402,GO:0005515,GO:0004622,GO:0046470,GO:0007608	CG2212-PA										G3DSA:2.60.120.10										
aly251.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly251.10	PHD finger protein 20-like protein 1	GO:0035327,GO:0005634,GO:0005705,GO:0045944,GO:0008270,GO:0003677,GO:0007095,GO:0022008,GO:0044545	CG10042-PB				SM00692,SM00333,SM00333,SM00391,SM00980		PF01429,PF05485	PS50982,PS50950,PS50157		PS01359,PS00028	G3DSA:3.30.40.10,G3DSA:3.30.890.10,G3DSA:2.30.30.140,G3DSA:2.30.30.270	SSF57716,SSF57903,SSF63748,SSF54171,SSF54160	712~746,1452~1472,506~533,663~683,89~109								
aly251.11	Proteasome subunit beta type-6	GO:0004175,GO:0090263,GO:0000082,GO:0010499,GO:0034641,GO:0051439,GO:0044281,GO:0051437,GO:0051436,GO:0042981,GO:0000209,GO:0005737,GO:0002474,GO:0005839,GO:0043161,GO:0005634,GO:0002479,GO:0005654,GO:0010467,GO:0043066,GO:0002223,GO:0090090,GO:0005794,GO:0000278,GO:0045087,GO:0006915,GO:0031145,GO:0006974,GO:0012501,GO:0006977,GO:0000502,GO:0070062,GO:0051603,GO:0005829,GO:0042590,GO:0004298,GO:0016032,GO:0006521	CG8392-PA						PF00227	PS51476	PR00141,PR00141,PR00141,PR00141		G3DSA:3.60.20.10	SSF56235			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045							
aly251.12	Protein hunchback (Fragment)	GO:0035290,GO:0035289,GO:0001763,GO:0003677,GO:0035282,GO:0044324,GO:0007362,GO:0043565,GO:0000122,GO:0005634,GO:0007400,GO:0046872,GO:0000981,GO:0000980,GO:0007427,GO:0008595,GO:0040034,GO:0007402,GO:0007355,GO:0007354,GO:0007424,GO:0048699,GO:0007419,GO:0003700,GO:0007431,GO:0003705,GO:0045944,GO:0006351,GO:0008293	CG9786-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly251.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly251.14	Peptidyl-prolyl cis-trans isomerase E	GO:0000413,GO:0006457,GO:0000974,GO:0071011,GO:0005634,GO:0000398,GO:0000166,GO:0003723,GO:0003755,GO:0006909,GO:0071013,GO:0003729	CG4886-PA			PIRSF001475	SM00360		PF00160,PF00076	PS50072,PS50102	PR00153,PR00153,PR00153,PR00153,PR00153	PS00170	G3DSA:3.30.70.330,G3DSA:2.40.100.10	SSF54928,SSF50891									
aly251.15	5-hydroxytryptamine receptor 2B	GO:0008284,GO:0050795,GO:0016310,GO:0007610,GO:0008144,GO:0014065,GO:0051000,GO:0045202,GO:0042310,GO:0051209,GO:0043123,GO:0030054,GO:0005737,GO:0014033,GO:0004930,GO:0071418,GO:0007210,GO:0003300,GO:0070528,GO:1904015,GO:0001587,GO:0050715,GO:0001965,GO:0060548,GO:0007186,GO:0010507,GO:0004993,GO:0048598,GO:0019722,GO:0006874,GO:2000253,GO:0005096,GO:0043066,GO:0014827,GO:0003007,GO:0034220,GO:0030425,GO:0005887,GO:0005886,GO:0001755,GO:0042493,GO:0008227,GO:0006182,GO:0051378,GO:0071502,GO:0007377,GO:0043406,GO:0043025,GO:0007202,GO:0007205,GO:0043647,GO:0001938,GO:0051781,GO:0035733,GO:0002031,GO:0010513,GO:0070374,GO:0016021,GO:0070371,GO:0001819	CG1056-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly251.2	MFS-type transporter SLC18B1	GO:0016021,GO:0055085	n/a						PF07690	PS50850	PR01035,PR01035		G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly251.3	Probable G-protein coupled receptor 152	GO:0007424,GO:0005201,GO:0051539,GO:0040005,GO:0004930,GO:0007475,GO:0008362,GO:0046331,GO:0005509,GO:0005887,GO:0031012,GO:0007186,GO:0005578	CG33196-PQ						PF01390	PS50024					1573~1576								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly251.4	Zinc finger protein 1	GO:0006697,GO:0007616,GO:0045938,GO:0005634,GO:0003700,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0008340,GO:0046872,GO:0006351	CG34100-PD				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly251.5	Folate transporter 1	GO:0006767,GO:0006810,GO:0008518,GO:0015884,GO:0005542,GO:0016020,GO:0006766,GO:0015350,GO:0044281,GO:0005887,GO:0005886,GO:0046655,GO:0008517	CG6574-PA			PIRSF028739		TIGR00806	PF01770				G3DSA:1.20.1250.20	SSF103473										
aly251.6	Single-pass membrane and coiled-coil domain-containing protein 4 homolog	GO:0005575,GO:0003674,GO:0016021,GO:0008150	CG33169-PA						PF15012														
aly251.7	Presqualene diphosphate phosphatase	GO:0003824,GO:0016021,GO:0016020,GO:0016787	CG31717-PA				SM00014		PF01569				G3DSA:1.20.144.10	SSF48317									
aly251.8	60S acidic ribosomal protein P1	GO:0003735,GO:0006414,GO:0022625,GO:0005840,GO:0006412	CG4087-PB	MF_01478					PF00428		PR00456,PR00456,PR00456												
aly251.9	Small G protein signaling modulator 3 homolog	GO:0032313,GO:0005096,GO:0005097	CG12241-PA				SM00593,SM00164,SM00326		PF02759,PF00253,PF00566,PF00018	PS50086,PS50002,PS50826			G3DSA:4.10.830.10,G3DSA:2.30.30.40,G3DSA:1.10.8.270	SSF57716,SSF140741,SSF140741,SSF47923,SSF47923,SSF50044									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2510.1	Organic cation transporter-like protein	GO:0030307,GO:0016021,GO:0007390,GO:0015695,GO:0040018,GO:0015101,GO:0008513,GO:0055085	CG42269-PE						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly2513.1	E3 ubiquitin-protein ligase CBL-B-A	GO:0004871,GO:0007476,GO:0023051,GO:0042059,GO:0008270,GO:0007166,GO:0008340,GO:0007298,GO:0010941,GO:0008069,GO:0005737,GO:0004842,GO:0005634,GO:0030971,GO:0033500,GO:0005509,GO:0006508,GO:0001784,GO:0042127,GO:0007175,GO:0007173,GO:0005938,GO:0001754,GO:0016874,GO:0048134,GO:0006897,GO:0009950,GO:0080134,GO:0007465,GO:0002376,GO:0005515	CG7037-PB						PF02262	PS51506			G3DSA:1.20.930.20,G3DSA:1.10.238.10	SSF47668	76~96								
aly2513.2	Unknown		n/a										G3DSA:2.120.10.30	SSF63829									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2517.1	Neuroligin-3	GO:0048675,GO:0050808,GO:0005887,GO:0060024,GO:0007612,GO:0061002,GO:0030425,GO:0050804,GO:0030139,GO:0045202,GO:0002087,GO:0060080,GO:2000969,GO:0030054,GO:0051932,GO:2000331,GO:0097105,GO:0097104,GO:0060999,GO:0007416,GO:2000310,GO:0043025,GO:0071625,GO:2000463,GO:0042043,GO:0097151,GO:0035176,GO:0009986,GO:1902474,GO:0048709,GO:0052689,GO:0008542,GO:0007158,GO:0060077,GO:0060076,GO:0030431,GO:0050839,GO:0030534,GO:1900271,GO:0090394,GO:0060291,GO:0006898,GO:0097110,GO:0051965,GO:2000809,GO:0051968,GO:0004872	CG34139-PD						PF00135				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474										
aly2517.2	Unknown		n/a																				
aly2517.3	Retrovirus-related Pol polyprotein from transposon 17.6	GO:0015074,GO:0004519,GO:0030017,GO:0003012,GO:0004190,GO:0045202,GO:0003676,GO:0042595,GO:0003964,GO:0008270	CG12505-PA						PF00078	PS50878			G3DSA:3.10.10.10,G3DSA:3.90.10.10,G3DSA:2.40.70.10,G3DSA:3.30.70.270	SSF56672,SSF50630										
aly2518.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly252.1	Unknown		n/a																				
aly252.10	Unknown	GO:0051536,GO:0016020,GO:0005272,GO:0016021,GO:0006814	CG31065-PB						PF00858				G3DSA:2.60.470.10,G3DSA:2.60.470.10										
aly252.11	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1 homolog, mitochondrial	GO:0045252,GO:0030976,GO:0005739,GO:0031966,GO:0006099,GO:0004591,GO:0006091,GO:0006096	CG1544-PA				SM00861		PF02779,PF16870,PF00676				G3DSA:3.40.50.970,G3DSA:3.40.50.970	SSF52518,SSF52518									
aly252.12	Heat shock protein 68	GO:0005811,GO:0006457,GO:0031427,GO:0005739,GO:0051082,GO:0042594,GO:0009408,GO:0008340,GO:0022008,GO:0005875,GO:0005524	CG5436-PA						PF00012		PR00301,PR00301,PR00301,PR00301,PR00301,PR00301	PS00329,PS01036	G3DSA:1.20.1270.10,G3DSA:3.30.420.40,G3DSA:3.90.640.10,G3DSA:2.60.34.10,G3DSA:3.30.30.30,G3DSA:3.30.420.40,G3DSA:3.30.420.40	SSF53067,SSF100920,SSF100934,SSF53067										
aly252.13	Transmembrane protein 135	GO:0016021,GO:0007031,GO:0005777	CG11737-PA						PF15982														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly252.14	CCR4-NOT transcription complex subunit 6	GO:2000327,GO:0030014,GO:0005737,GO:0000288,GO:0000289,GO:0010606,GO:0005634,GO:0016020,GO:0010467,GO:0006402,GO:0046872,GO:0048477,GO:0006351,GO:0008284,GO:0043928,GO:0090503,GO:0070966,GO:0035195,GO:0005829,GO:0004535,GO:0004532,GO:0006355,GO:0006357,GO:0003723,GO:0005515,GO:0017148,GO:0006417	CG31137-PC				SM00369,SM00369		PF13855	PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									
aly252.15	CCR4-NOT transcription complex subunit 6	GO:2000327,GO:0030014,GO:0005737,GO:0000288,GO:0000289,GO:0010606,GO:0005634,GO:0016020,GO:0010467,GO:0006402,GO:0046872,GO:0048477,GO:0006351,GO:0008284,GO:0043928,GO:0090503,GO:0070966,GO:0035195,GO:0005829,GO:0004535,GO:0004532,GO:0006355,GO:0006357,GO:0003723,GO:0005515,GO:0017148,GO:0006417	CG31137-PC						PF03372				G3DSA:3.60.10.10,G3DSA:3.60.10.10	SSF56219									
aly252.16	28S ribosomal protein S24, mitochondrial	GO:0003735,GO:0032543,GO:0006412,GO:0005762,GO:0005763	CG13608-PA						PF14955														
aly252.17	Unknown		n/a				SM00192,SM00192,SM00192			PS50068,PS50068,PS50068	PR00261,PR00261,PR00261		G3DSA:4.10.1220.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10	SSF57424,SSF57424,SSF57424	126~146								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly252.18	Unknown		n/a											SSF50494									
aly252.19	Unknown	GO:0022008	CG13321-PA				SM00696,SM00696		PF11901														
aly252.2	C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8	GO:0004867,GO:0005615,GO:0005886	n/a						PF07703														
aly252.20	Unknown		n/a																				
aly252.21	Collagen alpha 2(I) chain	GO:0005201,GO:0005587,GO:0005581,GO:0007391,GO:0005604,GO:0046872,GO:0005578,GO:0035848	CG4145-PC				SM00038		PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF01410	PS51461			G3DSA:2.10.70.10	SSF57603									
aly252.22	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly252.3	C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8	GO:0005615,GO:0019731,GO:0004867,GO:0006910,GO:0050832,GO:0046331,GO:0005515,GO:0004866,GO:0005886	CG7586-PA						PF12248,PF07678,PF00207,PF07677				G3DSA:2.60.40.690,G3DSA:1.50.10.20	SSF49410,SSF48239,SSF48239									
aly252.4	Neuropeptide F	GO:0007218,GO:0005576	n/a																				
aly252.5	Protein zwilch	GO:0005737,GO:0005828,GO:1990423,GO:0000776,GO:0007094,GO:0003674,GO:0007067,GO:0007093,GO:0051233,GO:0051301,GO:0000777	CG18729-PA						PF09817														
aly252.6	Chaoptin	GO:0035996,GO:0016028,GO:0042052,GO:0042051,GO:0050896,GO:0007601,GO:0046658,GO:0005886,GO:0007156	CG1744-PD				SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00082,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00369		PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855	PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52047,SSF52047,SSF52058,SSF52058									
aly252.7	Sodium/potassium-transporting ATPase subunit beta-1	GO:0006813,GO:0006812,GO:0008324,GO:0035725,GO:0006814,GO:0005391,GO:0005890,GO:0005515,GO:0005886,GO:0098655	CG9258-PA						PF00287,PF00287				G3DSA:2.60.40.1660										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly252.8	Unknown		n/a																				
aly252.9	Unknown	GO:0016021,GO:0005272,GO:0006814	CG33508-PA						PF00858				G3DSA:1.10.287.770										
aly2525.1	U4/U6 small nuclear ribonucleoprotein Prp4	GO:0016607,GO:0030532,GO:0071011,GO:0071013,GO:0000398,GO:0030621,GO:0005515,GO:0005688,GO:0005687,GO:0006397,GO:0008380,GO:0005681,GO:0017070	CG6322-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400, PF00400	PS50082,PS50082,PS50082,PS50294,PS50082,PS50082,PS50294,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978										
aly2525.2	U4/U6 small nuclear ribonucleoprotein Prp3	GO:0016607,GO:0046540,GO:0031935,GO:0000244,GO:0030532,GO:0071011,GO:0005634,GO:0000398,GO:0005688,GO:0005687,GO:0005681	CG7757-PA						PF06544,PF08572						356~376,163~190,111~136								
aly2525.3	DnaJ homolog subfamily B member 14	GO:0016021,GO:0016020,GO:0005789	CG3061-PA				SM00271		PF00226	PS50076	PR00625,PR00625,PR00625,PR00625		G3DSA:1.10.287.110,G3DSA:1.10.287.110	SSF46565,SSF46565									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly253.1	Usherin	GO:0060171,GO:1990075,GO:0017022,GO:0060113,GO:0002141,GO:0002142,GO:0005737,GO:0036064,GO:0016021,GO:0007605,GO:0035315,GO:0042803,GO:0032421,GO:0032391,GO:0016324,GO:0007601,GO:0050953,GO:0045184,GO:0048496,GO:0005604,GO:0050896,GO:0001917,GO:1990696,GO:0005518,GO:0045494	n/a																				
aly253.10	60S ribosomal protein L10a	GO:0015934,GO:0051298,GO:0022625,GO:0003735,GO:0007052,GO:0003723,GO:0000022,GO:0006412	CG7283-PA			PIRSF002155			PF00687				G3DSA:3.40.50.790,G3DSA:3.30.190.20,G3DSA:3.30.190.20	SSF56808									
aly253.11	Unknown		n/a																				
aly253.12	NADH dehydrogenase [ubiqui] flavoprotein 2, mitochondrial	GO:0008137,GO:0051537,GO:0005739,GO:0006120,GO:0005743,GO:0005747,GO:0070469,GO:0046872,GO:0003954	CG5703-PA			PIRSF000216		TIGR01958	PF01257				G3DSA:3.40.30.10	SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly253.13	Calcium-transporting ATPase type 2C member 1	GO:0005783,GO:0016339,GO:0007165,GO:0004871,GO:0006828,GO:0008544,GO:0043123,GO:0031532,GO:0016021,GO:0005777,GO:0051208,GO:0000166,GO:0030141,GO:0005509,GO:0030026,GO:0046872,GO:0005524,GO:0032468,GO:0005794,GO:0042044,GO:0019722,GO:0006874,GO:0006816,GO:0030133,GO:0030145,GO:0005886,GO:0071421,GO:0043231,GO:0005802,GO:0070588,GO:0000139,GO:0070509,GO:0005388,GO:0015410,GO:0032472	CG32451-PG				SM00831	TIGR01494,TIGR01494,TIGR01522	PF00702,PF00690,PF00122,PF00689		PR00120,PR00120,PR00120,PR00119,PR00119,PR00119,PR00119,PR00119,PR00119	PS00154	G3DSA:1.20.1110.10,G3DSA:1.20.1110.10,G3DSA:1.20.1110.10	SSF81665,SSF81665,SSF81665,SSF81653,SSF81660,SSF56784,SSF56784									
aly253.2	Unknown		CG14830-PA																				
aly253.3	Unknown		CG14830-PA																				
aly253.4	DNA topoisomerase 2	GO:0000182,GO:0051310,GO:0003677,GO:0007067,GO:0016590,GO:0003918,GO:0007126,GO:0008623,GO:0006342,GO:0005634,GO:0009295,GO:0006265,GO:0006261,GO:0046872,GO:0003696,GO:0005524,GO:0000400,GO:0007052,GO:0000795,GO:0007076,GO:0006312,GO:0000819,GO:0000712,GO:0005694,GO:0007095,GO:0003729	CG10223-PA				SM00433,SM00434		PF16898,PF00521,PF00204,PF02518,PF01751	PS50880	PR00418,PR00418,PR00418,PR00418,PR00418,PR00418,PR00418,PR00418,PR01158,PR01158,PR01158,PR01158,PR01158,PR01158,PR01158,PR01158,PR01158,PR01158,PR01158	PS00177	G3DSA:1.10.268.10,G3DSA:3.30.1360.40,G3DSA:3.40.50.670,G3DSA:3.30.230.10,G3DSA:3.30.1490.30,G3DSA:3.90.199.10,G3DSA:3.30.565.10	SSF55874,SSF54211,SSF56719	1187~1214,1157~1177									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly253.5	Transmembrane protein 223	GO:0016021,GO:0007399	CG12935-PA						PF14640														
aly253.6	E3 ubiquitin-protein ligase RNF144A	GO:0005794,GO:0016567,GO:0016021,GO:0030659,GO:0008270,GO:0005886,GO:0016874	CG33144-PA				SM00184,SM00184,SM00647,SM00647		PF01485,PF01485	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850,SSF57850,SSF57850									
aly253.7	Activating transcription factor 7-interacting protein 1	GO:0006355,GO:0005634,GO:0005694,GO:0006351	CG12340-PA						PF16794						140~160,223~243,453~473,706~733								
aly253.8	Unknown		CG14450-PA											SSF47781	220~243		REACT_216						
aly253.9	Zinc finger protein 501	GO:0031935,GO:0003700,GO:0005634,GO:0006355,GO:0048813,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG11352-PF				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667	182~206								
aly2531.1	Unknown		n/a												41~61								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2531.2	Unknown		n/a												70~90								
aly2531.3	Unknown		n/a																				
aly2531.4	Unknown		n/a																				
aly2532.1	Putative malate dehydrogenase 1B	GO:0005975,GO:0016615,GO:0016616,GO:0005623,GO:0003824,GO:0006099,GO:0045454,GO:0015035,GO:0006108,GO:0055114,GO:0009055	n/a										G3DSA:3.90.110.10										
aly2532.10	DNA polymerase theta	GO:0006303,GO:0008026,GO:0006281,GO:0005634,GO:0004386,GO:0003887,GO:0006260,GO:0071897,GO:0003677,GO:0006289,GO:0097681,GO:0005524,GO:0006261	CG6019-PA				SM00487,SM00482,SM00490		PF00476,PF00270,PF00271	PS51192,PS51194	PR00868,PR00868,PR00868,PR00868,PR00868,PR00868,PR00868	PS00447	G3DSA:1.10.150.20,G3DSA:1.10.150.20,G3DSA:3.40.50.300,G3DSA:3.30.70.370,G3DSA:3.30.70.370,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF158702,SSF52540,SSF52540,SSF52540,SSF56672		00240+2.7.7.7,00230+2.7.7.7								
aly2532.11	UPF0415 protein C7orf25 homolog	GO:0005575,GO:0008150,GO:0003674	CG42553-PA						PF07000														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2532.12	BRISC and BRCA1-A complex member 1	GO:0005737,GO:0031572,GO:0006302,GO:0005634,GO:0070552,GO:0070531,GO:0010212,GO:0045739,GO:0016568,GO:0070536	n/a																				
aly2532.13	PH and SEC7 domain-containing protein 3	GO:0016020,GO:0005802,GO:0016192,GO:0030182,GO:0005543,GO:0005086,GO:0045211,GO:0014069,GO:0005912,GO:0005515,GO:0032011,GO:0032012,GO:0005622,GO:0030054,GO:0043547	CG31158-PH				SM00222,SM00228,SM00233		PF01369,PF15410,PF00595	PS50106,PS50003,PS50190	PR00683,PR00683,PR00683		G3DSA:2.30.29.30,G3DSA:1.10.1000.11,G3DSA:2.30.42.10	SSF50729,SSF48425,SSF50156	685~712								
aly2532.14	CDGSH iron-sulfur domain-containing protein 2 homolog	GO:0043231,GO:0016021,GO:0051537,GO:0005789,GO:0005575,GO:0008150,GO:0003674,GO:0046872	CG1458-PA				SM00704		PF10660,PF09360														
aly2532.15	Unknown		n/a																				
aly2532.16	STAM-binding protein	GO:0005737,GO:0008284,GO:0070062,GO:0005634,GO:0019904,GO:0032154,GO:0007259,GO:0005654,GO:0004843,GO:0043524,GO:0000281,GO:0005886,GO:0014067,GO:0046872,GO:0016579,GO:0005769,GO:0008237,GO:0046580	CG2224-PA				SM00232		PF08969,PF01398				G3DSA:3.40.140.10,G3DSA:1.20.58.280	SSF102712,SSF140856									
aly2532.17	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2532.18	Xaa-Pro aminopeptidase 1	GO:0005737,GO:0004177,GO:0070062,GO:0030145,GO:0010815,GO:0070006,GO:0022008	CG6225-PA						PF16188,PF00557,PF16189,PF01321				G3DSA:3.40.350.10,G3DSA:3.90.230.10	SSF55920,SSF53092									
aly2532.19	Mannosyl-oligosaccharide alpha-1,2-mannosidase isoform A	GO:0005794,GO:0072347,GO:0006486,GO:0006487,GO:0016021,GO:0016020,GO:0000139,GO:0035010,GO:0004571,GO:0005509,GO:0008340,GO:0012505	CG42275-PI						PF01532		PR00747,PR00747,PR00747,PR00747,PR00747,PR00747,PR00747,PR00747		G3DSA:1.50.10.50	SSF48225									
aly2532.2	Ribonuclease P protein subunit p30	GO:0030677,GO:0004526,GO:0008033,GO:0005730,GO:0004540,GO:0022008	CG11606-PA						PF01876				G3DSA:3.20.20.140	SSF89550,SSF89550									
aly2532.20	Inactive ubiquitin carboxyl-terminal hydrolase 54	GO:0016318,GO:0001745,GO:0004221,GO:0036459,GO:0006511,GO:0008157,GO:0046666,GO:0046667,GO:0016579,GO:0004843	CG2904-PC							PS50235				SSF54001,SSF54001									
aly2532.21	Unknown		n/a																				
aly2532.22	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2532.23	DNA excision repair protein ERCC-1	GO:0006295,GO:0008022,GO:0006296,GO:0000109,GO:0048568,GO:0045190,GO:0008584,GO:0006949,GO:0000784,GO:0035264,GO:0009650,GO:0005737,GO:0010165,GO:0010259,GO:0006302,GO:0005634,GO:0008283,GO:0009744,GO:0005654,GO:0048477,GO:0003697,GO:0006310,GO:0035166,GO:0006283,GO:0006281,GO:0007584,GO:0000718,GO:0006289,GO:0005669,GO:0007283,GO:0000720,GO:0019904,GO:0000110,GO:0007131,GO:0006979,GO:0043234,GO:0000014,GO:0006312,GO:0001302,GO:0051276,GO:0000712,GO:0004519,GO:0036297,GO:0032205,GO:0048812,GO:0005515,GO:0070522,GO:0046982,GO:0003684	CG10215-PA					TIGR00597	PF14520,PF03834				G3DSA:1.10.150.20	SSF52980,SSF47781			REACT_216						
aly2532.24	Fanconi anemia group M protein	GO:0071821,GO:0006281,GO:0004518,GO:0004004,GO:0004386,GO:0005654,GO:0000712,GO:0003677,GO:0003682,GO:0031297,GO:0043240,GO:0005524	CG7922-PA				SM00487		PF00271,PF04851	PS51194,PS51192			G3DSA:3.40.50.300,G3DSA:1.20.1320.20,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540									
aly2532.25	Unknown		n/a																				
aly2532.26	Tetratricopeptide repeat protein 12	GO:0005575,GO:0008150,GO:0003674	CG6980-PA				SM00028,SM00028		PF13414	PS50293,PS50005,PS50005			G3DSA:1.25.40.10	SSF48452									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2532.27	Unknown		n/a																				
aly2532.28	Unknown	GO:0005802,GO:0016192,GO:0030182,GO:0005543,GO:0005086,GO:0005912,GO:0032012	CG31158-PH																				
aly2532.29	Unknown		n/a																				
aly2532.3	Protein LMBR1L	GO:0016021,GO:0006897,GO:0005886	CG5807-PA						PF04791		PR01692,PR01692,PR01692,PR01692,PR01692,PR01692												
aly2532.4	DNA polymerase zeta catalytic subunit	GO:0005730,GO:0008408,GO:0051539,GO:0000724,GO:0005634,GO:0006281,GO:0019985,GO:0006297,GO:0000166,GO:0003887,GO:0016035,GO:0006260,GO:0006261,GO:0003677,GO:0046872,GO:0005694,GO:0042276	CG1925-PA				SM00486		PF00136,PF03104,PF14260		PR00106,PR00106,PR00106	PS00116	G3DSA:1.10.287.690,G3DSA:3.30.420.10,G3DSA:3.90.1600.10,G3DSA:3.90.1600.10	SSF56672,SSF53098,SSF53098		00240+2.7.7.7,00230+2.7.7.7							
aly2532.5	Unknown	GO:0005488	n/a											SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2532.6	MICOS complex subunit MIC13 homolog	GO:0022008	CG7603-PA						PF15884														
aly2532.7	Proliferation-associated protein 2G4	GO:0005737,GO:0004177,GO:0006351,GO:0005730,GO:0030529,GO:0045597,GO:0006355,GO:0043066,GO:0003723,GO:0006417,GO:0006364	CG10576-PA					TIGR00495	PF00557				G3DSA:3.90.230.10,G3DSA:3.90.230.10,G3DSA:1.10.10.10	SSF46785,SSF55920,SSF55920										
aly2532.8	RWD domain-containing protein 1	GO:0005515	CG5515-PA				SM00591		PF05773	PS50908			G3DSA:3.10.110.10	SSF54495									
aly2532.9	Tubby-related protein 4	GO:0005737,GO:0035091,GO:0016567,GO:0061512,GO:0005929,GO:0035556	CG5586-PF						PF01167,PF01167	PS50082,PS50294		PS00758	G3DSA:2.130.10.10,G3DSA:3.20.90.10,G3DSA:3.20.90.10,G3DSA:3.20.90.10	SSF54518,SSF54518,SSF50978									
aly25398.1	Unknown		n/a																				
aly254.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly254.2	Unknown		n/a																				
aly254.3	Neural proliferation differentiation and control protein 1	GO:0005575,GO:0008150,GO:0016021,GO:0003674	CG44247-PA						PF06809														
aly2548.1	Unknown		n/a																				
aly2548.10	Calcium and integrin-binding family member 2	GO:0005178,GO:0042383,GO:0072562,GO:0007602,GO:0031594,GO:0008597,GO:0001917,GO:0055074,GO:0032403,GO:0005927,GO:0045494,GO:0005509	CG9236-PB							PS50222,PS50222		PS00018	G3DSA:1.10.238.10	SSF47473									
aly2548.11	Unknown	GO:0045931,GO:0008284,GO:0007113,GO:0051726,GO:0040018,GO:0007300,GO:0008054	CG5360-PA												482~502								
aly2548.12	Unknown	GO:0003674,GO:0005811,GO:0008150	CG42351-PC						PF16091														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2548.13	Trimeric intracellular cation channel type B	GO:0005267,GO:0005261,GO:0016021,GO:0016020,GO:0005789,GO:0015672	CG4239-PA						PF05197														
aly2548.14	UDP-glucose 4-epimerase	GO:0050662,GO:0035167,GO:0044237,GO:0006012,GO:0003974,GO:0003978	CG12030-PA					TIGR01179	PF16363		PR01713,PR01713,PR01713		G3DSA:3.90.25.10,G3DSA:3.90.25.10,G3DSA:3.40.50.720	SSF51735		00520+5.1.3.2,00052+5.1.3.2		PWY-7344,PWY-6397,PWY-6527,PWY-7328,PWY-6317,PWY-3821	UPA00214				
aly2548.15	DNA N6-methyl methyltransferase	GO:0008168,GO:0032259,GO:0003676,GO:0006139	CG14906-PC						PF05063	PS51143		PS00092		SSF53335									
aly2548.16	Protein disabled	GO:0005737,GO:0042169,GO:0007399,GO:0042051,GO:0045500,GO:0005118,GO:0007349,GO:0017124,GO:0072583,GO:0005515,GO:0008045,GO:0022008,GO:0030424,GO:0048488	CG9695-PF				SM00462		PF00640	PS01179			G3DSA:2.30.29.30	SSF50729									
aly2548.17	Unknown	GO:0005737,GO:0042169,GO:0007399,GO:0042051,GO:0045500,GO:0007349,GO:0007391,GO:0017124,GO:0072583,GO:0005515,GO:0008045,GO:0022008,GO:0030424,GO:0048488	CG9695-PF																				
aly2548.18	LysM and putative peptidoglycan-binding domain-containing protein 4	GO:0016021	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2548.19	Heterogeneous nuclear ribonucleoprotein K	GO:0005737,GO:0006351,GO:0035062,GO:0045165,GO:0000381,GO:0007446,GO:0008283,GO:0005634,GO:0035107,GO:0030529,GO:0005654,GO:0006355,GO:0000785,GO:0003723,GO:0003677,GO:0008380,GO:0006397,GO:0008134,GO:0005681,GO:0003729	CG13425-PC				SM00322,SM00322,SM00322		PF00013,PF00013,PF00013	PS50084,PS50084,PS50084			G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10	SSF54791,SSF54791,SSF54791									
aly2548.2	Unknown		n/a																				
aly2548.20	Transmembrane protein 110	GO:0016021	n/a						PF12400														
aly2548.21	Dynein heavy chain 7, axonemal	GO:0036156,GO:0008152,GO:0042623,GO:0036159,GO:0005929,GO:0007018,GO:0005858,GO:0000166,GO:0003774,GO:0001539,GO:2001019,GO:0016887,GO:0005524,GO:0003341,GO:0005874,GO:0005875,GO:0003777,GO:0005509	CG15804-PC				SM00382,SM00382		PF12777,PF08393,PF12774,PF03028,PF12775,PF12781,PF12780				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540	3621~3641,2661~2719,3850~3850								
aly2548.22	Probable splicing factor, arginine/serine rich 7	GO:0000381,GO:0071011,GO:0005634,GO:0000398,GO:0000166,GO:0006376,GO:0003723,GO:0008187,GO:0022008,GO:0071013,GO:0005681,GO:0003729	CG4602-PA				SM00360,SM00360		PF00076	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928	255~275								
aly2548.23	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2548.3	Unknown		n/a																				
aly2548.4	Unknown		n/a																				
aly2548.5	Unknown		n/a																				
aly2548.6	Unknown		n/a																				
aly2548.7	Protein tamozhennic	GO:0005737,GO:0008139,GO:0008536,GO:0008270,GO:0005515,GO:0042308,GO:0015031,GO:0007275	CG4057-PA				SM00547,SM00547		PF00641,PF00641	PS50199		PS01358		SSF90209	455~475								
aly2548.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2548.9	Unknown		CG43796-PA																				
aly2550.1	Homeobox protein orthopedia	GO:0043565,GO:0003700,GO:0005634,GO:0006355,GO:0046331,GO:0000976,GO:0003677,GO:0007379,GO:0007275,GO:0007417	CG10036-PK				SM00389		PF00046	PS50071,PS50803	PR00031,PR00031	PS00027	G3DSA:1.10.10.60	SSF46689									
aly2550.2	WD repeat-containing protein on Y chromosome	GO:0005575,GO:0003674,GO:0008150,GO:0005509,GO:0005515	CG40583-PB				SM00320,SM00320,SM00320			PS50294,PS50082			G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978									
aly2550.3	Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial	GO:0019441,GO:0070189,GO:0033512,GO:0047536,GO:0016212,GO:0097052,GO:0003824,GO:0009058,GO:0005739,GO:0030170,GO:0006103,GO:0006536,GO:0042803	CG6321-PA						PF00155				G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383									
aly2550.4	Retinal homeobox protein Rx	GO:0043565,GO:0007420,GO:0003700,GO:0005634,GO:0006355,GO:0006357,GO:0006351,GO:0022008	CG10052-PB				SM00389		PF03826,PF00046	PS50071,PS50803		PS00027	G3DSA:1.10.10.60	SSF46689									
aly2550.5	Unknown	GO:0030414	n/a						PF05375	PS51446				SSF57283									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2550.6	Homeobox protein ARX	GO:0042127,GO:0043565,GO:0003682,GO:0021759,GO:0021846,GO:0003700,GO:0005634,GO:0007411,GO:0006355,GO:0021831,GO:0021853,GO:0006351,GO:0072148,GO:0003677,GO:0001206,GO:0021800,GO:0044241,GO:0046622,GO:0000980	CG33152-PA				SM00389		PF00046	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689										
aly2550.7	Unknown		n/a																				
aly25549.1	Putative BEN domain-containing protein B1		n/a						PF10523	PS51457													
aly2555.1	Unknown		n/a				SM00456		PF00397	PS50020			G3DSA:2.20.70.10	SSF51045									
aly2555.2	Unknown	GO:0006030,GO:0005576,GO:0008061	CG14880-PB				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly2555.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2555.4	Unknown		n/a																				
aly2555.5	Unknown		n/a										G3DSA:3.40.50.620		133~153								
aly2555.6	Superoxide dismutase [Cu-Zn]	GO:0005737,GO:0005507,GO:0007568,GO:0005829,GO:0005777,GO:0005634,GO:0005739,GO:0006979,GO:0019430,GO:0006801,GO:0042803,GO:0004784,GO:0008340,GO:0046872,GO:0016209,GO:0055114,GO:0008270	CG11793-PA						PF00080		PR00068,PR00068,PR00068,PR00068	PS00087,PS00332	G3DSA:2.60.40.200	SSF49329				PWY-6854					
aly2555.7	Ribonuclease P protein subunit p40	GO:0090502,GO:0090501,GO:0008033,GO:0005634,GO:0004526,GO:0005655	n/a						PF08584														
aly2555.8	Protein takeout	GO:0007631,GO:0007623,GO:0007622,GO:0007617,GO:0005576,GO:0003674,GO:0042594,GO:0042595,GO:0008343,GO:0008049,GO:0005615	CG11853-PA				SM00700		PF06585														
aly2555.9	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2559.1	Golgi-associated plant pathogenesis-related protein 1	GO:0010634,GO:0070062,GO:0010718,GO:0000139,GO:0005576,GO:0070374,GO:0042803	CG4270-PA				SM00198,SM00198		PF00188,PF00188		PR00837,PR00837,PR00837,PR00837	PS01009,PS01009	G3DSA:3.40.33.10,G3DSA:3.40.33.10	SSF55797,SSF55797									
aly2559.2	5-hydroxytryptamine receptor 2A	GO:0006939,GO:0016023,GO:0043198,GO:0016021,GO:0007610,GO:0008227,GO:0005901,GO:0046883,GO:0050795,GO:0005887,GO:0005886,GO:0030424,GO:0007186,GO:0007210,GO:0004993	CG42796-PE						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly25599.1	Unknown	GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG2663-PA											SSF46938									
aly25599.2	Alpha-tocopherol transfer protein	GO:0032502,GO:0008431,GO:0005770,GO:0051180,GO:0046909,GO:0005215,GO:0005829,GO:0006810,GO:0090212,GO:0019842,GO:0005546,GO:0005622,GO:0043325,GO:0042360,GO:0060548,GO:0051452,GO:0009268,GO:0009636,GO:0001892,GO:0007584	CG2663-PA						PF00650	PS50191	PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087									
aly25599.3	Alpha-tocopherol transfer protein	GO:0008431,GO:0005770,GO:0006629,GO:0046909,GO:0005215,GO:0005829,GO:0006810,GO:0090212,GO:0005546,GO:0005622,GO:0043325,GO:0042360,GO:0060548,GO:0051452,GO:0009268,GO:0009636,GO:0001892,GO:0007584,GO:0051180	CG2663-PA						PF00650	PS50191	PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF46938,SSF52087	315~316								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly25599.4	Unknown	GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG2663-PA										G3DSA:3.40.525.10	SSF52087									
aly256.1	Hyaluronidase	GO:0004415,GO:0006952,GO:0005576,GO:0005975	n/a						PF01630,PF01630		PR00847,PR00847,PR00847,PR00846,PR00846,PR00846,PR00846		G3DSA:3.20.20.70,G3DSA:3.20.20.70	SSF51445		00531+3.2.1.35							
aly256.10	Doublesex- and mab-3-related transcription factor A2	GO:0003700,GO:0006355,GO:0005634,GO:0046872,GO:0043565	CG15504-PA				SM00301		PF00751	PS50809		PS40000	G3DSA:4.10.1040.10	SSF82927									
aly256.11	Unknown		n/a																				
aly256.12	5-hydroxyisourate hydrolase	GO:0033971,GO:0006810,GO:0006144,GO:0042597	CG30016-PA				SM00095	TIGR02962	PF00576		PR00189,PR00189,PR00189	PS00769,PS00768	G3DSA:2.60.40.180	SSF49472		00230+3.5.2.17		PWY-7394,PWY-5691					
aly256.13	RNA-binding protein 5	GO:0000381,GO:0000245,GO:0005634,GO:0000166,GO:0043065,GO:0008270,GO:0003676,GO:0005681,GO:0003729	CG4896-PD				SM00443		PF01585	PS50102,PS50174			G3DSA:4.10.1060.10,G3DSA:3.30.70.330	SSF54928	576~596								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly256.14	Unknown		CG42361-PA																				
aly256.15	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689	CG4382-PB						PF00135			PS00941,PS00122	G3DSA:3.40.50.1820	SSF53474									
aly256.16	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689	CG4757-PA						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly256.17	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689	CG4757-PA						PF00135,PF00135			PS00122	G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474									
aly256.18	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689	CG4382-PB						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly256.19	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689	CG4757-PA						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly256.2	Inward rectifier potassium channel irk-1	GO:0042391,GO:0043204,GO:0071805,GO:0006813,GO:0090099,GO:0016021,GO:0015467,GO:0035220,GO:0008277,GO:0048812,GO:0043005,GO:0043025,GO:0005242,GO:0046662	CG4370-PD						PF01007		PR01320,PR01320,PR01320,PR01320,PR01320		G3DSA:1.10.287.70,G3DSA:2.60.40.1400	SSF81324,SSF81296									
aly256.20	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689	CG4757-PA						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly256.21	Nicotinamide riboside kinase 1	GO:0019359,GO:0046872,GO:0050262,GO:0005524,GO:0009435	CG12016-PA						PF13238				G3DSA:3.40.50.300	SSF52540									
aly256.22	Unknown	GO:0009059,GO:0030176	CG42456-PA						PF07297														
aly256.23	Unknown		n/a						PF15684														
aly256.24	Unknown	GO:0005576,GO:0005121,GO:0008063	CG9196-PA											SSF57501									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly256.25	Unknown		n/a																				
aly256.26	Unknown		n/a																				
aly256.27	Unknown		n/a																				
aly256.28	Unknown		n/a																				
aly256.29	Unknown		n/a																				
aly256.3	Inward rectifier potassium channel 2	GO:0042391,GO:0071805,GO:0006813,GO:0090099,GO:0016021,GO:0051289,GO:0015467,GO:0035220,GO:0048812,GO:0005242,GO:0031224	CG4370-PD						PF01007,PF01007		PR01320,PR01320,PR01320,PR01320,PR01320		G3DSA:2.60.40.1400,G3DSA:2.60.40.1400,G3DSA:1.10.287.70	SSF81296,SSF81324									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly256.30	39S ribosomal protein L54, mitochondrial	GO:0070126,GO:0006996,GO:0070124,GO:0070125,GO:0005840,GO:0044822,GO:0003735,GO:0005743,GO:0005762,GO:0032543	CG9353-PA						PF08561														
aly256.31	Outer dense fiber protein 3B	GO:0016272	CG10252-PA						PF07004,PF07004														
aly256.32	Unknown		n/a																				
aly256.4	Unknown		n/a																				
aly256.5	Unknown	GO:0005737,GO:0016021,GO:0016627,GO:0006629	CG6282-PD						PF06966	PS50244							REACT_22258						
aly256.6	Unknown		n/a												33~67,108~132								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly256.7	NADPH oxidase 5	GO:0050663,GO:0000910,GO:0050661,GO:0050660,GO:0015992,GO:0005783,GO:0020037,GO:0008283,GO:0016175,GO:0016021,GO:0006915,GO:0043012,GO:0042554,GO:0015252,GO:0005509,GO:0010155,GO:0001525,GO:0001935,GO:2000379,GO:0055114,GO:0016491	CG34399-PC				SM00054,SM00054,SM00054,SM00054		PF08030,PF01794,PF08022,PF13499	PS51384,PS50222,PS50222,PS50222,PS50222,PS50222	PR00450,PR00450	PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:3.40.50.80,G3DSA:3.40.50.80,G3DSA:1.10.238.10,G3DSA:2.40.30.10	SSF52343,SSF52343,SSF47473,SSF47473,SSF63380										
aly256.8	Hydroxylysine kinase	GO:0005737,GO:0016772,GO:0047992	CG31751-PA						PF01636				G3DSA:3.30.200.20,G3DSA:3.90.1200.10	SSF56112									
aly256.9	Doublesex- and mab-3-related transcription factor A1	GO:0043565,GO:0007548,GO:0001541,GO:0060179,GO:0003700,GO:0005634,GO:0006355,GO:0005515,GO:0000987,GO:0046872,GO:0042803	CG15504-PA						PF03474					SSF46934									
aly25603.1	Unknown		n/a																				
aly256081.1	Unknown		n/a																				
aly25622.1	Prostaglandin reductase 1	GO:0005737,GO:0036132,GO:0070062,GO:0009636,GO:0008270,GO:0047522,GO:0032440	n/a						PF16884				G3DSA:3.90.180.10	SSF50129									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly25626.1	Unknown		n/a																				
aly2563.1	Protein unc-50 homolog	GO:0015031,GO:0006810,GO:0030173	CG9773-PA						PF05216														
aly2563.10	ATP synthase subunit b, mitochondrial	GO:0015986,GO:0006909,GO:0046933,GO:0005811,GO:0005739,GO:0015992,GO:0008553,GO:0015078,GO:0000276	CG8189-PA						PF05405					SSF161060	131~151								
aly2563.11	Unknown	GO:0008514,GO:0016020,GO:0015347,GO:0015711,GO:0006810	CG6417-PA										G3DSA:1.20.1250.20,G3DSA:1.20.1250.20										
aly2563.12	UTP--glucose-1-phosphate uridylyltransferase	GO:0005737,GO:0070062,GO:0005634,GO:0006011,GO:0008152,GO:0046872,GO:0003983	CG4347-PA			PIRSF000806			PF01704				G3DSA:3.90.550.10	SSF53448		00500+2.7.7.9,00040+2.7.7.9,00520+2.7.7.9,00052+2.7.7.9		PWY-7238,PWY-3801,PWY-7343,PWY-6527,PWY-6981					
aly2563.13	Solute carrier organic anion transporter family member 2A1	GO:0005319,GO:0006810,GO:0006869,GO:0008514,GO:0005215,GO:0015132,GO:0016020,GO:0015347,GO:0015711,GO:0005887,GO:0005886,GO:0043252,GO:0055085	CG6417-PA						PF03137	PS51465													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2563.14	Solute carrier organic anion transporter family member 2B1	GO:0016020,GO:0015721,GO:0008514,GO:0015125,GO:0006810,GO:0015347,GO:0015711,GO:0016324,GO:0001889,GO:0005515,GO:0016021,GO:0071718	CG6417-PA							PS51465													
aly2563.15	Proclotting enzyme	GO:0004252,GO:0005576,GO:0042381,GO:0006508	CG7432-PB				SM00020		PF00089,PF00089	PS50240,PS50240		PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494,SSF50494									
aly2563.16	Venom serine protease Bi-VSP	GO:0016504,GO:0004252,GO:0005576,GO:0006508	CG1299-PA				SM00680,SM00020		PF00089	PS50240		PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2563.17	Venom serine protease Bi-VSP	GO:0016504,GO:0004252,GO:0005576,GO:0006508	CG1299-PA				SM00020		PF00089	PS50240	PR00722,PR00722	PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2563.2	Proclotting enzyme	GO:0004252,GO:0005576,GO:0042381,GO:0006508	CG7432-PB				SM00020,SM00680		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2563.3	Glutamate-gated chloride channel	GO:0006810,GO:0016021,GO:0045211,GO:1902476,GO:0005230,GO:0016020,GO:0006821,GO:0034707,GO:0048812,GO:0005886,GO:0008068,GO:0006811,GO:0030054	CG7535-PN					TIGR00860	PF02931,PF02932		PR00252,PR00252,PR00252,PR00252,PR00253,PR00253,PR00253,PR00253	PS00236	G3DSA:2.70.170.10,G3DSA:1.20.58.390,G3DSA:1.20.58.390	SSF63712,SSF90112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2563.4	Adipokinetic prohormone	GO:0005179,GO:0007218,GO:0005576,GO:0007629	n/a						PF06377			PS00256											
aly2563.5	Solute carrier organic anion transporter family member 1B2	GO:0051384,GO:0015721,GO:0042493,GO:0001889,GO:0032496,GO:0015893,GO:0033993,GO:0015125,GO:0016020,GO:0015238,GO:0006857,GO:0006855,GO:0034097,GO:0005215,GO:0006810,GO:0015711,GO:0016323,GO:0015198,GO:0005886,GO:0043434,GO:0008514,GO:0015347,GO:0046677,GO:0016021	CG6417-PA						PF03137	PS51465													
aly2563.6	Ras-like protein 2	GO:0016020,GO:0003924,GO:0005622,GO:0005575,GO:0019003,GO:0007165,GO:0005515,GO:0005886,GO:0006184,GO:0007265,GO:0005525	CG1167-PA				SM00176,SM00174,SM00173,SM00175	TIGR00231	PF00071	PS51421	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly2563.7	Cyclin-H	GO:0032806,GO:0006468,GO:0016538,GO:0000079,GO:0005675,GO:0070985,GO:0019901,GO:0006355,GO:0007049,GO:0006367,GO:0006366,GO:0000990,GO:0008353,GO:0004693	CG7405-PA				SM00385	TIGR00569	PF16899,PF00134				G3DSA:1.10.472.10,G3DSA:1.10.472.10	SSF47954,SSF47954									
aly2563.8	Unknown	GO:0006810,GO:0008514,GO:0005215,GO:0016020,GO:0015347,GO:0015711	CG6417-PA						PF03137														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2563.9	Unknown	GO:0005575,GO:0008150,GO:0003674	CG32039-PA						PF15811						49~69								
aly25694.1	P protein	GO:0016020,GO:0005302,GO:0005215,GO:0016021,GO:0006810,GO:0033162,GO:0055085	CG12787-PC																				
aly25695.1	P protein	GO:0005737,GO:0016020,GO:0030318,GO:0008283,GO:0005302,GO:0005215,GO:0016021,GO:0006810,GO:0005789,GO:0005765,GO:0042438,GO:0007286,GO:0033162,GO:0015828,GO:0006726,GO:0055085,GO:0010008	CG12787-PC						PF03600						157~177								
aly257.1	Ice nucleation protein	GO:0050825,GO:0005201,GO:0009279,GO:0008150,GO:0031012	CG5765-PA																				
aly257.2	Unknown		n/a																				
aly25704.1	Probable protein disulfide-isomerase A6	GO:0005783,GO:0030968,GO:0005811,GO:0005788,GO:0003756,GO:2000427,GO:0045454,GO:0015035,GO:0006662	CG5809-PA					TIGR01126	PF00085	PS51352	PR00421,PR00421,PR00421	PS00194	G3DSA:3.40.30.10	SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2578.1	Unknown		n/a																				
aly2578.10	ATP-binding cassette sub-family G member 5	GO:0043190,GO:0042626,GO:0010212,GO:0015918,GO:0007588,GO:0045796,GO:0016324,GO:0005215,GO:0007584,GO:0042493,GO:0030299,GO:0033344,GO:0044281,GO:0016887,GO:0005886,GO:0042632,GO:0046982,GO:0010949,GO:0055085,GO:0005524,GO:0043235	CG11069-PA						PF00005	PS50893			G3DSA:3.40.50.300	SSF52540										
aly2578.11	ATP-binding cassette sub-family G member 8	GO:0015918,GO:0015914,GO:0010949,GO:0044281,GO:0016887,GO:0042626,GO:0005524,GO:0007588,GO:0043235,GO:0016324,GO:0005215,GO:0007584,GO:0006810,GO:0030299,GO:0005886,GO:0042632,GO:0055085,GO:0043190,GO:0045796,GO:0042493,GO:0033344,GO:0015248,GO:0046982	CG31121-PA						PF00005,PF01061	PS50893			G3DSA:3.40.50.300	SSF52540										
aly2578.12	Spermatogenesis associated 6-like protein		CG14079-PA						PF14909														
aly2578.13	Cryptochrome 1	GO:0005737,GO:0009881,GO:0048511,GO:0006281,GO:0005634,GO:0006355,GO:0018298,GO:0000166,GO:0003914,GO:0006351,GO:0003913	CG2488-PA						PF03441,PF00875	PS51645			G3DSA:1.25.40.80,G3DSA:1.10.579.10,G3DSA:3.40.50.620	SSF52425,SSF48173										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2578.14	Unknown		n/a																				
aly2578.15	Cystinosin homolog	GO:0016021,GO:0003333,GO:0015171,GO:0005765,GO:0015184,GO:0015811	CG17119-PA				SM00679,SM00679	TIGR00951	PF04193,PF04193														
aly2578.2	Calreticulin	GO:0031987,GO:0006457,GO:0005615,GO:0007422,GO:0042048,GO:0048854,GO:0005811,GO:0007476,GO:0030246,GO:0005788,GO:0045169,GO:0001964,GO:0051082,GO:0005509,GO:0022008,GO:0007417,GO:0030431	CG9429-PA			PIRSF002356			PF00262,PF00262		PR00626,PR00626,PR00626,PR00626,PR00626,PR00626	PS00805,PS00805,PS00805,PS00804,PS00803	G3DSA:2.60.120.200,G3DSA:2.60.120.200	SSF49899,SSF63887	346~376								
aly2578.3	Guanine nucleotide-binding protein-like 3 homolog	GO:0007494,GO:0008152,GO:0048588,GO:0090307,GO:0016887,GO:0042273,GO:0007431,GO:0042254,GO:0006200,GO:0005525,GO:0042127,GO:0046052,GO:0003924,GO:0046626,GO:0001652,GO:0043273,GO:0009267,GO:0006184,GO:0040014,GO:0090070,GO:0005730,GO:0006254	CG3983-PA						PF01926,PF08701	PS51721	PR00326,PR00326		G3DSA:3.40.50.300,G3DSA:1.10.1580.10	SSF52540	57~94								
aly2578.4	Rho-related GTP-binding protein RhoU	GO:0008360,GO:0042995,GO:0007010,GO:0016601,GO:0000139,GO:0000082,GO:0003924,GO:0030036,GO:0005622,GO:0005575,GO:0046872,GO:1903955,GO:0002102,GO:0008150,GO:0005886,GO:0007264,GO:0005925,GO:0005525	CG34104-PC				SM00174,SM00175,SM00173	TIGR00231	PF00071	PS51420	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2578.5	DNA polymerase epsilon subunit 4	GO:0043565,GO:0008622,GO:0043966,GO:0005622,GO:0003887,GO:0006974,GO:0005671,GO:0006260,GO:0046982	CG11301-PA						PF00808				G3DSA:1.10.20.10	SSF47113									
aly2578.6	Maltase A1	GO:0043169,GO:0005975,GO:0032450,GO:0003824,GO:0006006,GO:0004558	CG8696-PA				SM00642		PF00128				G3DSA:3.90.400.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF51445									
aly2578.7	Unknown		n/a																				
aly2578.8	5'-3' exoribonuclease 1	GO:0071044,GO:0000184,GO:0071028,GO:0005886,GO:0003676,GO:0003677,GO:0005737,GO:0016020,GO:0010603,GO:0004527,GO:0007369,GO:0007476,GO:0006401,GO:0046529,GO:0000723,GO:0005794,GO:0044822,GO:0007126,GO:0045111,GO:0042060,GO:0007283,GO:0016246,GO:0016075,GO:0090503,GO:0007569,GO:0004534,GO:0000932,GO:0007391,GO:0000956,GO:0005634,GO:0006396,GO:0034428	CG3291-PB						PF03159															
aly2578.9	Nuclear transcription factor Y subunit B-2	GO:0048749,GO:0043565,GO:0016602,GO:0003700,GO:0005634,GO:0043410,GO:0006355,GO:0043066,GO:0000976,GO:0006351,GO:0046982,GO:0045678,GO:0045893	CG10447-PA						PF00808		PR00615,PR00615,PR00615		G3DSA:1.10.20.10	SSF47113									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2582.1	Ig-like and fibronectin type-III domain-containing protein C25G4.10	GO:0016021,GO:0005515,GO:0005886	CG17839-PB				SM00409,SM00409,SM00409,SM00060,SM00060,SM00060,SM00060,SM00060,SM00408,SM00408,SM00408		PF01682,PF01682,PF01682,PF00047,PF07679,PF00041,PF00041,PF00041,PF00041,PF00041	PS50853,PS50853,PS50853,PS50835,PS50835,PS50853,PS50835,PS50853,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF49265,SSF49265,SSF49265,SSF48726,SSF49265,SSF48726,SSF49265										
aly2582.10	Adenosine kinase	GO:0044209,GO:0016773,GO:0004001,GO:0005575,GO:0006167,GO:0006166,GO:0005524	CG11255-PA						PF00294		PR00989,PR00989,PR00989,PR00989,PR00989	PS00584	G3DSA:3.30.1110.10,G3DSA:3.40.1190.20	SSF53613		00230+2.7.1.20		PWY-6619	UPA00588				
aly2582.11	60 kDa heat shock protein, mitochondrial	GO:0005811,GO:0006457,GO:0006626,GO:0006458,GO:0051082,GO:0005875,GO:0005743,GO:0042026,GO:0005739,GO:0005524,GO:0005759,GO:0009408,GO:0034605,GO:0007005	CG12101-PA	MF_00600				TIGR02348	PF00118		PR00298,PR00298,PR00298,PR00298,PR00298	PS00296	G3DSA:1.10.560.10,G3DSA:1.10.560.10,G3DSA:3.50.7.10	SSF54849,SSF52029,SSF48592,SSF48592	362~389								
aly2582.12	Tyrosine-protein phosphatase non-receptor type 13	GO:0005856,GO:0016319,GO:0070062,GO:0035071,GO:0008092,GO:0048846,GO:0006470,GO:0004725,GO:0044297,GO:0005737,GO:0048102,GO:0030027,GO:0048036,GO:0043005,GO:0005886,GO:0035335,GO:0036312,GO:0014066,GO:0005634,GO:0040040	CG1228-PG				SM00295,SM00228		PF00373,PF09379,PF00595,PF09380	PS50057,PS50106			G3DSA:2.30.42.10,G3DSA:1.20.80.10,G3DSA:2.30.29.30	SSF50729,SSF50156,SSF47031										
aly2582.13	Vesicle transport through interaction with t-SNAREs homolog 1A	GO:0005794,GO:0016021,GO:0006888,GO:0016192,GO:0008021,GO:0043025,GO:0006886,GO:0090161,GO:0000139,GO:0042147,GO:0044306,GO:0050882,GO:0030173,GO:0005484,GO:0048471,GO:0048280,GO:0005768,GO:0031201,GO:0030136	CG3279-PA						PF05008,PF12352				G3DSA:1.20.5.110,G3DSA:1.20.58.400	SSF47661,SSF58038	68~88,34~58								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2582.14	Unknown		n/a																				
aly2582.15	General vesicular transport factor p115	GO:0005737,GO:0008565,GO:0007030,GO:0006888,GO:0005783,GO:0005730,GO:0051726,GO:0006904,GO:0006886,GO:0016020,GO:0044822,GO:0048211,GO:0000139,GO:0048280,GO:0045056,GO:0005794,GO:0012507,GO:0005795,GO:0048471,GO:0061025,GO:0005829	CG1422-PA						PF04869,PF04871					SSF48371	648~668,720~747								
aly2582.16	Factor VIII intron 22 protein	GO:0005737,GO:0005634,GO:0005515	CG8134-PA										G3DSA:1.25.40.10	SSF48452									
aly2582.17	Serine/threonine-protein kinase RIO3	GO:0004674,GO:0006468,GO:0007059,GO:0005524,GO:0004672	CG3008-PA			PIRSF038146	SM00090		PF01163			PS01245	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly2582.18	60S ribosomal protein L34	GO:0003735,GO:0005622,GO:0022625,GO:0006412,GO:0005840	CG9354-PB	MF_00349					PF01199		PR01250,PR01250,PR01250,PR01250	PS01145											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2582.19	Unknown		n/a																				
aly2582.2	Odorant receptor 30a	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG13106-PA						PF02949														
aly2582.20	Bone morphogenetic protein receptor type-1B	GO:0048100,GO:0006703,GO:0016021,GO:0042078,GO:0008101,GO:1902043,GO:0046872,GO:0030154,GO:0006468,GO:0030425,GO:0048636,GO:0035108,GO:0030509,GO:0045887,GO:0001763,GO:0007304,GO:0005025,GO:0030501,GO:0001745,GO:0007274,GO:0050431,GO:0001948,GO:0060041,GO:0005771,GO:0007476,GO:0030707,GO:0006954,GO:0004675,GO:0004674,GO:0004672,GO:0002062,GO:0002063,GO:0007181,GO:0043025,GO:0005524,GO:0045705,GO:0060350,GO:0031290,GO:0035215,GO:0061036,GO:1902731,GO:0007424,GO:0007488,GO:0046332,GO:0045595,GO:0001501,GO:0001654,GO:0090254,GO:0005886,GO:0030166,GO:0001550,GO:0007179,GO:0007178,GO:0045597,GO:0007507,GO:0001502,GO:0016477,GO:0009953,GO:0046845,GO:0022407,GO:0045927,GO:0045669,GO:0007448,GO:0010629,GO:0007391,GO:0005024,GO:0042698,GO:0006357,GO:0005515,GO:0004702,GO:0061327,GO:0045570,GO:0043010,GO:0005769,GO:0030718	CG14026-PC				SM00220,SM00467		PF00069,PF08515,PF01064	PS51256,PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:2.10.60.10,G3DSA:3.30.200.20	SSF57302,SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2582.21	RNA-binding protein lark	GO:0008104,GO:0008062,GO:0030036,GO:0009790,GO:0007303,GO:0008270,GO:0003676,GO:0007067,GO:0005737,GO:0005634,GO:0000166,GO:0048477,GO:0007623,GO:0071011,GO:0071013,GO:0045475,GO:0045995,GO:0040011,GO:0007562,GO:0000398,GO:0003723,GO:0045804,GO:0003729	CG8597-PB				SM00360,SM00360,SM00343		PF00098,PF00076,PF00076	PS50102,PS50102,PS50158			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:4.10.60.10	SSF54928,SSF54928										
aly2582.22	Unknown		n/a												113~140								
aly2582.23	Stress-activated protein kinase JNK	GO:0048675,GO:0048674,GO:0048615,GO:0019731,GO:0030425,GO:0071243,GO:0035006,GO:0043508,GO:0007411,GO:0035313,GO:0007298,GO:0071907,GO:0005737,GO:0007254,GO:0048803,GO:0043652,GO:0005634,GO:0000165,GO:0030707,GO:0007258,GO:0001736,GO:0004674,GO:0010508,GO:1903688,GO:0004672,GO:0005524,GO:0048666,GO:0006468,GO:0034614,GO:0042060,GO:0071276,GO:0006952,GO:0009267,GO:0009408,GO:0034599,GO:0030424,GO:0006979,GO:0016055,GO:0007391,GO:0004705,GO:0004707,GO:0048812,GO:0046529,GO:0005515,GO:0046844,GO:0046843	CG5680-PB				SM00220		PF00069	PS50011	PR01772,PR01772,PR01772,PR01772,PR01772,PR01772,PR01772,PR01772,PR01772	PS01351,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112			REACT_6900						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2582.24	Transcription initiation factor TFIID subunit 9	GO:0000124,GO:0007221,GO:0051123,GO:0006352,GO:0005634,GO:0001075,GO:0090575,GO:0006357,GO:0006367,GO:0006366,GO:0005669,GO:0046982,GO:0008134	CG6474-PA						PF02291				G3DSA:1.10.20.10	SSF47113									
aly2582.25	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	GO:0050662,GO:0003857,GO:0070403,GO:0006635,GO:0005743,GO:0005811,GO:0005777,GO:0005739,GO:0005654,GO:0004300,GO:0042060,GO:0042594,GO:0005759,GO:0008340,GO:0016507,GO:0005875,GO:0016509	CG4389-PA			PIRSF000105			PF02737,PF00725			PS00067	G3DSA:3.40.50.720,G3DSA:1.10.1040.10	SSF48179,SSF51735		00623+1.1.1.35,00650+5.1.2.3+4.2.1.17+1.1.1.35,00903+4.2.1.17,00592+4.2.1.17,00281+4.2.1.17+1.1.1.35,00120+1.1.1.35,00640+4.2.1.17,00627+4.2.1.17,00071+5.1.2.3+4.2.1.17+1.1.1.35,00062+4.2.1.17+1.1.1.35,00930+4.2.1.17+1.1.1.35,00071+4.2.1.17+1.1.1.35,00720+4.2.1.17+1.1.1.35,00310+4.2.1.17+1.1.1.35,00410+4.2.1.17,00650+4.2.1.17+1.1.1.35,00360+4.2.1.17,00362+4.2.1.17,00380+4.2.1.17+1.1.1.35,00280+4.2.1.17+1.1.1.35		PWY-6435,PWY-6944,PWY-7046,PWY-7216,PWY-1361,PWY-735,PWY-7606,PWY-5177,PWY-6583,PWY-5109,PWY-7094,PWY-6883,PWY-5138,PWY-6945,PWY-5136,PWY-6946,PWY-6863,PWY-7007,PWY-5789,PWY-7401	UPA00659				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2582.26	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	GO:0006635,GO:0046676,GO:0042594,GO:0032868,GO:0003857,GO:0005875,GO:0016491,GO:0005737,GO:0050662,GO:0005811,GO:0005777,GO:0005739,GO:0005654,GO:0004300,GO:0005759,GO:0014823,GO:0042060,GO:0008340,GO:0044255,GO:0055114,GO:0042493,GO:0005743,GO:0016509,GO:0070403,GO:0016507,GO:0044281	CG4389-PA			PIRSF000105			PF00725,PF02737			PS00067	G3DSA:1.10.1040.10,G3DSA:3.40.50.720	SSF48179,SSF51735		00623+1.1.1.35,00650+5.1.2.3+4.2.1.17+1.1.1.35,00903+4.2.1.17,00592+4.2.1.17,00281+4.2.1.17+1.1.1.35,00120+1.1.1.35,00640+4.2.1.17,00627+4.2.1.17,00071+5.1.2.3+4.2.1.17+1.1.1.35,00062+4.2.1.17+1.1.1.35,00930+4.2.1.17+1.1.1.35,00071+4.2.1.17+1.1.1.35,00720+4.2.1.17+1.1.1.35,00310+4.2.1.17+1.1.1.35,00410+4.2.1.17,00650+4.2.1.17+1.1.1.35,00360+4.2.1.17,00362+4.2.1.17,00380+4.2.1.17+1.1.1.35,00280+4.2.1.17+1.1.1.35		PWY-6435,PWY-6944,PWY-7046,PWY-7216,PWY-1361,PWY-735,PWY-7606,PWY-5177,PWY-6583,PWY-5109,PWY-7094,PWY-6883,PWY-5138,PWY-6945,PWY-5136,PWY-6946,PWY-6863,PWY-7007,PWY-5789,PWY-7401	UPA00659				
aly2582.27	Inositol polyphosphate multikinase	GO:0000823,GO:0047326,GO:0046427,GO:0008440,GO:0005730,GO:0005654,GO:0001841,GO:0032958,GO:0000824,GO:0005524	CG13688-PA						PF03770					SSF56104,SSF56104									
aly2582.28	AN1-type zinc finger protein 4	GO:0008270	CG15368-PA				SM00154		PF01428	PS51039			G3DSA:4.10.1110.10	SSF118310									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2582.29	AN1-type zinc finger protein 4	GO:0005840,GO:0022625,GO:0006464,GO:0006412,GO:0003735,GO:0006511,GO:0008270,GO:0005515,GO:0005875	CG2960-PB				SM00213		PF00240	PS50053	PR00348,PR00348,PR00348		G3DSA:3.10.20.90	SSF54236									
aly2582.3	Odorant receptor Or2	GO:0005549,GO:0007608,GO:0042048,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984	CG13106-PA						PF02949														
aly2582.30	40S ribosomal protein S26	GO:0003735,GO:0005622,GO:0022627,GO:0006412,GO:0005840	CG10305-PB						PF01283			PS00733											
aly2582.31	PEST proteolytic signal-containing nuclear protein	GO:0005654,GO:0016567,GO:0007049,GO:0043161	n/a						PF15473														
aly2582.32	CDK5RAP1-like protein	GO:0046872,GO:0000079,GO:0016740,GO:0051539,GO:0009451	CG6345-PA				SM00729	TIGR00089,TIGR01574	PF04055,PF01938,PF00919	PS50926,PS51449		PS01278	G3DSA:3.80.30.20	SSF102114									
aly2582.33	Ankyrin repeat domain-containing protein 6	GO:0005737,GO:0090090,GO:2000096,GO:0042067,GO:0005634,GO:0046330,GO:0005515,GO:0001737,GO:0001736	CG12342-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF13637,PF12796	PS50088,PS50088,PS50088,PS50297,PS50088			G3DSA:1.25.40.20	SSF48403	411~431,299~319								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2582.34	Serine protease 30	GO:0046658,GO:0004252,GO:0017080,GO:0006814,GO:0006508	CG13318-PA						PF00089	PS50240			G3DSA:2.60.40.10,G3DSA:2.40.10.10	SSF50494									
aly2582.35	Nucleolar pre-ribosomal-associated protein 1	GO:0022008,GO:0044822,GO:0005730	CG12499-PA						PF11707,PF16201						472~492								
aly2582.36	Unknown		n/a																				
aly2582.37	Stimulator of interferon genes protein	GO:0032608,GO:0005783,GO:0035438,GO:0005789,GO:0035458,GO:0032092,GO:0016021,GO:0005777,GO:0002230,GO:0048471,GO:0008134,GO:0042802,GO:0033160,GO:0005794,GO:0045087,GO:0006915,GO:0019901,GO:0032481,GO:0061507,GO:0005886,GO:0042993,GO:0031625,GO:0051607,GO:0071360,GO:0002218,GO:0005741,GO:0045944,GO:0042803	CG1667-PB						PF15009														
aly2582.38	Nucleoporin-like protein 2	GO:0005737,GO:0005643,GO:0005634,GO:0031965,GO:0005654,GO:0044822,GO:0015031,GO:0051028,GO:0046872,GO:0001750	CG18787-PB				SM00356		PF00642	PS50103			G3DSA:4.10.1000.10	SSF90229									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2582.39	U5 small nuclear ribonucleoprotein 40 kDa protein	GO:0005737,GO:0005732,GO:0030532,GO:0071011,GO:0071013,GO:0044822,GO:0003988,GO:0008380,GO:0005654,GO:0000375,GO:0010467,GO:0005515,GO:0007067,GO:0005682,GO:0006396	CG3436-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50294,PS50082,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678,PS00678,PS00678	G3DSA:2.130.10.10	SSF50978										
aly2582.4	Unknown	GO:0005549,GO:0016020,GO:0007608,GO:0004984	n/a						PF02949														
aly2582.40	Nucleoside diphosphate kinase 6	GO:0030308,GO:0006228,GO:0005739,GO:0005622,GO:0006241,GO:0004550,GO:0005524,GO:0006165,GO:0045839,GO:0046872,GO:0006183	CG5310-PA				SM00562		PF00334		PR01243,PR01243,PR01243	PS00469	G3DSA:3.30.70.141	SSF54919		00230+2.7.4.6,00240+2.7.4.6		PWY-7210,PWY-7198,PWY-7176,PWY-7220,PWY-7184,PWY-7187,PWY-7205,PWY-7224,PWY-7197,PWY-7226,PWY-7227,PWY-7221,PWY-6545,PWY-7222						
aly2582.41	Enkurin domain-containing protein 1	GO:0005881,GO:0015630	CG11125-PA						PF13864	PS51665					290~310								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2582.42	Unknown		n/a																				
aly2582.43	Protein charybde	GO:0005737,GO:0045926,GO:0009968,GO:0008258,GO:0006915,GO:0003674,GO:0032006,GO:0008219,GO:0006979	CG7533-PC						PF07809						39~59								
aly2582.44	Unknown		CG15601-PA				SM00595		PF10545	PS51029													
aly2582.45	Unknown	GO:0046331	CG5953-PA				SM00595		PF10545	PS51029													
aly2582.46	Unknown	GO:0046331	CG5953-PA						PF10545	PS51029													
aly2582.47	Unknown	GO:0003677	CG13204-PA				SM00595		PF10545,PF02944	PS51029													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2582.48	Unknown	GO:0003677	CG13204-PA				SM00595		PF10545,PF02944	PS51029					271~274								
aly2582.49	Unknown		n/a																				
aly2582.5	Odorant receptor 22c	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG15377-PA						PF02949														
aly2582.50	Unknown	GO:0042600	CG15570-PA								PR01217,PR01217,PR01217,PR01217												
aly2582.6	Odorant receptor 22a	GO:0005549,GO:0007608,GO:0071683,GO:0016021,GO:0016020,GO:0030425,GO:0050911,GO:0004888,GO:0005886,GO:0004984,GO:0032590	CG12193-PA						PF02949														
aly2582.7	Cytochrome P450 4V2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016021,GO:0016020,GO:0005789,GO:0005506,GO:0010430,GO:0055114,GO:0009055	CG16761-PA						PF00067,PF00067		PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2582.8	F-box/LRR-repeat protein 15	GO:0005737,GO:0009953,GO:0000086,GO:0031146,GO:0016567,GO:0048512,GO:0045475,GO:0043153,GO:0030513,GO:0030282,GO:0019005	CG8873-PA				SM00367,SM00367,SM00367,SM00367,SM00367,SM00367						G3DSA:3.80.10.10	SSF52047										
aly2582.9	Histone acetyltransferase KAT6A	GO:0016319,GO:2000737,GO:0006473,GO:0003677,GO:0010628,GO:0008270,GO:0000786,GO:0016605,GO:0000123,GO:0005730,GO:0033563,GO:0005634,GO:0004402,GO:0016573,GO:0043966,GO:0046425,GO:0008134,GO:0045892,GO:0045893,GO:0007405,GO:0036099,GO:0006334,GO:0090398,GO:0070776,GO:0006355,GO:0016407,GO:0006351,GO:0030099	CG11290-PA				SM00526		PF01853	PS51726,PS51504			G3DSA:3.30.60.60,G3DSA:1.10.10.10,G3DSA:3.40.630.30	SSF55729,SSF46785	1698~1718								
aly2584.1	Unknown	GO:0005575,GO:0003674,GO:0008150	CG15589-PA																				
aly2584.2	Unknown	GO:0003674,GO:0008150,GO:0005887	CG1148-PB						PF07898														
aly2584.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2584.4	Unknown		n/a												90~124,40~60								
aly2584.5	Venom allergen 5	GO:0005576,GO:0003674,GO:0032504	CG3640-PA						PF00188				G3DSA:3.40.33.10	SSF55797									
aly2584.6	Unknown		n/a												200~220								
aly258728.1	Probable manganese-transporting ATPase C10C6.6	GO:0000166,GO:0006812,GO:0016021,GO:0019829,GO:0005789,GO:0016887,GO:0015662,GO:0046872,GO:0005524	CG6230-PA																				
aly2588.1	Rap1 GTPase-activating protein 1	GO:0051056,GO:0005099,GO:0005829,GO:0003924,GO:0060293,GO:0016020,GO:0005096,GO:0000139,GO:0032861,GO:0042803,GO:1903697,GO:0007165,GO:0008152,GO:0046582,GO:0007265,GO:0017016,GO:0043087,GO:0002121,GO:0043547	CG44086-PH				SM00390		PF02145,PF02188	PS50877,PS50085				SSF111347	770~797									
aly258887.1	Fatty acyl-CoA reductase 1	GO:0005778,GO:0080019,GO:0016021,GO:0050062,GO:0010025,GO:0046474,GO:0035336,GO:0008611	CG1441-PA						PF07993								REACT_22258						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly259.1	Unknown	GO:0003676	n/a											SSF53098,SSF53098									
aly259.10	Alpha-tocopherol transfer protein-like	GO:0016918,GO:0005215,GO:0016020,GO:0006810,GO:0005622	CG10546-PA				SM01100		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087,SSF46938	56~76								
aly259.11	Chondroitin sulfate proteoglycan 4	GO:0000187,GO:0030207,GO:0030204,GO:0030203,GO:0030206,GO:0051286,GO:0048771,GO:0030208,GO:0044281,GO:0004871,GO:0007169,GO:0035556,GO:0001525,GO:0007517,GO:0005925,GO:0070062,GO:0031258,GO:0051491,GO:0016203,GO:0005796,GO:0008283,GO:0016324,GO:0009986,GO:0019901,GO:0043202,GO:0005887,GO:0022008,GO:0008347,GO:0005975,GO:0050731,GO:0005576,GO:0005515	CG10275-PB				SM00282,SM00282		PF16184,PF16184,PF16184,PF16184,PF16184,PF16184,PF16184,PF16184,PF02210,PF02210	PS51257,PS50025,PS50025			G3DSA:2.60.120.200,G3DSA:2.60.120.200	SSF49899,SSF49899									
aly259.12	Chromatin complexes subunit BAP18	GO:0008574,GO:0008017,GO:0007018,GO:0000090,GO:0016589,GO:0016568,GO:0003777,GO:0003677,GO:0005871,GO:0003682,GO:0071339,GO:0005524	CG32955-PG				SM00717		PF00249				G3DSA:1.10.10.60	SSF46689									
aly259.13	Chromatin complexes subunit BAP18	GO:0008574,GO:0008017,GO:0007018,GO:0000090,GO:0016589,GO:0016568,GO:0003777,GO:0003677,GO:0005871,GO:0003682,GO:0071339,GO:0005524	CG32955-PG						PF00249				G3DSA:1.10.10.60	SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly259.14	LIM homeobox transcription factor 1-beta (Fragment)	GO:0043565,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0007275,GO:0006351	CG32105-PB				SM00389,SM00132,SM00132		PF00412,PF00412,PF00046	PS50071,PS50023,PS50023		PS00478,PS00478,PS00027	G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:1.10.10.60	SSF57716,SSF46689,SSF57716	226~246								
aly259.15	Unknown		n/a																				
aly259.16	Unknown	GO:0003676	n/a										G3DSA:3.30.420.10										
aly259.17	Unknown		n/a																				
aly259.18	F-box/WD repeat-containing protein 7	GO:0035147,GO:0045926,GO:0030332,GO:0016567,GO:0060438,GO:0005634,GO:0031146,GO:0060253,GO:0042023,GO:0019005,GO:0030162,GO:0008054,GO:0005515,GO:0071456,GO:0007411,GO:0007096,GO:0007088,GO:0004842,GO:1903146,GO:1900038	CG15010-PC				SM00256,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF00400,PF00400,PF12937	PS50082,PS50082,PS50181,PS50082,PS50082,PS50082,PS50294,PS50082,PS50082	PR00320,PR00320,PR00320,PR00320	PS00678,PS00678,PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:1.20.1280.50,G3DSA:2.130.10.10	SSF50978,SSF81383										
aly259.19	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly259.2	Unknown		n/a																				
aly259.20	Protein bric-a-brac 1	GO:0007548,GO:0048092,GO:0048086,GO:0007480,GO:0003700,GO:0007455,GO:0005634,GO:0007478,GO:0048071,GO:0048070,GO:0006355,GO:0006351,GO:0005515,GO:0003677,GO:0003680,GO:0008585,GO:0046660	CG9097-PB				SM00225		PF05225,PF00651	PS50097,PS50960			G3DSA:3.30.710.10	SSF46689,SSF54695										
aly259.21	CCR4-NOT transcription complex subunit 1	GO:0030014,GO:0032947,GO:0048387,GO:0005737,GO:0007517,GO:0005778,GO:0000289,GO:0001829,GO:0000122,GO:0016020,GO:0005654,GO:1900153,GO:2000036,GO:0006402,GO:0033147,GO:0030331,GO:0044822,GO:0061014,GO:0060213,GO:0019904,GO:0022008,GO:0005615,GO:0090503,GO:0035195,GO:0010606,GO:0000932,GO:0048813,GO:0070016,GO:0006351,GO:0005515,GO:0017148,GO:0042974,GO:0007095	CG34407-PH						PF16415,PF04054,PF16418,PF16417,PF12842														
aly259.22	DNA-binding protein D-ETS 3	GO:0043565,GO:0003700,GO:0005634,GO:0030154,GO:0006355,GO:0006357,GO:0003677,GO:0000981	CG7018-PA				SM00413		PF00178	PS50061	PR00454,PR00454,PR00454,PR00454	PS00346,PS00345	G3DSA:1.10.10.10	SSF46785									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly259.23	Succinate dehydrogenase [ubiqui] flavoprotein subunit, mitochondrial	GO:0050660,GO:0005739,GO:0005743,GO:0006099,GO:0022900,GO:0008177,GO:0004776,GO:0005749	CG17246-PB						PF02910,PF00890				G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:4.10.80.40,G3DSA:3.90.700.10,G3DSA:1.20.58.100	SSF46977,SSF56425,SSF51905,SSF51905									
aly259.24	Unknown		n/a										G3DSA:1.20.1300.10	SSF81343									
aly259.25	Protein SCAI	GO:0005737,GO:0030336,GO:0016021,GO:0003714,GO:0031965,GO:1903507,GO:0035024,GO:0006355,GO:0006351,GO:0005634	CG13293-PB						PF12070														
aly259.26	Unknown		CG43078-PH												289~309								
aly259.27	High affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A	GO:0048675,GO:0009187,GO:0006198,GO:0048149,GO:0007619,GO:0004114,GO:0007617,GO:0007614,GO:0007612,GO:0007613,GO:0007611,GO:0007165,GO:0046958,GO:0019933,GO:0001661,GO:0040040,GO:0008355,GO:0000003,GO:0004115,GO:0046872,GO:0048477,GO:0007623,GO:0008306,GO:0045475,GO:0007268,GO:0005829,GO:0046331	CG32498-PB				SM00471		PF00233		PR00387,PR00387,PR00387,PR00387,PR00387,PR00387	PS00126	G3DSA:1.10.1300.10	SSF109604	627~647								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly259.28	Paraplegin	GO:0004222,GO:0007399,GO:0016021,GO:0005739,GO:0008089,GO:0008237,GO:0051082,GO:0008270,GO:0016887,GO:0006508,GO:0007005,GO:0031966,GO:0008233,GO:0005524	CG2658-PA	MF_01458			SM00382	TIGR01241	PF01434,PF00004				G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540,SSF140990	216~236,667~687								
aly259.29	Unknown		CG17570-PA																				
aly259.3	Unknown		n/a																				
aly259.30	Unknown	GO:0003676	n/a						PF03184														
aly259.31	Unknown		n/a																				
aly259.32	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly259.33	Unknown	GO:0003677	n/a						PF05225					SSF46689									
aly259.34	Unknown		n/a																				
aly259.35	IQ and AAA domain-containing protein 1-like	GO:0005524	CG16789-PA						PF00004				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	160~185,208~228,414~443								
aly259.4	TPPP family protein CG45057	GO:0005575,GO:0048812,GO:0003674	CG45057-PE						PF05517					SSF47473									
aly259.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly259.6	Basement membrane-specific heparan sulfate proteoglycan core protein	GO:0016319,GO:0008022,GO:0030204,GO:0006909,GO:0005887,GO:0060351,GO:0030425,GO:0030424,GO:0021551,GO:0007419,GO:0008104,GO:0008046,GO:0042157,GO:0070593,GO:0007411,GO:0007413,GO:0032490,GO:0001523,GO:0030203,GO:0001525,GO:0070062,GO:0048846,GO:0005615,GO:0048704,GO:0005576,GO:0043005,GO:0002062,GO:0046872,GO:0043025,GO:0042802,GO:0042803,GO:0048666,GO:0050976,GO:0005796,GO:0005925,GO:0007603,GO:0043202,GO:0003823,GO:0005886,GO:0031012,GO:0007420,GO:0005605,GO:0005975,GO:0050770,GO:0007422,GO:0022617,GO:0001958,GO:0048738,GO:0030198,GO:0048814,GO:0006027,GO:0006024,GO:0044281	CG33950-PAT				SM00179,SM00179,SM00179,SM00179,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00282,SM00282,SM00282,SM00281,SM00281,SM00281		PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF02210,PF02210,PF02210,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00053,PF00053,PF00053,PF00053,PF00053,PF00052,PF00052,PF00052,PF13927,PF13927,PF13927,PF13927,PF13895,PF13895,PF13895	PS50835,PS50068,PS50835,PS50025,PS50068,PS50835,PS50026,PS50835,PS51115,PS50835,PS50027,PS50835,PS51115,PS50026,PS50835,PS50068,PS50027,PS50027,PS50068,PS50835,PS50068,PS50068,PS50026,PS50025,PS50068,PS50068,PS50835,PS50027,PS50835,PS50026,PS50835,PS50068,PS50068,PS50068,PS50835,PS50068,PS50068,PS50835,PS50068,PS50025,PS50835,PS50027,PS50026,PS50068,PS50068,PS51115	PR00261,PR00261,PR00261,PR00261,PR00261,PR00261,PR00261	PS01209,PS01186,PS00022,PS01209,PS00022,PS01209,PS00022,PS01209,PS00022,PS01209,PS01186,PS01209,PS00022,PS01209,PS01186,PS00022,PS01209,PS00022,PS01209,PS01248,PS00022,PS01209,PS01186,PS01248,PS00022,PS01209,PS00010,PS00022,PS01248,PS01186,PS01186,PS01209,PS01186,PS01248,PS01248,PS00022,PS01186,PS01209,PS01248,PS01248	G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.10.25.10,G3DSA:2.60.40.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.170.300.10,G3DSA:2.60.40.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.120.200,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.120.200,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10	SSF49899,SSF48726,SSF57424,SSF57196,SSF57424,SSF48726,SSF57424,SSF57424,SSF49899,SSF48726,SSF57424,SSF57424,SSF57196,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF57424,SSF57424,SSF57424,SSF48726,SSF48726,SSF48726,SSF49899,SSF57424,SSF57424,SSF48726,SSF48726,SSF57196								
aly259.7	Low-density lipoprotein receptor-related protein 2	GO:0006898,GO:0020028,GO:0005903,GO:0005905,GO:0008188,GO:0033280,GO:0005737,GO:0010165,GO:0004930,GO:0005615,GO:0016021,GO:0016020,GO:0045056,GO:0046879,GO:0005509,GO:0032403,GO:0007186,GO:0043234,GO:0032526,GO:0006766,GO:0031100,GO:0016324,GO:0060070,GO:0030165,GO:0010951,GO:0044332,GO:0050750,GO:0016197,GO:0007568,GO:0030492,GO:0005768,GO:0045121,GO:0042493,GO:0031526,GO:0042813,GO:0017147,GO:0042953,GO:0016500,GO:0004872	CG34411-PC				SM00192		PF00057,PF01390	PS50068,PS50024		PS01209	G3DSA:4.10.400.10,G3DSA:3.30.70.960	SSF82671,SSF57424									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly259.8	Aldose 1-epimerase	GO:0005737,GO:0005975,GO:0016853,GO:0004034,GO:0019318,GO:0030246,GO:0006012,GO:0005576,GO:0006006,GO:0070062	CG10467-PA						PF01263				G3DSA:2.70.98.10,G3DSA:2.70.98.10	SSF74650,SSF74650									
aly259.9	Unknown		n/a												108~128								
aly2593.1	Elongation of very long chain fatty acids protein AAEL008004	GO:0006633,GO:0009922,GO:0016021,GO:0030497,GO:0005575,GO:0016740,GO:0030176	CG5278-PA						PF01151							00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					
aly2593.2	Elongation of very long chain fatty acids protein 4	GO:0007111,GO:0007110,GO:0007112,GO:0000915,GO:0000212,GO:0016021,GO:0030497,GO:0005789,GO:0009922,GO:0016740,GO:0030176,GO:0019367,GO:0042761,GO:0051225,GO:0005783	CG6921-PB						PF01151							00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2593.3	Elongation of very long chain fatty acids protein 2	GO:0009922,GO:0036109,GO:0005783,GO:0016021,GO:0043651,GO:0030497,GO:0005789,GO:0005575,GO:0019432,GO:0034626,GO:0035338,GO:0044281,GO:0044255,GO:0033559,GO:0042761,GO:0006636	CG5278-PA						PF01151							00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598							
aly2593.4	Elongation of very long chain fatty acids protein 7	GO:0007111,GO:0007110,GO:0007112,GO:0000915,GO:0000212,GO:0016021,GO:0030497,GO:0005789,GO:0009922,GO:0019432,GO:0016740,GO:0034626,GO:0035338,GO:0044281,GO:0019367,GO:0044255,GO:0042761,GO:0051225,GO:0005783	CG6921-PB						PF01151							00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598							
aly2594.1	Kin of IRRE-like protein 3	GO:0072102,GO:0048812,GO:0021740,GO:0043198,GO:0016021,GO:0007606,GO:0030424,GO:0005575,GO:0001764,GO:0005576,GO:0003674,GO:0005886,GO:0030097,GO:0002121	CG33512-PB				SM00409,SM00409,SM00408,SM00408		PF07679,PF00047	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726										
aly2599.1	Unknown		n/a																				
aly2599.2	Unknown	GO:0016021,GO:0050909	n/a						PF08395														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2599.3	Coiled-coil domain-containing protein 113	GO:0005737,GO:0005654,GO:0043234,GO:0034451,GO:0042384	CG13693-PA						PF13870						374~394,39~59,158~178								
aly26.1	Synaptogyrin-3	GO:0031594,GO:0030672,GO:0032411,GO:0008021,GO:0016079,GO:0016021,GO:0016020,GO:0017158,GO:0021762,GO:0022008,GO:0030054,GO:0048489	CG10808-PA							PS51225													
aly26.10	Ankyrin repeat and fibronectin type-III domain-containing protein 1	GO:0007165	CG45058-PG				SM00248,SM00248,SM00314		PF13637	PS50200,PS50853,PS50297,PS50088			G3DSA:2.60.40.10,G3DSA:1.25.40.20	SSF48403,SSF49265	1010~1030								
aly26.11	Hydroxysteroid dehydrogenase like protein 2	GO:0016616,GO:0005811,GO:0005777,GO:0008152,GO:0005875,GO:0016491	CG5590-PA						PF02036,PF00106		PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720,G3DSA:3.30.1050.10	SSF51735,SSF55718									
aly26.12	Adenylosuccinate lyase	GO:0004018,GO:0044208,GO:0005829,GO:0070626,GO:0009152,GO:0006163,GO:0003824,GO:0006189,GO:0044281,GO:0006167,GO:0006144,GO:0055086	CG3590-PA				SM00998	TIGR00928	PF10397,PF00206		PR00145,PR00145,PR00145,PR00149,PR00149,PR00149	PS00163	G3DSA:1.10.275.10,G3DSA:1.20.200.10	SSF48557		00250+4.3.2.2,00230+4.3.2.2		PWY-7219,PWY-6123,PWY-6124,PWY-7234	UPA00075,UPA00074				
aly26.13	Chitotriosidase-1	GO:0009617,GO:0005975,GO:0005615,GO:0008843,GO:0006955,GO:0000272,GO:0005764,GO:0005576,GO:0008061,GO:0004568,GO:0006030,GO:0006032	CG9357-PA				SM00494,SM00494,SM00494,SM00636		PF01607,PF01607,PF01607,PF00704	PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:3.20.20.80	SSF57625,SSF57625,SSF57625,SSF51445,SSF51445	2247~2247								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly26.14	Unknown		n/a										G3DSA:2.40.128.20	SSF50814									
aly26.15	Exocyst complex component 6	GO:0016192,GO:0000145,GO:0042331,GO:0016081,GO:0006904,GO:0055037,GO:0031410,GO:0017137,GO:0090522,GO:0015031,GO:0022416,GO:0032456,GO:0016080,GO:0007269,GO:0007411,GO:0007298,GO:0072659,GO:0005768,GO:0043679	CG7034-PA			PIRSF025007			PF04091						34~54								
aly26.16	Aconitate hydratase, mitochondrial	GO:0051538,GO:0051539,GO:0043209,GO:0005634,GO:0005811,GO:0005739,GO:0006099,GO:0006101,GO:0008152,GO:0006102,GO:0003994,GO:0005506	CG9244-PB						PF00694,PF00330,PF00330		PR00415,PR00415,PR00415,PR00415,PR00415,PR00415	PS01244	G3DSA:3.30.499.10,G3DSA:3.30.499.10,G3DSA:3.20.19.10,G3DSA:3.40.1060.10	SSF52016,SSF53732		00290+4.2.1.33			UPA00048				
aly26.17	60S ribosomal protein L22 2	GO:0005840,GO:0022625,GO:0005622,GO:0003735,GO:0007052,GO:0000022,GO:0006412	CG7434-PA						PF01776														
aly26.18	Unknown		n/a																				
aly26.19	E3 ubiquitin-protein ligase RING2-A	GO:0035518,GO:0036353,GO:0030708,GO:0006351,GO:0031519,GO:0005730,GO:0006342,GO:0030713,GO:0000122,GO:0008278,GO:0071339,GO:0045498,GO:0008270,GO:0005515,GO:0035102,GO:0007275,GO:0022008,GO:0016874,GO:0005634,GO:0007062	CG5595-PA				SM00184		PF16207,PF00097	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly26.2	Histone acetyltransferase KAT8	GO:0072487,GO:0043981,GO:0035064,GO:0010506,GO:0046972,GO:0009047,GO:0000123,GO:0006325,GO:0005634,GO:0000805,GO:0004402,GO:0005654,GO:0016747,GO:0016573,GO:0046872,GO:0016456,GO:0071339,GO:0005667,GO:0018394,GO:0008134,GO:0031965,GO:0045892,GO:0045893,GO:0000776,GO:0051091,GO:0007549,GO:0043982,GO:0004468,GO:0044545,GO:0005705,GO:0043984,GO:0006355,GO:0016407,GO:0006351,GO:0005515,GO:0030099,GO:0003682,GO:0003729	CG3025-PA						PF11717,PF01853	PS51726			G3DSA:3.40.630.30,G3DSA:2.30.30.270,G3DSA:2.30.30.270	SSF55729,SSF54160										
aly26.20	Unknown		CG12880-PA						PF16027														
aly26.21	Alkyldihydroxyacetonephosphate synthase	GO:0050660,GO:0008762,GO:0008609,GO:0005777,GO:0003824,GO:0055114,GO:0071949,GO:0008611,GO:0008610	CG10253-PA						PF01565,PF02913	PS51387			G3DSA:3.30.465.10,G3DSA:3.30.43.10	SSF55103,SSF55103,SSF56176		00520+1.3.1.98,00550+1.3.1.98		PWY-6386,PWY-6387	UPA00219				
aly26.22	Innexin inx2	GO:0016324,GO:0005737,GO:0010496,GO:0007440,GO:0016328,GO:0055085,GO:0042048,GO:0016021,GO:0016327,GO:0016331,GO:0016323,GO:0007293,GO:0006811,GO:0007154,GO:0005243,GO:0030727,GO:0005921	CG4590-PA						PF00876	PS51013	PR01262,PR01262,PR01262,PR01262,PR01262,PR01262												
aly26.23	Protein BUD31 homolog	GO:0071011,GO:0005634,GO:0071013,GO:0022008,GO:0000398	CG1639-PA						PF01125		PR00322,PR00322,PR00322,PR00322,PR00322	PS00997,PS00998			22~42								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly26.24	Unknown		n/a								PR01217,PR01217,PR01217,PR01217												
aly26.25	Unconventional myosin-XV	GO:0005737,GO:0007626,GO:0042472,GO:0070062,GO:0042623,GO:0007605,GO:0006886,GO:0007391,GO:0032420,GO:0030175,GO:0016461,GO:0016459,GO:0005515,GO:0046847,GO:0043025,GO:0003774,GO:0005524	CG43657-PD				SM00242,SM00015,SM00015,SM00015,SM00295,SM00139,SM00139		PF00063,PF00612,PF00612,PF00784,PF00784	PS50096,PS51456,PS50096,PS50057,PS51016,PS50096	PR00193,PR00193,PR00193,PR00193,PR00193		G3DSA:2.30.29.30	SSF52540,SSF50729	2401~2421,783~808									
aly26.26	Unknown		CG13566-PB																				
aly26.27	APOBEC1 complementation factor	GO:0005737,GO:0050821,GO:0030895,GO:0035770,GO:0005783,GO:0046011,GO:0006397,GO:0071011,GO:0016556,GO:0016554,GO:0000398,GO:0000166,GO:0005654,GO:0003727,GO:0010467,GO:0003723,GO:0007310,GO:0022008,GO:0003729,GO:0046843	CG17838-PJ				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928										
aly26.28	Unknown		n/a																				
aly26.29	Developmentally-regulated GTP-binding protein 2	GO:0005737,GO:0016020,GO:0007165,GO:0005739,GO:0005525	CG6195-PA					TIGR00231	PF16897,PF02824,PF01926	PS51710	PR00326,PR00326,PR00326,PR00326	PS00905	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540		00970+6.1.1.3							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly26.3	Ras-related protein Rac1	GO:0048675,GO:0019897,GO:0007394,GO:0006909,GO:0042052,GO:0016335,GO:0008258,GO:0030032,GO:0032794,GO:0050807,GO:0031941,GO:0030036,GO:0034334,GO:0007419,GO:0007164,GO:0007391,GO:0031175,GO:0007411,GO:0007298,GO:0007413,GO:0071907,GO:0071902,GO:0007017,GO:0051963,GO:0007254,GO:0016028,GO:0045216,GO:0048615,GO:0097206,GO:0031532,GO:0002433,GO:0030707,GO:0051491,GO:0051450,GO:0048814,GO:0005525,GO:0016203,GO:0050975,GO:0008078,GO:0035212,GO:0008283,GO:0042067,GO:0007424,GO:0003924,GO:0048747,GO:0035011,GO:0035010,GO:0007516,GO:0008045,GO:0007409,GO:0005886,GO:0007520,GO:0007264,GO:0008347,GO:0000902,GO:0035099,GO:0007015,GO:0010593,GO:0007426,GO:0050770,GO:0051726,GO:0005829,GO:0007422,GO:0046664,GO:0030866,GO:0016199,GO:0007390,GO:0006974,GO:0048813,GO:0035320,GO:0090303,GO:0007435,GO:0005515,GO:0051017,GO:0045610,GO:0046843	CG2248-PA				SM00175,SM00174,SM00173	TIGR00231	PF00071	PS51420	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly26.30	ER membrane protein complex subunit 3	GO:0005794,GO:0030140,GO:0016021,GO:0016020,GO:0072546,GO:0042060,GO:0003674,GO:0060041,GO:0034975,GO:0045494	CG6750-PA						PF01956,PF01956														
aly26.31	Endonuclease III-like protein 1	GO:0006284,GO:0006285,GO:0051539,GO:0006281,GO:0000703,GO:0005739,GO:0006974,GO:0003824,GO:0006296,GO:0003677,GO:0003690,GO:0046872,GO:0005634,GO:1903146	CG9272-PA	MF_03183			SM00478,SM00525		PF00730,PF00633				G3DSA:1.10.340.30,G3DSA:1.10.1670.10	SSF48150			REACT_216						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly26.32	Nucleolar protein 12	GO:0008284,GO:0035214,GO:0005730,GO:0030307,GO:0019843,GO:0043066,GO:0003674,GO:0045572,GO:0007000	CG32418-PA						PF09805						185~205,32~67								
aly26.33	TATA-binding protein-associated factor 172	GO:0019730,GO:0006963,GO:0004003,GO:0045087,GO:0003677,GO:0004386,GO:0003700,GO:0045892,GO:0042742,GO:0008063,GO:0035562,GO:0005634,GO:0005524	CG4261-PB				SM00487,SM00490		PF00176,PF00271,PF12054,PF12054	PS51194,PS51192			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF52540,SSF52540	172~173,186~192								
aly26.34	Axin	GO:0005737,GO:0007507,GO:0038032,GO:0010941,GO:0007447,GO:0043547,GO:0042594,GO:0007455,GO:0005634,GO:0016055,GO:0005096,GO:0008013,GO:0019901,GO:0004871,GO:0005886,GO:0035019,GO:0006909,GO:0007476,GO:0048477,GO:0030178	CG7926-PA				SM00021,SM00315		PF00778,PF08833,PF00615	PS50841,PS50132			G3DSA:1.10.196.10,G3DSA:1.10.196.10,G3DSA:1.10.167.10	SSF54236,SSF48097									
aly26.35	Histone H2A deubiquitinase MYSM1	GO:0003682,GO:0006338,GO:0005634,GO:0035522,GO:0003713,GO:0042393,GO:0045944,GO:0006351,GO:0003677,GO:0046872,GO:0004843,GO:0008237	n/a						PF14464				G3DSA:3.40.140.10	SSF102712,SSF102712,SSF46689									
aly26.36	Sulfide:quinone oxidoreductase, mitochondrial	GO:0000098,GO:0070221,GO:0070813,GO:0000096,GO:0070224,GO:0005743,GO:0034641,GO:0044281,GO:0048038,GO:0055114,GO:0016491	CG14997-PB						PF07992,PF07992	PS51257	PR00368,PR00368,PR00368		G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905									
aly26.37	Sulfide:quinone oxidoreductase, mitochondrial	GO:0000098,GO:0070221,GO:0070813,GO:0000096,GO:0070224,GO:0005743,GO:0034641,GO:0044281,GO:0048038,GO:0055114,GO:0016491	CG14997-PB										G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905,SSF51905									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly26.38	Carboxypeptidase N subunit 2	GO:0072562,GO:0005515,GO:0070062	CG5195-PA				SM00365,SM00365,SM00365,SM00365,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly26.39	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	GO:0033539,GO:0050660,GO:0042594,GO:0006635,GO:0051289,GO:0046359,GO:0000062,GO:0031966,GO:0001104,GO:0005759,GO:0048813,GO:0051384,GO:0005739,GO:0006367,GO:0004085,GO:0003995,GO:0016592,GO:0055114	CG4703-PA			PIRSF016578			PF02771,PF00441,PF02770			PS00072,PS00073	G3DSA:2.40.110.10,G3DSA:1.20.140.10,G3DSA:1.10.540.10	SSF47203,SSF56645									
aly26.4	Dihydropyrimidine dehydrogenase [NADP(+)]	GO:0005737,GO:0006222,GO:0046872,GO:0051539,GO:0000166,GO:0006207,GO:0051536,GO:0017113,GO:0004158,GO:0004159,GO:0006214,GO:0006212,GO:0019483,GO:0055114	CG2194-PC					TIGR01037	PF14697,PF14691,PF01180,PF07992	PS51379,PS51379,PS51379	PR00419,PR00419,PR00419	PS00912,PS00198	G3DSA:1.10.1060.10,G3DSA:3.20.20.70,G3DSA:3.30.70.20,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54862,SSF54862,SSF46548,SSF51395,SSF51971									
aly26.40	Vacuolar protein sorting associated protein 18 homolog	GO:0048069,GO:0007634,GO:0006728,GO:0015721,GO:0006904,GO:0008333,GO:0048757,GO:0008270,GO:0007040,GO:0007298,GO:0051301,GO:0045176,GO:0006886,GO:0031902,GO:0030897,GO:0060036,GO:0048072,GO:0006622,GO:0006726,GO:0035542,GO:0006727,GO:0008057,GO:0008340,GO:0007032,GO:0030674,GO:0007220,GO:0006897,GO:0016192,GO:0016197,GO:0005764,GO:0005765,GO:0033263,GO:0005515,GO:0005768,GO:0043485,GO:0045202	CG3093-PA						PF05131,PF00637	PS50236					810~840								
aly26.41	BAG domain-containing protein Samui	GO:0030544,GO:0007275	n/a				SM00264		PF02179	PS51035			G3DSA:1.20.58.120	SSF63491	623~643								

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly26.42	Unknown	GO:0005575,GO:0008150,GO:0003674	CG7044-PA										G3DSA:1.25.10.10	SSF48371									
aly26.43	39S ribosomal protein L12, mitochondrial	GO:0016049,GO:0005840,GO:0005811,GO:0005622,GO:0003735,GO:0005743,GO:0005762,GO:0005763,GO:0003682,GO:0006412,GO:0007005	CG5012-PA	MF_00368					PF16320,PF00542				G3DSA:3.30.1390.10	SSF48300,SSF54736									
aly26.44	Cryptochrome 1	GO:0008020,GO:0071000,GO:0009416,GO:0003913,GO:0007623,GO:0005737,GO:0050660,GO:0042332,GO:0005634,GO:0009882,GO:0000060,GO:0009637,GO:0048511,GO:0048471,GO:0006351,GO:0009881,GO:0050958,GO:0006281,GO:0009588,GO:0018298,GO:0007602,GO:0042752,GO:0045892,GO:0045475,GO:0009649,GO:0009785,GO:0043234,GO:0005641,GO:0005515,GO:0043153,GO:0050980	CG3772-PA						PF00875,PF03441,PF03441	PS51645			G3DSA:1.25.40.80,G3DSA:1.10.579.10,G3DSA:3.40.50.620	SSF48173,SSF52425	419~439								
aly26.45	Cytosolic Fe-S cluster assembly factor NUBP2 homolog	GO:0005737,GO:0051539,GO:0000166,GO:0016226,GO:0046872,GO:0005524	CG4858-PA	MF_03039					PF10609			PS01215	G3DSA:3.40.50.300	SSF52540									
aly26.46	Protein tweety	GO:1902476,GO:0016021,GO:0034707,GO:0006821,GO:0005886,GO:0005254	CG1693-PA						PF04906,PF04906														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly26.47	Unknown		n/a																				
aly26.48	Sulfotransferase 1C4	GO:0005829,GO:0051923,GO:0008146,GO:0006805,GO:0044281,GO:0050427	CG6704-PA						PF00685				G3DSA:3.40.50.300	SSF52540									
aly26.49	Unknown		n/a																				
aly26.5	Alpha-(1,3)-fucosyltransferase 10	GO:0006486,GO:0016021,GO:0008417,GO:0000139,GO:0005886,GO:0032580,GO:0046920	CG4435-PA						PF00852,PF17039					SSF53756					UPA00378				
aly26.50	Unknown		n/a																				
aly26.51	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly26.52	Unknown	GO:0005575,GO:0008150,GO:0003674	CG9628-PB																				
aly26.53	Unknown	GO:0060576,GO:0007496,GO:0019991,GO:0003674,GO:0005887,GO:0061028,GO:0005920	CG6981-PB																				
aly26.54	Unknown		n/a																				
aly26.55	TATA-binding protein-associated factor 172	GO:0019730,GO:0006963,GO:0004003,GO:0045087,GO:0003677,GO:0004386,GO:0003700,GO:0045892,GO:0042742,GO:0008063,GO:0035562,GO:0005634,GO:0005524	CG4261-PB						PF12054														
aly26.56	Unknown		n/a																				
aly26.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly26.7	DNA-directed RNA polymerase III subunit RPC5	GO:0051607,GO:0005813,GO:0005634,GO:0005654,GO:0006351,GO:0005515,GO:0005666,GO:0003899,GO:0006383,GO:0045087	CG10582-PA						PF04801														
aly26.8	Multiple inositol polyphosphate phosphatase 1	GO:0034417,GO:0005788,GO:0004721,GO:0003993,GO:0052826	CG4123-PB			PIRSF000894			PF00328				G3DSA:3.40.50.1240	SSF53254									
aly26.9	Eukaryotic translation initiation factor 3 subunit B	GO:0006446,GO:0005852,GO:0016282,GO:0005829,GO:0000166,GO:0003676,GO:0033290,GO:0031369,GO:0003729,GO:0006413,GO:0001731,GO:0003743	CG4878-PB	MF_03001		PIRSF036424	SM00360		PF13893,PF08662	PS50102			G3DSA:2.130.10.10,G3DSA:2.120.10.30,G3DSA:3.30.70.330	SSF82171,SSF82171,SSF54928										
aly260.1	Tolloid-like protein 1	GO:0004222,GO:0007275,GO:0030154,GO:0008586,GO:0007415,GO:0010629,GO:0005576,GO:0005509,GO:0008045,GO:0016485,GO:0007411,GO:0006508,GO:0008270	CG6863-PB			PIRSF001199	SM00181,SM00181,SM00042,SM00042,SM00042,SM00042,SM00179,SM00235		PF00431,PF00431,PF00431,PF00431,PF00431, PF14670,PF01400,PF07645	PS01180,PS50026,PS01180, PS01180,PS01180,PS01180, PS50026	PR00480,PR00480,PR00480,PR00480,PR00480	PS01186,PS01186,PS01187,PS01187,PS00010,PS00010	G3DSA:2.10.25.10,G3DSA:3.40.390.10,G3DSA:2.60.120.290,G3DSA:2.10.25.10,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290	SSF49854,SSF49854,SSF57196,SSF57196,SSF49854,SSF55486,SSF49854,SSF49854										
aly260.2	Ubiquitin thioesterase OTU1	GO:0016289,GO:0006520,GO:0005575,GO:0046872,GO:0016579,GO:0004843	CG4603-PB							PS50802		PS00028	G3DSA:3.10.20.90	SSF54236,SSF54001									
aly260.3	Calcium-binding mitochondrial carrier protein Aralar1	GO:0006810,GO:0016021,GO:0005811,GO:0022857,GO:0042060,GO:0005743,GO:0005740,GO:0005739,GO:0005509,GO:0006839,GO:0055085	CG2139-PE				SM00054,SM00054,SM00054		PF13202,PF13202,PF00036,PF00153,PF00153,PF00153	PS50920,PS50222,PS50920,PS50222,PS50920,PS50222	PR00926,PR00926,PR00926,PR00926,PR00926,PR00926	PS00018,PS00018,PS00018	G3DSA:1.50.40.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473,SSF47473,SSF103506										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly260.4	Putative gamma-glutamyltransferase YwrD	GO:0003810,GO:0003840,GO:0036374,GO:0006749,GO:0048812	CG4829-PB						PF01019		PR01210,PR01210,PR01210,PR01210,PR01210,PR01210			SSF56235		00460+2.3.2.2,00430+2.3.2.2,00480+2.3.2.2+3.4.19.13		PWY-4041,PWY-5826					
aly260.5	Unknown	GO:0005549,GO:0016020,GO:0007608,GO:0004984	n/a						PF02949														
aly260.6	Acid sphingomyelinase-like phosphodiesterase 3a	GO:0006685,GO:0004767,GO:0005615,GO:0016798	CG32052-PC										G3DSA:3.60.21.10	SSF56300									
aly2611.1	Unknown	GO:0007157,GO:0005576,GO:0003674	CG12621-PD						PF13927	PS50835,PS50835			G3DSA:2.60.40.10	SSF48726									
aly2612.1	Protein virilizer	GO:0007549,GO:0000381,GO:0003676,GO:0005634,GO:0000375,GO:0007539,GO:0048024,GO:0007298,GO:0006397,GO:0016021,GO:0007530	CG3496-PA						PF15912						664~670								
aly2612.10	Chitobiosyldiphosphodolichol beta-mannosyltransferase	GO:0005783,GO:0006486,GO:0016021,GO:0016020,GO:0097502,GO:0005789,GO:0019187,GO:0004578,GO:0000030	CG18012-PA						PF13692					SSF53756,SSF53756	405~425								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2612.11	RNA-binding protein 40	GO:0003676,GO:0006397,GO:0005634,GO:0000398,GO:0000166,GO:0005654,GO:0034693,GO:0003723,GO:0005689,GO:0005693,GO:0008380,GO:0003729	CG44249-PA				SM00360,SM00360		PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									
aly2612.12	Nucleolar protein 11	GO:0005634,GO:0006351,GO:0030490,GO:1901838,GO:0005730	CG9300-PA																				
aly2612.13	Alcohol dehydrogenase class-3	GO:0005737,GO:2000169,GO:0004552,GO:0080007,GO:0004022,GO:0006066,GO:0080164,GO:0051903,GO:0006069,GO:0008542,GO:0055114,GO:0008270	CG6598-PA					TIGR02818	PF00107,PF08240			PS00059	G3DSA:3.90.180.10,G3DSA:3.40.50.720	SSF50129,SSF50129,SSF51735		00010+1.1.1.1,00260+1.1.1.1,00071+1.1.1.1,00626+1.1.1.1,00982+1.1.1.1,00625+1.1.1.1,00980+1.1.1.1,00		PWY-5751,PWY-6342,PWY-7118,PWY-6871,PWY-7013,PWY-7396,PWY-7557,PWY-5057,PWY-6802,PWY-6587,PWY-					
aly2612.14	Uncharacterized protein C18orf8	GO:0005765	CG8270-PB						PF07035				G3DSA:2.120.10.30	SSF69322									
aly2612.15	Coiled-coil and C2 domain-containing protein 2A	GO:0005737,GO:0035869,GO:0036038,GO:0042384,GO:0060271,GO:0007224,GO:0005856,GO:0005515	CG43370-PD				SM00239						G3DSA:2.60.40.150	SSF49562									
aly2612.16	Diphosphoinositol polyphosphate phosphohydrolase 2	GO:0005737,GO:0016787,GO:0052848,GO:0052845,GO:0052844,GO:0005634,GO:0052846,GO:0052840,GO:0043647,GO:0009117,GO:0052843,GO:0008486,GO:0030515,GO:0046872,GO:0052847	CG6391-PA						PF00293	PS51462		PS00893	G3DSA:3.90.79.10	SSF55811									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2612.17	Guanylate kinase-associated protein mars	GO:0051382,GO:0000087,GO:0023052,GO:0005876,GO:0005737,GO:0043146,GO:0007346,GO:0005819,GO:0005634,GO:0000922,GO:0005654,GO:0043148,GO:0008017,GO:0007052,GO:0072686,GO:0005886,GO:0007267,GO:0007059,GO:0051642,GO:0051726,GO:0005828,GO:0008157	CG17064-PA						PF03359						41~61,610~630									
aly2612.18	Netrin-1	GO:0005737,GO:0008284,GO:0005604,GO:0016337,GO:2000289,GO:0045773,GO:0070983,GO:0071944,GO:0030334,GO:0033564,GO:0005576,GO:0001764,GO:0008045,GO:0030517,GO:0007411,GO:0040023,GO:0005578,GO:0008347,GO:0042472	CG18657-PA				SM00136,SM00180		PF00055,PF00053	PS51117		PS01248	G3DSA:2.10.25.10,G3DSA:2.60.120.260	SSF57196										
aly2612.19	Netrin-B	GO:0016200,GO:0007432,GO:2000289,GO:0070983,GO:0008039,GO:0005576,GO:0008045,GO:0007411,GO:0005578,GO:0008347	CG10521-PA				SM00180,SM00180,SM00643		PF01759,PF00053,PF00053	PS50027,PS50027,PS50189		PS01248,PS01248	G3DSA:2.10.25.10,G3DSA:2.40.50.120,G3DSA:2.10.25.10	SSF57196,SSF57196,SSF50242										
aly2612.2	E3 ubiquitin-protein ligase ZNRF2	GO:0005737,GO:0043234,GO:0042734,GO:0005765,GO:0061630,GO:0030659,GO:0008270,GO:0005886,GO:0016874,GO:0030054,GO:0010008	CG14435-PA				SM00184		PF13639	PS50089			G3DSA:3.30.40.10	SSF57850										
aly2612.20	Unknown	GO:0016772	CG11892-PB				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2612.21	Unknown		n/a																				
aly2612.22	Uridine-cytidine kinase like 1	GO:0005737,GO:0044211,GO:0016032,GO:0016773,GO:0044206,GO:0008152,GO:0004849,GO:0005634,GO:0005524	CG4798-PB					TIGR00235	PF00485,PF14681		PR00988,PR00988,PR00988,PR00988,PR00988,PR00988		G3DSA:3.40.50.2020,G3DSA:3.40.50.300	SSF53271,SSF52540		00983+2.7.1.48,00240+2.7.1.48		PWY-7193	UPA00574,UPA00579				
aly2612.23	Xylose isomerase	GO:0042732,GO:0005737,GO:0000287,GO:0006098,GO:0009045	n/a							PS51415	PR00688,PR00688,PR00688,PR00688,PR00688,PR00688		G3DSA:3.20.20.150,G3DSA:3.20.20.150	SSF51658		00051+5.3.1.5,00040+5.3.1.5							
aly2612.24	Threonylcarbamoyladenosine tRNA methylthiotransferase	GO:0008033,GO:0051539,GO:0016021,GO:0009451,GO:0005575,GO:0016740,GO:0012505,GO:0046872	CG6550-PA				SM00729	TIGR01578,TIGR00089	PF04055,PF00919,PF01938	PS50926,PS51449		PS01278	G3DSA:3.80.30.20	SSF102114									
aly2612.25	D(1C) dopamine receptor	GO:0004930,GO:0016021,GO:0004952,GO:0005887,GO:0007186,GO:0008227	CG12796-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly2612.3	Uncharacterized Golgi apparatus membrane protein-like protein CG5021	GO:0016192,GO:0009306,GO:0016021,GO:0003674,GO:0030173,GO:0008150	CG5021-PC						PF05832														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2612.4	TATA element modulatory factor	GO:0005783,GO:0033327,GO:0008584,GO:0010629,GO:0042742,GO:0003677,GO:0005634,GO:0032275,GO:0043066,GO:0005794,GO:0061136,GO:0030317,GO:0017137,GO:2000845,GO:0008150,GO:0007286,GO:0007289,GO:0001675,GO:0003700,GO:0071407,GO:0000139,GO:0006355,GO:0006351,GO:0001819	CG4557-PA						PF12329						17~37,769~796,572~606,381~401,692~733,617~687,800~834									
aly2612.5	TATA element modulatory factor	GO:0005794,GO:0006351,GO:0005783,GO:0033327,GO:0006355,GO:0071407,GO:0005634,GO:0007286,GO:2000845,GO:0000139,GO:0032275,GO:0010629,GO:0043066,GO:0042742,GO:0007289,GO:0003677,GO:0008584,GO:0001675,GO:0030317,GO:0061136,GO:0001819	n/a						PF12325						30~143,167~215									
aly2612.6	Serine/threonine-protein kinase SMG1	GO:0005737,GO:0050808,GO:0000724,GO:0016773,GO:0016310,GO:0005634,GO:0004672,GO:0018105,GO:0046777,GO:0004674,GO:0000184,GO:0044822,GO:0016301,GO:0035195,GO:0016246,GO:0046983,GO:0046872,GO:0007274,GO:0046854,GO:0005524,GO:0048489	CG32743-PA				SM00146		PF15785,PF00454	PS50290,PS51189			G3DSA:1.10.1070.11,G3DSA:1.10.1070.11,G3DSA:3.30.1010.10	SSF56112,SSF56112,SSF48371	1827~1854									
aly2612.7	Ribosomal RNA-processing protein 7 homolog A	GO:0005737,GO:0034456,GO:0001825,GO:0000166,GO:0000028,GO:0006364,GO:0032545,GO:0044822	CG9107-PA						PF12923	PS50102			G3DSA:3.30.70.330	SSF54928	236~256,153~183									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2612.8	Cleavage and polyadenylation specificity factor subunit 4	GO:0090502,GO:0005847,GO:0004521,GO:0008270,GO:0003676,GO:0006378,GO:0006379,GO:0022008,GO:0003723	CG3642-PA				SM00356,SM00356,SM00356,SM00356,SM00356		PF14964,PF00642,PF00642	PS50103,PS50103,PS50103,PS50103,PS50103			G3DSA:4.10.1000.10,G3DSA:4.10.1000.10,G3DSA:4.10.60.10,G3DSA:4.10.60.10	SSF90229,SSF90229									
aly2612.9	NHP2-like protein 1	GO:0007399,GO:0007422,GO:0071011,GO:0010608,GO:0005634,GO:0005730,GO:0042254,GO:0000398,GO:0005681,GO:0003723,GO:0030532,GO:0006397,GO:0008380,GO:0060415,GO:0003729	CG3949-PB						PF01248		PR00883,PR00883,PR00883,PR00883,PR00881,PR00881,PR00881,PR00881	PS01082	G3DSA:3.30.1330.30	SSF55315			REACT_71						
aly2613.1	Chromatin modification-related protein YNG2	GO:1900404,GO:0008285,GO:0051321,GO:2000873,GO:0032777,GO:0006281,GO:0005829,GO:0004402,GO:0070776,GO:0008270,GO:0016573	CG9293-PA				SM00249						G3DSA:3.30.40.10	SSF57903									
aly2613.2	Unknown		n/a																				
aly2613.3	Chaoptin	GO:0035996,GO:0016028,GO:0042052,GO:0050896,GO:0007601,GO:0005575,GO:0046658,GO:0008150,GO:0005515,GO:0005886,GO:0003674,GO:0007156	CG42346-PC				SM00369,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365		PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF00041,PF13306	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS50853,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:2.60.40.10,G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52058,SSF49265,SSF52058	1377~1378								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2613.4	Chaoptin	GO:0035996,GO:0016028,GO:0042052,GO:0050896,GO:0007601,GO:0005575,GO:0046658,GO:0008150,GO:0005886,GO:0003674,GO:0007156	CG42346-PC				SM00369,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364		PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF00041	PS51450,PS51450,PS50853,PS51450	PR00019,PR00019		G3DSA:2.60.40.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF49265,SSF52058,SSF52058,SSF52058,SSF52058									
aly26140.1	Sarcalumenin	GO:0033018,GO:0003924,GO:0006816,GO:0005509,GO:0005525	CG9297-PB											SSF52540									
aly2618.1	Uncharacterized MFS-type transporter C09D4.1	GO:0016021,GO:0055085	CG1358-PC						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly2618.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2618.3	Unknown		n/a												581~601,860~880,381~401,181~261,82~102								
aly2618.4	Unknown	GO:0005515	n/a						PF00018				G3DSA:2.30.30.40	SSF50044									
aly2618.5	Unknown		n/a												189~213								
aly2625.1	Unknown		n/a																				
aly26260.1	Far upstream element-binding protein 3	GO:0005737,GO:0006351,GO:0000381,GO:0045893,GO:0005634,GO:0016020,GO:0044822,GO:0045944,GO:0007283,GO:0001077,GO:0010628,GO:0003723,GO:0005515,GO:0006366,GO:0048024,GO:0048025,GO:0005685,GO:0003729,GO:0000978,GO:0006397	CG8912-PC				SM00322		PF00013	PS50084			G3DSA:3.30.1370.10	SSF54791										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2627.1	Lipase 1	GO:0004806,GO:0006629,GO:0007586,GO:0016788,GO:0016042,GO:0005576	CG6113-PC			PIRSF000862			PF04083				G3DSA:3.40.50.1820	SSF53474									
aly2627.10	Rab GTPase-activating protein 1	GO:0032313,GO:0005829,GO:0005096,GO:0005097,GO:0005815,GO:0003677,GO:0007049	CG7112-PB				SM00462		PF12473,PF00640	PS01179			G3DSA:2.30.29.30	SSF50729									
aly2627.11	Rab GTPase-activating protein 1-like	GO:0032313,GO:0005096,GO:0005097	CG7112-PB				SM00164		PF00566	PS50086			G3DSA:1.10.8.270	SSF47923,SSF47923	398~456								
aly2627.12	Uncharacterized protein C9orf172	GO:0008157	CG42748-PK											SSF144232									
aly2627.13	Retinol dehydrogenase 14	GO:0008106,GO:0005783,GO:0005634,GO:0016020,GO:0005739,GO:0005789,GO:0005765,GO:0008152,GO:0042572,GO:0001649,GO:0016491	CG2070-PA						PF00106,PF00106		PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2627.14	Ras-related protein Rab-9B	GO:0008021,GO:0005802,GO:0016192,GO:0030670,GO:0055037,GO:0005770,GO:0003924,GO:0031982,GO:0005764,GO:0032482,GO:0045335,GO:0019003,GO:0045202,GO:0042147,GO:0006886,GO:0015031,GO:0005886,GO:0008152,GO:0005769,GO:0005525	CG9994-PA				SM00174,SM00176,SM00173,SM00175	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly2627.15	Unknown		n/a																				
aly2627.16	Nuclear hormone receptor FTZ-F1 beta	GO:0006351,GO:0030522,GO:0035072,GO:0035211,GO:0045433,GO:0003700,GO:0005634,GO:0006919,GO:0003712,GO:0016321,GO:0006355,GO:0008270,GO:0043401,GO:0003677,GO:0000978,GO:0003707,GO:0004879,GO:0060968	CG8676-PB				SM00399,SM00430		PF00105,PF00104	PS51030	PR00398,PR00398,PR00398,PR00398,PR00047,PR00047,PR00047,PR00047	PS00031	G3DSA:3.30.50.10,G3DSA:1.10.565.10,G3DSA:1.10.565.10,G3DSA:1.10.565.10,G3DSA:1.10.565.10	SSF57716,SSF48508,SSF48508,SSF48508,SSF48508,SSF48508	731~751		REACT_71						
aly2627.17	Zinc metalloproteinase nas-4	GO:0006508,GO:0022008,GO:0005576,GO:0004222,GO:0008270	CG15255-PA				SM00235		PF01400		PR00480,PR00480,PR00480,PR00480,PR00480		G3DSA:3.40.390.10	SSF55486									
aly2627.18	Paired mesoderm homeobox protein 1	GO:0043565,GO:0003700,GO:0005634,GO:0006355,GO:0003677,GO:0007275	CG9876-PA				SM00389		PF00046	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2627.19	Mitochondrial cardiolipin hydrolase	GO:0046872,GO:0043186,GO:0046843,GO:0016021,GO:0005739,GO:0016042,GO:0003824,GO:0005741,GO:0030717,GO:0004519,GO:0051321,GO:0034587,GO:0048477,GO:0031047	CG12314-PA						PF13091	PS50035			G3DSA:3.30.870.10	SSF56024									
aly2627.2	Thioredoxin-like protein 1	GO:0005737,GO:0006662,GO:0006457,GO:0070062,GO:0000103,GO:0005634,GO:0006974,GO:0016671,GO:0000502,GO:0034599,GO:0015035,GO:0045454,GO:0055114,GO:0015036	CG5495-PA						PF00085,PF06201	PS51352,PS51532	PR00421,PR00421,PR00421	PS00194	G3DSA:3.40.30.10,G3DSA:2.60.120.470	SSF52833,SSF49785									
aly2627.20	Estradiol 17-beta-dehydrogenase 8	GO:0006703,GO:0006633,GO:0016614,GO:0004303,GO:0047035,GO:0008152,GO:0005759,GO:0016491	CG3603-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735									
aly2627.21	Deoxynucleotidyltransferase terminal-interacting protein 2	GO:0006355,GO:0005634,GO:0006351,GO:0044822,GO:0005730	CG1142-PA						PF08698														
aly2627.22	Chymotrypsin-2	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG31265-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2627.23	Arrestin, lateral eye	GO:0005737,GO:0042335,GO:0031647,GO:0007369,GO:0007601,GO:0045746,GO:0035641,GO:0007165,GO:0061099,GO:0002168	CG1487-PA				SM01017		PF02752,PF00339		PR00309,PR00309,PR00309		G3DSA:2.60.40.840,G3DSA:2.60.40.640	SSF81296,SSF81296									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2627.24	Unknown		n/a																				
aly2627.25	Unknown	GO:0006030,GO:0005576,GO:0008061,GO:0016490	CG10287-PA				SM00494,SM00494,SM00494		PF01607,PF01607,PF01607	PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625,SSF57625									
aly2627.26	Kynurenine--oxoglutarate transaminase 3	GO:0005739,GO:0070189,GO:0044822,GO:0006520,GO:0016212,GO:0097052,GO:0009058,GO:0047804,GO:0030170,GO:0006103,GO:0047315	CG6950-PC						PF00155				G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383									
aly2627.27	UPF0605 protein CG18335	GO:0005575,GO:0003674,GO:0008150	CG18335-PA						PF10629														
aly2627.28	Probable elongator complex protein 3	GO:0008023,GO:0051124,GO:0045202,GO:0050808,GO:0008607,GO:0005737,GO:0048789,GO:0000123,GO:0005634,GO:0004402,GO:0016573,GO:0006368,GO:0002168,GO:0007626,GO:0018394,GO:0045859,GO:0033588,GO:0030431,GO:0002098,GO:0046872,GO:0008080,GO:2000289,GO:0051536,GO:0016407,GO:0006357,GO:0030097	CG15433-PA						PF16199														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2627.29	Probable elongator complex protein 3	GO:0008023,GO:0051124,GO:0045202,GO:0050808,GO:0008607,GO:0005737,GO:0048789,GO:0000123,GO:0005634,GO:0004402,GO:0016573,GO:0006368,GO:0002168,GO:0007626,GO:0018394,GO:0045859,GO:0033588,GO:0030431,GO:0002098,GO:0046872,GO:0008080,GO:2000289,GO:0051536,GO:0016407,GO:0006357,GO:0030097	CG15433-PA						PF10629,PF10629														
aly2627.3	U4/U6.U5 tri-snRNP-associated protein 2	GO:0000245,GO:0071011,GO:0000398,GO:0036459,GO:0006511,GO:0008270,GO:0051301,GO:0005681,GO:0008380,GO:0007049,GO:0006397	CG7288-PA				SM00290		PF02148,PF00443	PS50271,PS50235			G3DSA:3.30.40.10	SSF57850,SSF54001									
aly2627.30	Unknown		n/a																				
aly2627.31	Protein TIC 214	GO:0015031,GO:0016021,GO:0009706	n/a																				
aly2627.32	Unknown		CG31676-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2627.33	Unknown		CG6583-PA																				
aly2627.34	Uncharacterized oxidoreductase SSP0419	GO:0008152,GO:0016491	CG31549-PA						PF00106		PR00080,PR00080,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly2627.35	Probable G-protein coupled receptor CG31760	GO:0008066,GO:0005886,GO:0016021,GO:0007214,GO:0004930	CG31760-PC						PF00003	PS50259					632~652								
aly2627.36	Protein MIS12 homolog	GO:0051382,GO:0005634,GO:0007059,GO:0000444,GO:0007067,GO:0051301	n/a						PF05859						141~161,110~130								
aly2627.37	Unknown		n/a																				
aly2627.38	Protein purity of essence	GO:0007399,GO:0042066,GO:0050896,GO:0007601,GO:0007291,GO:0005516,GO:0007286,GO:0004842,GO:0008270	CG14472-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2627.39	E3 ubiquitin-protein ligase UBR4	GO:0005737,GO:0042066,GO:0005813,GO:0016021,GO:0016020,GO:0005654,GO:0016874,GO:0007291,GO:0042787,GO:0005516,GO:0016032,GO:0007286,GO:0004842,GO:0008270	CG14472-PA																				
aly2627.4	E3 ubiquitin-protein ligase UBR4	GO:0005737,GO:0016032,GO:0042066,GO:0005813,GO:0016021,GO:0016020,GO:0005654,GO:0016874,GO:0007291,GO:0042787,GO:0008270,GO:0005515,GO:0007286,GO:0004842,GO:0005516	CG14472-PA				SM00396		PF02207,PF13764	PS51157			G3DSA:2.130.10.10	SSF50978,SSF48371,SSF48371	3208~3228								
aly2627.40	Tctex1 domain containing protein 2		CG5359-PA						PF03645						1~21								
aly2627.41	Unknown		n/a																				
aly2627.5	Protein purity of essence	GO:0007399,GO:0042066,GO:0050896,GO:0007601,GO:0007291,GO:0005516,GO:0007286,GO:0004842,GO:0008270	CG14472-PA						PF13764														
aly2627.6	Aquaporin AQPAe.a	GO:0006810,GO:0005215,GO:0016021,GO:0016020,GO:0005372,GO:0015250,GO:0006833,GO:0003014,GO:0030104,GO:0055085,GO:0046662	CG9023-PF					TIGR00861	PF00230		PR00783,PR00783,PR00783,PR00783,PR00783,PR00783		G3DSA:1.20.1080.10	SSF81338									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2627.7	SET and MYND domain-containing protein 4	GO:0005737,GO:0008168,GO:0010629,GO:0046872,GO:0042826	CG7759-PA				SM00028,SM00028,SM00028,SM00028		PF13414,PF00856,PF07719	PS50293,PS50293,PS50280,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:2.170.270.10,G3DSA:2.170.270.10	SSF48452,SSF48452,SSF82199,SSF82199,SSF144232	346~366								
aly2627.8	Stress-activated map kinase-interacting protein 1	GO:0051124,GO:0031932,GO:0006915,GO:0019901,GO:0048813,GO:0003674,GO:0001932	CG10105-PA						PF16979,PF05422,PF16978						143~163								
aly2627.9	Unknown		n/a												57~91								
aly2628.1	Unknown		n/a																				
aly2631.1	Dopamine D2-like receptor	GO:0004930,GO:0007212,GO:0007195,GO:0016021,GO:0007606,GO:0001591,GO:0007194,GO:0004952,GO:0005887,GO:0007268,GO:0007186,GO:0008227	CG33517-PH						PF00001	PS50262	PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly2631.10	ELAV-like protein 4	GO:0006397,GO:0003730,GO:0005634,GO:0000166,GO:0017091,GO:0007293,GO:0003723,GO:0036093,GO:0003729,GO:0048477,GO:0006396,GO:0060856	CG3151-PJ				SM00360,SM00360,SM00360		PF00076,PF00076,PF00076	PS50102,PS50102,PS50102	PR00961,PR00961,PR00961		G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2631.11	Unknown		CG2278-PB																				
aly2631.12	Mitogen-activated protein kinase kinase kinase 9	GO:0046777,GO:0007256,GO:0007257,GO:0007254,GO:0004674,GO:0043065,GO:0048803,GO:0004712,GO:0004713,GO:0048804,GO:0004672,GO:0005524,GO:0042803,GO:0006468,GO:0006915,GO:0046330,GO:0009408,GO:0006351,GO:0071361,GO:0007394,GO:0007391,GO:0005622,GO:0005575,GO:0006355,GO:0004706,GO:0046529,GO:0005515,GO:0004708,GO:0046843	CG2272-PB				SM00220,SM00326		PF14604,PF07714	PS50002,PS50011	PR00452,PR00452,PR00452,PR00452,PR00109,PR00109,PR00109,PR00109	PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:2.30.30.40,G3DSA:3.30.200.20	SSF50044,SSF56112	383~438								
aly2631.13	MAGUK p55 subfamily member 5	GO:0016332,GO:0032287,GO:0045197,GO:0045196,GO:0035003,GO:0007009,GO:0007163,GO:0007043,GO:0043220,GO:0005923,GO:0019904,GO:0005737,GO:0002009,GO:0045176,GO:0070062,GO:0016021,GO:0016020,GO:0045179,GO:0046939,GO:0090002,GO:0005654,GO:0035749,GO:0040003,GO:0016324,GO:0016327,GO:0004385,GO:0042461,GO:0032288,GO:0045186,GO:0046331,GO:0005913,GO:0005912,GO:0005886,GO:0035750,GO:0005918,GO:0043234,GO:0043219,GO:0002011,GO:0001738,GO:0005515,GO:0012505	CG32717-PG				SM00072,SM00228,SM00228		PF00595,PF07653,PF00625	PS50002,PS50106,PS50052		PS00856	G3DSA:2.30.30.40,G3DSA:2.30.42.10,G3DSA:3.30.63.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:2.30.42.10	SSF50156,SSF50044,SSF52540	411~431,1002~1022	00230+2.7.4.8		PWY-7221					
aly2631.14	Unknown	GO:0070822	CG4400-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2631.15	Unknown		n/a																				
aly2631.16	Unknown		n/a																				
aly2631.17	Unknown		n/a																				
aly2631.2	Dopamine D2-like receptor	GO:0004930,GO:0007212,GO:0007195,GO:0016021,GO:0007606,GO:0001591,GO:0007194,GO:0004952,GO:0005887,GO:0007268,GO:0007186,GO:0008227	CG33517-PH						PF00001	PS50262	PR00534,PR00534,PR00534,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly2631.3	HMG box transcription factor BBX	GO:0005737,GO:0003700,GO:0005634,GO:0060348,GO:0005654,GO:0006355,GO:0006351,GO:0003677	CG1414-PB				SM00398		PF00505	PS50118			G3DSA:1.10.30.10	SSF47095	391~411,210~230								
aly2631.4	Anaphase-promoting complex subunit 1	GO:0048749,GO:0070979,GO:0005634,GO:0031145,GO:0090302,GO:0007067,GO:0022008,GO:0051301,GO:0005680	CG9198-PA						PF12859														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2631.5	Chymotrypsin-2	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG5255-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2631.6	Chymotrypsin-1	GO:0004252,GO:0005615,GO:0006508	CG31269-PB				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2631.7	Unknown		n/a																				
aly2631.8	Zinc finger protein 287	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0007476,GO:0046331,GO:0045892,GO:0045893,GO:0003676,GO:0003677,GO:0007155,GO:0042035,GO:0046872,GO:0030178,GO:0006351	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2631.9	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase	GO:0006651,GO:0005829,GO:0046673,GO:0004871,GO:0035556,GO:0008377,GO:0002385,GO:0016028,GO:0043547,GO:0001580,GO:0016027,GO:0016042,GO:0005509,GO:0006644,GO:0007608,GO:0019722,GO:0007601,GO:2000370,GO:0005096,GO:0007602,GO:0046488,GO:0009649,GO:0008344,GO:0004435,GO:0008654,GO:0016056,GO:0051482,GO:0016059,GO:0005622,GO:0043153,GO:0004629,GO:0005515,GO:0043052,GO:0045494	CG3620-PF				SM00239,SM00148,SM00149		PF09279,PF06631,PF00388,PF01688,PF00387	PS50007,PS50008,PS50004	PR00390,PR00390,PR00390,PR00390,PR00390		G3DSA:2.30.29.30,G3DSA:2.60.40.150,G3DSA:3.20.20.190,G3DSA:3.20.20.190,G3DSA:1.20.1230.10,G3DSA:1.10.238.10	SSF51695,SSF69989,SSF50729,SSF49562,SSF47473	917~937,963~1019,818~845	00562+3.1.4.11	REACT_14797,REACT_15295	PWY-6367,PWY-6351,PWY-7039						
aly263279.1	Unknown		n/a												77~104,137~157								
aly2633.1	Cadherin-86C	GO:0016339,GO:0016020,GO:0035003,GO:0008360,GO:0005509,GO:0005887,GO:0044331,GO:0007156,GO:0016021	CG42601-PF				SM00112,SM00112,SM00112,SM00112		PF00028,PF00028	PS50268,PS50268,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205	PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49313,SSF49313,SSF49313									
aly2633.10	Myophilin	GO:0003779,GO:0031032	CG5023-PA				SM00033		PF00307,PF00402	PS51122,PS50021	PR00889,PR00889,PR00889,PR00889,PR00889,PR00888,PR00888,PR00888,PR00888,PR00888,PR00888,PR00888,PR00888		G3DSA:1.10.418.10	SSF47576									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2633.2	Unknown		n/a																				
aly2633.3	Muscle-specific protein 20	GO:1901739,GO:0003779,GO:0007155,GO:0008360,GO:0005509,GO:0005515,GO:0007520,GO:0043292	CG4696-PA				SM00033		PF00402,PF00307	PS50021,PS51122	PR00888,PR00888,PR00888,PR00888,PR00888,PR00888,PR00888	PS01052	G3DSA:1.10.418.10	SSF47576									
aly2633.4	Mitogen-activated protein kinase kinase kinase 15	GO:0048082,GO:0006468,GO:0012501,GO:0004702,GO:0005622,GO:0004674,GO:0046330,GO:0008360,GO:0032874,GO:0004672,GO:0046872,GO:0004709,GO:0005524	CG4720-PC				SM00220		PF13281,PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly2633.5	Headcase protein	GO:0005737,GO:0007424,GO:0035155,GO:0007430,GO:0030154,GO:0007476,GO:0050768,GO:0002165,GO:0003674,GO:0048675,GO:0016246,GO:0022008,GO:0035071,GO:0035147	CG15532-PC						PF16002,PF15353														
aly2633.6	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0004185,GO:0006952,GO:0005576,GO:0035006,GO:0007311,GO:0008063,GO:0006508,GO:0035008,GO:0008233,GO:0008236	CG3066-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2633.7	Unknown		n/a										G3DSA:2.70.220.10	SSF63707									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2633.8	Odorant receptor 4	GO:0005549,GO:0016021,GO:0016020,GO:0007608,GO:0004984	CG12697-PA						PF02949														
aly2633.9	Circadian clock-controlled protein	GO:0007623,GO:0005615	CG14457-PB				SM00700		PF06585														
aly2637.1	Octopamine receptor beta-2R	GO:0043565,GO:0010579,GO:0003700,GO:0016021,GO:0007606,GO:0007612,GO:0006355,GO:0045887,GO:0007189,GO:0001963,GO:0005887,GO:0007191,GO:0004989,GO:0007186,GO:0008227,GO:0060158	CG18553-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR01102,PR01102,PR01102,PR01102,PR01102	PS00237	G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly2637.2	Unknown		n/a																				
aly264.1	Probable tubulin polyglutamylase TTLL1	GO:0005737,GO:0018095,GO:0035082,GO:0005874,GO:0018166,GO:0004835,GO:0016874,GO:0003351	CG32238-PA						PF03133,PF03133	PS51221				SSF56059									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly264.2	Probable tubulin polyglutamylase TTLL1	GO:0005737,GO:0018095,GO:0060271,GO:0035082,GO:0005874,GO:0018166,GO:0006464,GO:0003351,GO:0044782,GO:0016874,GO:0004835	CG32238-PA						PF03133	PS51221			G3DSA:3.30.470.20	SSF56059,SSF56059									
aly264.3	Probable tubulin polyglutamylase TTLL1	GO:0005737,GO:0018095,GO:0035082,GO:0005874,GO:0018166,GO:0006464,GO:0003351,GO:0016874,GO:0004835	CG32238-PA						PF03133	PS51221				SSF56059,SSF56059									
aly264.4	Transcription initiation factor TFIID subunit 1	GO:0060261,GO:0051123,GO:0001075,GO:0008270,GO:0003677,GO:0007049,GO:0043565,GO:0005634,GO:0004674,GO:0006367,GO:0004672,GO:0035174,GO:0005524,GO:0016573,GO:0046425,GO:0008134,GO:0006461,GO:0022008,GO:0001129,GO:0000117,GO:0007221,GO:0051726,GO:0006355,GO:0045944,GO:0006352,GO:0005669	CG17603-PE				SM00297,SM00297,SM00384,SM00384		PF15288,PF09247,PF12157,PF00439,PF00439	PS50014,PS50014	PR00929,PR00929,PR00503,PR00503,PR00503,PR00503	PS00633,PS00633	G3DSA:1.10.1100.10,G3DSA:1.20.920.10,G3DSA:1.20.920.10	SSF47370,SSF47370,SSF47055	1057~1077,1206~1240,1501~1528,1100~1142,1624~1658								
aly264.5	Unknown	GO:0018166,GO:0018095,GO:0004835	CG32238-PA																				
aly264.6	Unknown	GO:0018166,GO:0018095,GO:0004835	CG32238-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly264.7	Transcription initiation factor TFIID subunit 1-like	GO:0017025,GO:0006366,GO:0001075,GO:0008270,GO:0003677,GO:0007140,GO:0043565,GO:0005634,GO:0004402,GO:0070577,GO:0005654,GO:0004674,GO:0010467,GO:0006367,GO:0004672,GO:0006368,GO:0035174,GO:0006468,GO:0016573,GO:0046425,GO:0008134,GO:0006461,GO:0045893,GO:0022008,GO:0001129,GO:0000117,GO:0051726,GO:0006355,GO:0006357,GO:0045944,GO:0016032,GO:0005669	CG17603-PE																				
aly264031.1	Unknown		n/a																				
aly2643.1	Unknown		n/a																				
aly2643.2	G-protein coupled receptor 143	GO:0032438,GO:0050848,GO:0035240,GO:0035643,GO:0005737,GO:0004930,GO:0016021,GO:0016020,GO:0072544,GO:0072545,GO:0035584,GO:0032402,GO:0032400,GO:0007186,GO:0033162,GO:0005794,GO:0016324,GO:0007601,GO:0007218,GO:0006726,GO:0005886,GO:0048015,GO:0042470,GO:0005765,GO:0007165	n/a						PF02101	PS50262	PR00965,PR00965,PR00965,PR00965,PR00965			SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2643.3	A-kinase anchor protein 10, mitochondrial	GO:0005737,GO:0038032,GO:0051018,GO:0005829,GO:0007596,GO:0005739,GO:0008104,GO:0007165,GO:0005886	CG4132-PA				SM00315,SM00315		PF00615,PF00615	PS50132,PS50132			G3DSA:1.10.167.10,G3DSA:1.10.167.10	SSF48097,SSF48097,SSF48097									
aly2643.4	Unknown		n/a																				
aly2643.5	Malectin	GO:0044267,GO:0006457,GO:0005783,GO:0018279,GO:0016021,GO:0016020,GO:0030246,GO:0019899,GO:0005789,GO:0043687	CG9257-PA						PF11721														
aly2643.6	Sex peptide receptor	GO:0045434,GO:0008528,GO:0007218,GO:0045932,GO:0016021,GO:0005886,GO:0004930,GO:0035013,GO:0048042,GO:0005887,GO:0008188,GO:0007193,GO:0007186,GO:0008344	CG8985-PB						PF10324	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly2643.7	Unknown		n/a																				
aly2643.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly26484.1	Unknown		n/a																				
aly2653.1	F-box/LRR-repeat protein 20	GO:0005737,GO:0005515,GO:0001662	CG9003-PB				SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00256		PF12937	PS50181			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047										
aly2653.2	Aldo-keto reductase AKR2E4	GO:0004032,GO:0008202,GO:0055114,GO:0016491	CG12766-PA						PF00248		PR00069,PR00069,PR00069,PR00069	PS00062	G3DSA:3.20.20.100	SSF51430										
aly2653.3	Unknown		n/a																				
aly2653.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2653.5	Talin-1	GO:0005200,GO:0006909,GO:0015629,GO:0060439,GO:0007596,GO:0035160,GO:0006928,GO:0007044,GO:0007043,GO:0007411,GO:0007298,GO:0005925,GO:0005737,GO:0044267,GO:0001726,GO:0070062,GO:0007430,GO:0002576,GO:0007475,GO:0003779,GO:0030168,GO:0016203,GO:0005178,GO:0016032,GO:0006936,GO:0009986,GO:0005158,GO:0036498,GO:0008360,GO:0045892,GO:0030274,GO:0005886,GO:0007155,GO:0032587,GO:0007526,GO:0007016,GO:0005911,GO:0005815,GO:0030968,GO:0005829,GO:0030866,GO:0005576,GO:0017166,GO:0005515,GO:0070527	CG6831-PB				SM00307		PF01608,PF08913	PS50945			G3DSA:1.20.1410.10,G3DSA:1.20.1440.10,G3DSA:1.20.1440.10	SSF47220,SSF109885	672~692								
aly2653.6	Talin-1	GO:0005200,GO:0006909,GO:0015629,GO:0060439,GO:0035160,GO:0007298,GO:0005925,GO:0005856,GO:0001726,GO:0007430,GO:0007475,GO:0003779,GO:0016203,GO:0005178,GO:0009986,GO:0005158,GO:0008360,GO:0045892,GO:0007155,GO:0032587,GO:0007526,GO:0007016,GO:0005829,GO:0005515	CG6831-PB						PF01608				G3DSA:1.20.1490.10,G3DSA:1.20.1440.10,G3DSA:1.20.1440.10	SSF109885	255~275								
aly2653.7	Talin-1	GO:0005200,GO:0006909,GO:0015629,GO:0060439,GO:0035160,GO:0007298,GO:0005925,GO:0005856,GO:0001726,GO:0007430,GO:0007475,GO:0003779,GO:0016203,GO:0005178,GO:0009986,GO:0005158,GO:0008360,GO:0045892,GO:0007155,GO:0032587,GO:0007526,GO:0007016,GO:0005829,GO:0005515	CG6831-PB										G3DSA:1.20.1440.10,G3DSA:1.20.1440.10		55~82								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2653.8	Unknown		n/a												156~176,338~358,304~324								
aly2659.1	Protein toll	GO:0009897,GO:0007416,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0007165,GO:0008063,GO:0006955,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0010508,GO:0002229,GO:0042802,GO:0016201,GO:0009880,GO:0008329,GO:0007507,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005886,GO:0007155,GO:0007352,GO:0043234,GO:0006952,GO:0051607,GO:0002752,GO:0009950,GO:0009620,GO:0046790,GO:0004888,GO:0045944,GO:0030097,GO:0045610,GO:0005769,GO:0035007	CG8595-PA				SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00255,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365		PF01582,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS50104,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.40.50.10140,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52200,SSF52058,SSF52058									
aly2659.10	Crossover junction endonuclease MUS81	GO:0006310,GO:0005730,GO:0046872,GO:0006281,GO:0004518,GO:0005634,GO:0000737,GO:0072429,GO:0048257,GO:0003677,GO:0007095,GO:0007131,GO:0008821	CG3026-PA				SM00891		PF02732				G3DSA:3.40.50.10130,G3DSA:1.10.8.310	SSF52980,SSF47802									
aly2659.11	Sialomucin core protein 24	GO:0048149,GO:0007616,GO:0035324,GO:0007611,GO:0007162,GO:0003674,GO:0007165,GO:0007275,GO:0010008,GO:0007517,GO:0031410,GO:0007476,GO:0005886,GO:0008355,GO:0042127,GO:0008285,GO:0032504,GO:0005887,GO:0006955,GO:0007155,GO:0007157,GO:0098549,GO:0005764,GO:0005765,GO:0005576,G	CG16707-PE						PF05283														
aly2659.12	Lipase 3	GO:0004806,GO:0006629,GO:0016788,GO:0016042	CG6113-PC			PIRSF000862			PF00561				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2659.2	GILT-like protein F37H8.5	GO:0005737,GO:0005576	CG9427-PA						PF03227														
aly2659.3	SET and MYND domain-containing protein 5	GO:0008168,GO:0046872,GO:0005515	CG3353-PA				SM00317		PF00856	PS50280			G3DSA:2.170.270.10,G3DSA:2.170.270.10	SSF82199,SSF82199									
aly2659.4	Solute carrier family 22 member 12	GO:0070062,GO:0016324,GO:0016021,GO:0042493,GO:1903825,GO:0008513,GO:0022857,GO:0030165,GO:0005886,GO:0015747,GO:0015143,GO:0031526,GO:0055085,GO:0046415	CG7442-PA						PF00083				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly2659.5	Structural maintenance of chromosomes protein 3	GO:0008280,GO:0030893,GO:0006281,GO:0005634,GO:0007476,GO:0006275,GO:0000775,GO:0046331,GO:0000785,GO:0051301,GO:0007064,GO:0051321,GO:0022008,GO:0003682,GO:0001737,GO:0008278,GO:0005524,GO:0007062	CG9802-PA			PIRSF005719	SM00968		PF02463,PF06470				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF75553	760~787,852~925,797~831,676~717,395~454,964~991,260~357,186~213,483~503								
aly2659.6	Phospholipase D3	GO:0070062,GO:0016021,GO:0005789,GO:0003824,GO:0070290,GO:0008152,GO:0004630,GO:0016042	CG9248-PB				SM00155		PF13918,PF00614	PS50035			G3DSA:3.30.870.10,G3DSA:3.30.870.10	SSF56024,SSF56024									
aly2659.7	THO complex subunit 7 homolog	GO:0043234,GO:0005737,GO:0005634,GO:0016607,GO:0003674,GO:0003723,GO:0000347,GO:0051028,GO:0000445,GO:0008380,GO:0006406,GO:0006397	CG17143-PA						PF05615						138~165								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2659.8	Solute carrier family 35 member F1	GO:0016021,GO:0006810	n/a						PF06027														
aly2659.9	RNA polymerase-associated protein CTR9 homolog	GO:0000122,GO:0035327,GO:0045944,GO:0006351,GO:0005515,GO:0016593,GO:0051571,GO:0032968,GO:0080182	CG2469-PB				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF00515,PF13414,PF13414,PF13414	PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50293,PS50005,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452	784~808,461~488								
aly265983.1	Peroxisome biogenesis protein 6	GO:0005737,GO:0007031,GO:0006635,GO:0016558,GO:0005777,GO:0017111,GO:0005524	CG11919-PD						PF00004				G3DSA:3.40.50.300	SSF52540									
aly2661.1	Carotenoid isomerooxygenase	GO:0004497,GO:0016063,GO:0035238,GO:0007604,GO:0007603,GO:0007602,GO:0010436,GO:0003834,GO:0009110,GO:0016119,GO:0042572,GO:0046872,GO:0042574,GO:0004744	CG9347-PA						PF03055														
aly2661.10	Unknown		n/a																				
aly2661.11	VWFA and cache domain-containing protein CG16868	GO:0005575,GO:0008150,GO:0016021,GO:0003674,GO:0006816	CG16868-PA						PF02743				G3DSA:3.30.450.20,G3DSA:3.30.450.20	SSF103190									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2661.12	Unknown		CG30428-PA						PF13873														
aly2661.2	Retinol dehydrogenase 11	GO:0016614,GO:0016062,GO:0004745,GO:0016021,GO:0052650,GO:0007603,GO:0005789,GO:0001917,GO:0008152,GO:0042572,GO:0005622,GO:0042574,GO:0001523,GO:0016491	CG7675-PB						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly2661.3	Lipase member H	GO:0004806,GO:0006629,GO:0016020,GO:0052689,GO:0016042,GO:0005576	CG17292-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly2661.4	Phospholipase A1 2	GO:0004806,GO:0006629,GO:0052740,GO:0044179,GO:0016042,GO:0005576,GO:0052739,GO:0008970	CG17292-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly2661.5	Cytochrome P450 4c3	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2661.6	Unknown		n/a																				
aly2661.7	Neuromedin-U receptor 2	GO:0005229,GO:0036401,GO:0007204,GO:0006821,GO:0008188,GO:0001607,GO:0007417,GO:0004930,GO:0016021,GO:0042924,GO:0043006,GO:0048265,GO:0007186,GO:0005525,GO:0007625,GO:1902476,GO:0007218,GO:0006816,GO:0002023,GO:0005887,GO:0005886,GO:0048016,GO:0007200,GO:0005829,GO:0050482,GO:0005622	CG8784-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly2661.8	Retinol dehydrogenase 13	GO:0042462,GO:0016614,GO:0010842,GO:0005743,GO:0008152,GO:0009644,GO:0016491	CG7675-PB						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735	77~97								
aly2661.9	La-related protein 7	GO:0042386,GO:0035363,GO:0005634,GO:0035172,GO:0030529,GO:0097322,GO:0046331,GO:0003723,GO:0003676,GO:0003677,GO:0030097,GO:0022008,GO:0000166,GO:0006396	CG12058-PA				SM00360,SM00715		PF05383,PF00076	PS50102,PS50961	PR00302,PR00302,PR00302		G3DSA:3.30.70.330,G3DSA:1.10.10.10	SSF46785,SSF54928									
aly2668.1	Putative nuclease HARBI1	GO:0005737,GO:0005813,GO:0005634,GO:0046872,GO:0004518	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2668.10	Vacuolar protein sorting associated protein 33B	GO:0016197,GO:0030897,GO:0031091,GO:0016192,GO:0005765,GO:0006904,GO:0007476,GO:0061025,GO:0035542,GO:0032418,GO:0033263,GO:0019905,GO:0015031,GO:0005515,GO:0006955,GO:0070889,GO:0048471,GO:0032400,GO:0031902	CG5127-PA						PF00995				G3DSA:3.40.50.1910,G3DSA:3.40.50.1910	SSF56815,SSF56815									
aly2668.11	Probable isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	GO:0000287,GO:0016616,GO:0051287,GO:0005811,GO:0005739,GO:0006099,GO:0005759,GO:0004449,GO:0005875,GO:0055114	CG12233-PD					TIGR00175	PF00180			PS00470	G3DSA:3.40.718.10	SSF53659		00020+1.1.1.41	REACT_1046	PWY-6549,PWY-5690					
aly2668.12	Probable isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	GO:0000287,GO:0051287,GO:0005811,GO:0005739,GO:0006099,GO:0005759,GO:0004449,GO:0005875	CG12233-PD						PF00180				G3DSA:3.40.718.10	SSF53659									
aly2668.13	Nucleolar protein 6	GO:0022008,GO:0005730,GO:0006364,GO:0003723	CG12785-PA						PF03813														
aly2668.14	Uncharacterized family 31 glucosidase KIAA1161	GO:0017177,GO:0005975,GO:0048741,GO:0043568,GO:0016021,GO:0031965,GO:0004553,GO:0004558,GO:0051897	CG11909-PA						PF01055				G3DSA:3.20.20.70,G3DSA:3.20.20.70	SSF51445,SSF51011									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2668.15	Uncharacterized family 31 glucosidase KIAA1161	GO:0017177,GO:0005975,GO:0048741,GO:0043568,GO:0016021,GO:0031965,GO:0004553,GO:0004558,GO:0051897	CG11909-PA						PF01055				G3DSA:3.20.20.70,G3DSA:3.20.20.70	SSF51011,SSF51445									
aly2668.16	Uncharacterized family 31 glucosidase KIAA1161	GO:0017177,GO:0005975,GO:0048741,GO:0043568,GO:0016021,GO:0031965,GO:0004553,GO:0004558,GO:0051897	CG11909-PA						PF01055				G3DSA:3.20.20.70,G3DSA:3.20.20.70	SSF51445,SSF51011									
aly2668.17	Tubulin-specific chaperone A	GO:0007021,GO:0005737,GO:0015631,GO:0005874,GO:0051082	CG1890-PA						PF02970				G3DSA:1.20.58.90	SSF46988	23~47								
aly2668.18	Programmed cell death protein 7	GO:2001235,GO:0006915,GO:0051384,GO:0070234,GO:0005689	n/a						PF16021						85~119,157~206								
aly2668.19	DDB1- and CUL4-associated factor 12	GO:0005737,GO:0016567,GO:0080008,GO:0005515,GO:0005815	CG3313-PA										G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2668.2	Ras-specific guanine nucleotide-releasing factor 2	GO:0005089,GO:0005088,GO:0003677,GO:0046579,GO:0005789,GO:0035022,GO:0035023,GO:0005737,GO:2000134,GO:0045500,GO:2000310,GO:0007480,GO:0008595,GO:0008360,GO:0005886,GO:0007265,GO:0007264,GO:0031234,GO:0030676,GO:0007015,GO:0007426,GO:0007399,GO:0060291,GO:0016199,GO:0005515,GO:0008293,GO:0046982	CG7793-PA				SM00233,SM00233,SM00325,SM00229,SM00147		PF00618,PF00621,PF00617,PF00169	PS50096,PS50009,PS50212,PS50010,PS50003		PS00720	G3DSA:2.30.29.30,G3DSA:2.30.29.30,G3DSA:1.20.870.10,G3DSA:1.20.870.10,G3DSA:1.10.840.10,G3DSA:1.20.900.10	SSF50729,SSF48065,SSF48366,SSF48366,SSF50729	459~486,199~219								
aly2668.20	Unknown		n/a																				
aly2668.3	Monocarboxylate transporter 12	GO:0005308,GO:0015293,GO:0008028,GO:0016021,GO:1902598,GO:0005887,GO:0055085	CG3409-PA						PF07690				G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly2668.4	Monocarboxylate transporter 12	GO:0005308,GO:0035879,GO:0015129,GO:0008028,GO:0016021,GO:1902598,GO:0015293,GO:0005887,GO:0055085	CG3409-PA						PF07690,PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	273~293								
aly2668.5	Monocarboxylate transporter 12	GO:0005308,GO:0035879,GO:0015129,GO:0008028,GO:0016021,GO:1902598,GO:0015293,GO:0005887,GO:0055085	CG3456-PA						PF07690,PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2668.6	BTB/POZ domain-containing protein 2	GO:0005575,GO:0000932,GO:0022008,GO:0003674,GO:0005515	CG43226-PD				SM00225,SM00875		PF07707,PF00651,PF08005	PS50097			G3DSA:3.30.710.10	SSF54695									
aly2668.7	Katanin p60 ATPase-containing subunit A-like 2	GO:0005737,GO:0016887,GO:0051013,GO:0008568,GO:0031122,GO:0005515,GO:0008152,GO:0005874,GO:0005524	CG10793-PA				SM00667,SM00382		PF00004	PS50896			G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540									
aly2668.8	Dolichol-phosphate mannosyltransferase subunit 3	GO:0031647,GO:0005789,GO:0030176,GO:0033185,GO:0006506,GO:0035269,GO:0004582	CG33977-PA						PF08285						64~84				UPA00378				
aly2668.9	Phosphatidylinositol 3-kinase catalytic subunit type 3	GO:0046934,GO:0000910,GO:0033227,GO:0006897,GO:0035004,GO:0036092,GO:0016303,GO:0006914,GO:0035005,GO:0030496,GO:0035032,GO:0000045,GO:0048015,GO:0005488,GO:0009267,GO:0046854,GO:0005622,GO:0010506,GO:0005524	CG5373-PA				SM00146,SM00142		PF00454,PF00454,PF00613,PF00792	PS51547,PS51545,PS50290		PS00916,PS00915	G3DSA:3.30.1010.10,G3DSA:1.25.40.70,G3DSA:1.10.1070.11,G3DSA:1.25.40.70,G3DSA:2.60.40.150	SSF48371,SSF49562,SSF56112										
aly2669.1	Transcriptional regulator ATRX	GO:0016605,GO:0042393,GO:0070603,GO:0031933,GO:0006338,GO:0030330,GO:0006336,GO:0005634,GO:0006281,GO:0010571,GO:0004386,GO:0006334,GO:1901581,GO:0006351,GO:0003677,GO:0032206,GO:0045944,GO:0031297,GO:0072711,GO:0005524,GO:0008270	CG8290-PA							PS51533		PS00518	G3DSA:3.30.40.10	SSF57903	616~636								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2669.10	Unknown		n/a																				
aly2669.2	Major facilitator superfamily domain-containing protein 6	GO:0016021,GO:0016020,GO:0005575,GO:0003674,GO:0008150,GO:0055085	CG10121-PC						PF12832	PS51257			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly2669.3	Pericentriolar material 1 protein	GO:0005737,GO:0034451,GO:0005813,GO:0090316,GO:0042384,GO:0035735,GO:0005929,GO:0042802	n/a						PF15717						685~705,452~496,608~635,811~831,330~350,233~263								
aly2669.4	Unknown		n/a																				
aly2669.5	Zinc transporter 9	GO:0006812,GO:0005634,GO:0008324,GO:0055085,GO:0006355,GO:0006351,GO:0006829,GO:0016021	CG8632-PB					TIGR01297	PF01545				G3DSA:3.90.530.10,G3DSA:1.20.1510.10	SSF161111,SSF46955									
aly2669.6	Probable Ufm1-specific protease 2	GO:0016790,GO:0005575,GO:0008150,GO:0012505,GO:0071567,GO:0006508	CG16979-PA						PF07910					SSF54001									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2669.7	Exosome complex component RRP43	GO:0005737,GO:0000178,GO:0000288,GO:0005730,GO:0005829,GO:0000176,GO:0000177,GO:0000175,GO:0017091,GO:0010467,GO:0006364,GO:0043928,GO:0005634,GO:0006397	CG9606-PA						PF01138					SSF55666,SSF54211,SSF54211			REACT_21257						
aly2669.8	60S ribosomal protein L31	GO:0005840,GO:0022625,GO:0005622,GO:0003735,GO:0007052,GO:0000022,GO:0006412	CG1821-PC						PF01198			PS01144	G3DSA:3.10.440.10	SSF54575									
aly2669.9	Unknown		n/a																				
aly267.1	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG6475-PD						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly267.2	Unknown	GO:0005575,GO:0007606,GO:0003674	CG10946-PA										G3DSA:2.60.40.10	SSF48726									
aly267.3	Limbic system associated membrane protein	GO:0050767,GO:0016337,GO:0043005,GO:0009986,GO:0007606,GO:0005575,GO:0035641,GO:0003674,GO:0005911,GO:0005886,GO:0043025,GO:0031225	CG10946-PA				SM00408,SM00409		PF07686	PS50835			G3DSA:2.60.40.10	SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly267.4	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG4302-PA						PF00201					SSF53756									
aly267.5	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG4302-PA						PF00201					SSF53756									
aly267.6	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG4302-PA						PF00201					SSF53756									
aly26709.1	Unknown		n/a																				
aly2672.1	Frataxin homolog, mitochondrial	GO:0019896,GO:0006879,GO:0051881,GO:0042542,GO:0006783,GO:0004322,GO:0006811,GO:0005739,GO:0016226,GO:0008199,GO:0045823,GO:0034986	CG14085-PA					TIGR03421,TIGR03422	PF14906,PF01491	PS50810	PR00904,PR00904,PR00904,PR00904	PS01344	G3DSA:3.30.920.10	SSF55387		00860+1.16.3.1							
aly2672.2	Carbonic anhydrase 5B, mitochondrial	GO:0031233,GO:0004089,GO:0006730,GO:0005739,GO:0008270	CG6906-PA				SM01057		PF00194	PS51144			G3DSA:3.10.200.10	SSF51069									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2672.3	Unknown		n/a						PF14646						139~159								
aly2672.4	Unknown		n/a																				
aly2672.5	Carbonic anhydrase 2	GO:0015701,GO:0038166,GO:0006730,GO:0032849,GO:0030424,GO:0010043,GO:0005902,GO:2001150,GO:0051453,GO:0044070,GO:0005737,GO:0002009,GO:0045177,GO:0070062,GO:0043209,GO:0008270,GO:0001822,GO:0004089,GO:0004064,GO:2001225,GO:0032230,GO:0045780,GO:0016323,GO:0005886,GO:0043627,GO:0009268,GO:0005615,GO:0046903,GO:0042475,GO:0005829,GO:0045672,GO:0071498,GO:0044281	CG11284-PA				SM01057		PF00194	PS51144			G3DSA:3.10.200.10	SSF51069										
aly2672.6	Unknown	GO:0016021,GO:0009593,GO:0015276	CG13576-PA										G3DSA:3.40.190.10	SSF53850,SSF53850									
aly2672.7	Tyrosine kinase receptor Cad96Ca	GO:0006468,GO:0045792,GO:0016339,GO:0016020,GO:0045177,GO:0042060,GO:0018108,GO:0004714,GO:0090303,GO:0004713,GO:0005887,GO:0004672,GO:0007156,GO:0007030,GO:0005524,GO:0005509	CG10244-PA				SM00219,SM00112		PF07714,PF00028	PS50011,PS50268	PR00109,PR00109,PR00109,PR00109,PR00109	PS00109,PS00107	G3DSA:3.30.200.20,G3DSA:3.30.200.20,G3DSA:2.60.40.60,G3DSA:1.10.510.10	SSF56112,SSF49313										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2672.8	Tachykinin-like peptides receptor 86C	GO:0007218,GO:0006935,GO:0016021,GO:0007217,GO:0004950,GO:0005887,GO:0008188,GO:0004995,GO:0002121,GO:0007186	CG6515-PB						PF00001	PS50262	PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly26727.1	Myosin-VIIa	GO:0005737,GO:0008407,GO:0032027,GO:0045572,GO:0045927,GO:0042623,GO:0007605,GO:0042067,GO:0035317,GO:0008586,GO:0035220,GO:0001736,GO:0030048,GO:0048800,GO:0016459,GO:0030898,GO:0008152,GO:0035218,GO:0003774,GO:0005524	CG42840-PE						PF00063	PS51456				SSF52540									
aly26763.1	Tripeptidyl-peptidase 2	GO:0005737,GO:0004252,GO:0005615,GO:0004177,GO:0008240,GO:0051260,GO:0005739,GO:0008238,GO:0006508	CG3991-PD																				
aly2679.1	Unknown		n/a																				
aly2680.1	Aminopeptidase N	GO:0004177,GO:0070062,GO:0005793,GO:0009897,GO:0016021,GO:0030154,GO:0005765,GO:0008270,GO:0006508,GO:0001525,GO:0008237,GO:0005615	CG14516-PB						PF01433,PF11838		PR00756,PR00756,PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF63737,SSF55486									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2680.2	Membrane alanyl aminopeptidase	GO:0004177,GO:0008270,GO:0005886,GO:0006508,GO:0008237,GO:0031225	CG31198-PA						PF11838,PF01433		PR00756,PR00756,PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF63737,SSF55486									
aly2680.3	Membrane alanyl aminopeptidase (Fragment)	GO:0004177,GO:0008270,GO:0005886,GO:0006508,GO:0008237,GO:0031225	CG31198-PA						PF11838,PF01433		PR00756,PR00756,PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF55486,SSF63737									
aly2680.4	Membrane alanyl aminopeptidase (Fragment)	GO:0004177,GO:0008270,GO:0005886,GO:0006508,GO:0008237,GO:0031225	CG31198-PA						PF11838,PF01433		PR00756,PR00756,PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF55486,SSF63737									
aly2680.5	Membrane alanyl aminopeptidase (Fragment)	GO:0004177,GO:0008270,GO:0005886,GO:0006508,GO:0008237,GO:0031225	CG31198-PA						PF01433,PF11838		PR00756,PR00756,PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF63737,SSF55486									
aly2680.6	Membrane alanyl aminopeptidase (Fragment)	GO:0004177,GO:0008270,GO:0005886,GO:0006508,GO:0008237,GO:0031225	CG31198-PA						PF11838,PF11838,PF01433,PF01433		PR00756,PR00756,PR00756,PR00756,PR00756		G3DSA:1.10.390.10,G3DSA:1.10.390.10	SSF63737,SSF55486,SSF55486,SSF63737	1778~1787								
aly2680.7	Unknown	GO:0008270,GO:0003676	n/a				SM00343,SM00343		PF09668	PS50158		PS00141	G3DSA:4.10.60.10	SSF57756,SSF50630									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2682.1	Scavenger receptor class B member 1	GO:0006898,GO:0016324,GO:0016021,GO:0016020,GO:0045056,GO:0016323,GO:0005901,GO:0005886,GO:0007155,GO:0070506	CG40006-PA						PF01130,PF01130		PR01609,PR01609,PR01609												
aly2682.2	Unknown		n/a																				
aly2683.1	Zinc finger protein 878	GO:0006351,GO:0003676,GO:0003700,GO:0005634,GO:0006355,GO:0000790,GO:0008270,GO:0005515,GO:0003677,GO:0046872,GO:0043035	CG2711-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly2683.2	Unknown		CG42727-PA											SSF53335									
aly2683.3	Transcriptional repressor CTCF	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG1233-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13909	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly2683.4	Transmembrane protein 258	GO:0005575,GO:0008150,GO:0016021,GO:0003674	CG9669-PA						PF05251														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2683.5	Cadherin-23	GO:0007424,GO:0045177,GO:0047485,GO:0007605,GO:0016339,GO:0016020,GO:0005509,GO:0005887,GO:0005886,GO:0007156,GO:0016021	CG3389-PB				SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112		PF00028	PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205	PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313										
aly2683.6	Lipid storage droplets surface-binding protein 1	GO:0005737,GO:0032994,GO:0034389,GO:0006642,GO:0006869,GO:0005811,GO:1990044,GO:0010883,GO:0019915,GO:0010898,GO:0022008	CG10374-PA						PF03036						361~392								
aly2683.7	Splicing factor 3A subunit 1	GO:0044822,GO:0005654,GO:0071004,GO:0000381,GO:0071011,GO:0005634,GO:0000389,GO:0010467,GO:0000398,GO:0008380,GO:0005681,GO:0007052,GO:0003723,GO:0005686,GO:0007067,GO:0005684,GO:0071013,GO:0006396,GO:0006397	CG16941-PA				SM00648,SM00648		PF01805,PF01805,PF12230	PS50128,PS50128				SSF109905,SSF109905	534~537,559~559									
aly26830.1	P protein	GO:0016020,GO:0005302,GO:0005215,GO:0016021,GO:0006810,GO:0033162,GO:0055085	CG12787-PC																				
aly26868.1	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6467-PA						PF00089				G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly26912.1	Unknown	GO:0004806,GO:0005829,GO:0005811,GO:0016042,GO:0006642,GO:0008203	CG11055-PB										G3DSA:3.40.50.1820										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2692.1	Unknown		n/a																				
aly2692.2	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2	GO:0031697,GO:1990090,GO:0016020,GO:0017160,GO:0032926,GO:0030336,GO:0003094,GO:0030425,GO:0051898,GO:0045202,GO:0004871,GO:0005923,GO:0005737,GO:0072015,GO:0030159,GO:0005634,GO:0005770,GO:0038180,GO:0032403,GO:0048471,GO:0036057,GO:0008285,GO:0051291,GO:0004385,GO:0046332,GO:0030165,GO:0032516,GO:0010976,GO:0005886,GO:0071850,GO:0016482,GO:0043234,GO:0060395,GO:0070699,GO:0019902,GO:0005515,GO:0014069,GO:0043113,GO:0002092	CG30388-PA				SM00228,SM00228,SM00228,SM00228,SM00456,SM00456		PF00595,PF00595,PF00595,PF00397,PF00397	PS50020,PS50106,PS50106,PS50020,PS50106		PS01159	G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.20.70.10,G3DSA:2.20.70.10,G3DSA:2.30.42.10	SSF50156,SSF51045,SSF50156,SSF50156,SSF50156,SSF51045									
aly2692.3	Trypsin CFT-1	GO:0004252,GO:0005615,GO:0006508	CG32374-PA				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2692.4	Inositol 1,4,5-trisphosphate receptor	GO:0016319,GO:0030322,GO:0005783,GO:0005262,GO:0005220,GO:0007591,GO:0005789,GO:0042594,GO:0050909,GO:0016021,GO:0016020,GO:0000280,GO:0051209,GO:0060259,GO:0007608,GO:0035071,GO:0006874,GO:0007601,GO:0007629,GO:0055089,GO:0006979,GO:0048016,GO:0030536,GO:0005829,GO:0070588,G	CG1063-PB				SM00472,SM00472,SM00472,SM00472		PF02815,PF08709,PF01365,PF01365,PF00520,PF08454	PS50919,PS50919,PS50919,PS50919,PS50919	PR00779,PR00779,PR00779,PR00779,PR00779,PR00779,PR00779,PR00779,PR00779		G3DSA:1.25.10.30,G3DSA:1.25.10.30,G3DSA:2.80.10.50,G3DSA:2.80.10.50	SSF100909,SSF82109,SSF100909,SSF82109			REACT_14797,REACT_11061,REACT_15380,REACT_604,REACT_162,REACT_15295,REACT_1505					
aly2692.5	Trypsin, alkaline A	GO:0006508,GO:0005576,GO:0005615,GO:0004252	CG30031-PA				SM00020		PF00089	PS50240			G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2692.6	Serine/threonine-protein kinase WNK3	GO:0032414,GO:0090188,GO:0090263,GO:0035220,GO:0010800,GO:0030177,GO:0007411,GO:0090004,GO:0005923,GO:0005737,GO:0046777,GO:0004674,GO:0043066,GO:0004672,GO:0005524,GO:0010765,GO:0006468,GO:2000688,GO:0005912,GO:2000682,GO:0019869,GO:0051928,GO:2000021,GO:2000651	CG7177-PK				SM00220		PF00069,PF12202	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:3.10.20.90	SSF56112	664~684,1000~1034,828~855									
aly2692.7	Protein MON2 homolog	GO:0005794,GO:0016192,GO:0031532,GO:0005802,GO:0005086,GO:0005488,GO:0015031,GO:0005519,GO:0005768,GO:0007318	CG8683-PB						PF09324,PF16206,PF12783,PF16213,PF16213				G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371	538~558								
aly2692.8	Protein MON2 homolog	GO:0005794,GO:0016192,GO:0031532,GO:0005802,GO:0005086,GO:0015031,GO:0005519,GO:0005768,GO:0007318	CG8683-PB						PF16206														
aly2692.9	Craniofacial development protein 2	GO:0005737,GO:0005634	n/a										G3DSA:3.60.10.10	SSF56219									
aly2694.1	Unknown		CG30419-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2694.10	Msx2-interacting protein	GO:0001085,GO:0001191,GO:0007219,GO:0070062,GO:0017053,GO:0000122,GO:0003700,GO:0044822,GO:0003714,GO:0000166,GO:0005654,GO:0045892,GO:0045893,GO:0016032,GO:0050769,GO:0003697,GO:0006351	n/a																				
aly2694.11	Iron-sulfur cluster assembly 2 homolog, mitochondrial	GO:0005198,GO:0051536,GO:0005739,GO:0016226,GO:0046331,GO:0046872	CG13623-PA					TIGR00049	PF01521				G3DSA:2.60.300.12	SSF89360									
aly2694.12	Unknown		CG16926-PA																				
aly2694.13	Succinate dehydrogenase [ubiqui] flavoprotein subunit, mitochondrial	GO:0050660,GO:0005739,GO:0005743,GO:0006099,GO:0022900,GO:0008177,GO:0004776,GO:0005749,GO:0055114,GO:0016491	CG17246-PB			PIRSF000171		TIGR01812,TIGR01816	PF00890,PF02910			PS00504	G3DSA:1.20.58.100,G3DSA:3.90.700.10,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:4.10.80.40	SSF46977,SSF56425,SSF51905,SSF51905		00720+1.3.5.1,00190+1.3.5.1,00020+1.3.5.1,00650+1.3.5.1		PWY-561,PWY-4302,PWY-3781,PWY-7279,PWY-6969,PWY-6728,PWY-7254,PWY-5690					
aly2694.14	Transcription initiation factor TFIID subunit 11	GO:0051123,GO:0001075,GO:0005634,GO:0003713,GO:0006355,GO:0006367,GO:0005669,GO:0046982,GO:0008134	CG4079-PA						PF04719				G3DSA:1.10.20.10	SSF47113	173~208								
aly2694.15	Zinc finger C2HC domain-containing protein 1A	GO:0046872	CG30460-PC						PF13913,PF13913														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2694.16	ADP-ribosylation factor 2	GO:0016197,GO:0048749,GO:0005794,GO:0006471,GO:0003924,GO:0005525,GO:0005622,GO:0005575,GO:0007269,GO:0015031,GO:0007264,GO:0048488,GO:0003956	CG11027-PA						PF00025				G3DSA:3.40.50.300	SSF52540									
aly2694.17	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial	GO:0004300,GO:0005739,GO:0008152,GO:0003824	CG6984-PA						PF00378				G3DSA:3.90.226.10	SSF52096									
aly2694.18	ATP-dependent RNA helicase DHX36	GO:0008026,GO:0000781,GO:0001503,GO:0005737,GO:0070062,GO:0009615,GO:0005634,GO:0010501,GO:0042826,GO:0045087,GO:0005524,GO:0006351,GO:0044212,GO:0044822,GO:0004004,GO:0004386,GO:0032481,GO:0001047,GO:0002151,GO:0008094,GO:0051880,GO:0005829,GO:0032206,GO:0003725,GO:0045944,GO:0043330,GO:0006396	CG9323-PA				SM00847,SM00490,SM00487		PF00270,PF07717,PF04408,PF00271	PS51194,PS51192		PS00690	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									
aly2694.19	Polypeptide N-acetylgalactosaminyltransferase 3	GO:0005795,GO:0005794,GO:0031589,GO:0016266,GO:0006493,GO:0016021,GO:0004653,GO:0030246,GO:0070278,GO:0009312,GO:0033628,GO:0046872,GO:0016757,GO:0008376,GO:0000139	CG4445-PA						PF00535				G3DSA:2.80.10.50,G3DSA:3.90.550.10	SSF50370,SSF53448									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2694.2	3-oxoacyl-[acyl-carrier-protein] reductase FabG	GO:0050661,GO:0051287,GO:0030497,GO:0004316,GO:0008152,GO:0016491	CG31548-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080	PS00061	G3DSA:3.40.50.720	SSF51735									
aly2694.20	Unknown		n/a																				
aly2694.21	Unknown		n/a																				
aly2694.22	Unknown		n/a												33~60								
aly2694.3	3-oxoacyl-[acyl-carrier-protein] reductase FabG	GO:0006633,GO:0016614,GO:0006635,GO:0008670,GO:0004316,GO:0008152,GO:0051287,GO:0016491	CG3699-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2694.4	Unknown		n/a						PF01826				G3DSA:2.10.25.10	SSF57567									
aly2694.5	Unknown		n/a																				
aly2694.6	Unknown		n/a						PF01826				G3DSA:2.10.25.10	SSF57567									
aly2694.7	Unknown		n/a																				
aly2694.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2694.9	Protein split ends	GO:0048749,GO:0006351,GO:0007422,GO:0007379,GO:0005634,GO:0016055,GO:0035222,GO:0008586,GO:0000166,GO:0050832,GO:0006355,GO:0030177,GO:0007173,GO:0048106,GO:0003676,GO:0003723,GO:0007411,GO:0035321,GO:0007403,GO:0008347,GO:0007400	CG18497-PA				SM00360,SM00360,SM00360		PF07744,PF00076	PS50102,PS50917,PS50102			G3DSA:3.30.70.330,G3DSA:2.40.290.10	SSF54928,SSF54928,SSF100939	1188~1208,1543~1565,1993~2013,986~1013,1043~1063,456~458,1421~1464								
aly27.1	Reticulon-4 receptor-like 2	GO:0009897,GO:0031103,GO:0005515,GO:0009986,GO:0045121,GO:0042059,GO:0046658,GO:0046331,GO:0004872,GO:0005887,GO:0070062	CG1804-PB				SM00369,SM00369,SM00369,SM00369,SM00369,SM00082		PF13855,PF07679	PS50835			G3DSA:2.60.40.10,G3DSA:3.80.10.10	SSF48726,SSF52058									
aly27.10	Unknown		CG8813-PA																				
aly27.11	Rho GTPase-activating protein 6	GO:0005737,GO:0007015,GO:0043547,GO:0051497,GO:0016004,GO:0007202,GO:0005096,GO:0005622,GO:0005575,GO:0010518,GO:0043274,GO:0007165,GO:0048041,GO:0005100,GO:0043087,GO:0051895,GO:0015629	CG42316-PD				SM00324		PF00620	PS50238			G3DSA:1.10.555.10	SSF48350			REACT_11044						
aly27.12	Rho GTPase-activating protein 6	GO:0005737,GO:0007015,GO:0043547,GO:0051497,GO:0016004,GO:0007202,GO:0005096,GO:0005622,GO:0005575,GO:0010518,GO:0043274,GO:0007165,GO:0048041,GO:0005100,GO:0043087,GO:0051895,GO:0015629	CG42316-PD																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly27.13	Unknown		n/a																				
aly27.14	Putative oxidoreductase GLYR1 homolog	GO:0050662,GO:0008442,GO:0051287,GO:0005705,GO:0006098,GO:0004616	CG4747-PB			PIRSF000103			PF14833,PF03446				G3DSA:3.40.50.720,G3DSA:1.10.1040.10	SSF48179,SSF51735									
aly27.15	Transposable element P transposase	GO:0004803,GO:0006313,GO:0015074,GO:0016740,GO:0003693,GO:0046872	n/a				SM00980		PF12017,PF05485					SSF57716	124~151								
aly27.16	Leucine-rich repeat and immunoglobulin-like domain containing nogo receptor-interacting protein 2	GO:0016021,GO:0048812,GO:0051965,GO:0005515	CG16974-PA				SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00082,SM00408,SM00409,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364		PF07679,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS50835,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:2.60.40.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF48726,SSF52058	590~610								
aly27.17	Putative oxidoreductase GLYR1 homolog	GO:0050662,GO:0008442,GO:0051287,GO:0005705,GO:0006098,GO:0004616	CG4747-PB				SM00293		PF00855,PF03446	PS50812			G3DSA:3.40.50.720,G3DSA:2.30.30.160	SSF51735,SSF63748									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly27.18	Unknown		n/a												154~181,225~245								
aly27.19	Protein YIPF1	GO:0016021,GO:0016020	CG4645-PA						PF04893														
aly27.2	Unknown		n/a																				
aly27.20	Pre-mRNA cleavage complex 2 protein Pcf11	GO:0005737,GO:0006379,GO:0006378,GO:0031124,GO:0005849,GO:0000398,GO:0005654,GO:0010467,GO:0003723,GO:0006366,GO:0006369,GO:0022008,GO:0000993,GO:0008380,GO:0003729	CG10228-PD				SM00582		PF04818	PS51391			G3DSA:1.25.40.90	SSF48464	175~195								
aly27.21	Pre-mRNA cleavage complex 2 protein Pcf11	GO:0005737,GO:0006379,GO:0006378,GO:0031124,GO:0005849,GO:0000398,GO:0005654,GO:0010467,GO:0003723,GO:0006366,GO:0006369,GO:0022008,GO:0000993,GO:0008380,GO:0003729	CG10228-PD												225~256								
aly27.22	Probable asparagine--tRNA ligase, mitochondrial	GO:0005737,GO:0004812,GO:0006421,GO:0004816,GO:0005739,GO:0000166,GO:0003676,GO:0006418,GO:0005759,GO:0005524	CG6796-PA					TIGR00457	PF00152,PF01336	PS50862	PR01042,PR01042,PR01042		G3DSA:2.40.50.140,G3DSA:3.30.930.10	SSF50249,SSF55681		00970+6.1.1.22	REACT_71						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly27.23	Krueppel homolog 2	GO:0016021,GO:0012505	CG9159-PA						PF03661														
aly27.24	Unknown		n/a																				
aly27.3	Yemanuclein-alpha	GO:0001940,GO:0005634,GO:0035042,GO:0005654,GO:0003700,GO:0006357,GO:0042585,GO:0003677,GO:0048477,GO:0007143,GO:0000776,GO:0000777	CG14513-PB						PF14075,PF08729						452~472									
aly27.4	Amyloid beta A4 precursor protein-binding family B member 2	GO:0005737,GO:0043065,GO:0001540,GO:0030308,GO:0030027,GO:0005634,GO:0016020,GO:0030426,GO:0007050,GO:0006355,GO:0030198,GO:0001764,GO:0045202,GO:0005515,GO:0043066,GO:0007411,GO:0035556,GO:0008134	n/a				SM00462,SM00462,SM00456		PF00640	PS50020,PS01179			G3DSA:2.30.29.30,G3DSA:2.30.29.30,G3DSA:2.20.70.10	SSF50729,SSF51045,SSF50729									
aly27.5	Unknown		n/a																				
aly27.6	Unknown		CG30015-PC												1304~1331								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly27.7	Endoplasmic reticulum-Golgi intermediate compartment protein 2	GO:0005737,GO:0005794,GO:0006888,GO:0043231,GO:0005793,GO:0005730,GO:0016021,GO:0016020,GO:0033116,GO:0005789,GO:0003674,GO:0005634,GO:0030134	CG4293-PB						PF07970,PF13850														
aly27.8	Ragulator complex protein LAMTOR1	GO:0007032,GO:0005764,GO:0045121,GO:0016049,GO:0071230,GO:0060620,GO:0032439,GO:0032418,GO:0043547,GO:0043410,GO:0005765,GO:0071986,GO:0005886,GO:0007040,GO:0010872,GO:0042632,GO:0001919,GO:0010874,GO:0031902,GO:0034613,GO:0032008	CG14184-PA						PF15454														
aly27.9	Unknown		n/a																				
aly270.1	ADAMTS-like protein 1	GO:0044267,GO:0036066,GO:0004222,GO:0043687,GO:0005788,GO:0006493,GO:0008270,GO:0006508,GO:0008233,GO:0005578,GO:0008237	CG31619-PC				SM00209,SM00209,SM00209,SM00209,SM00209,SM00209,SM00209,SM00209,SM00209,SM00408,SM00409		PF08686,PF07679,PF00090,PF00090,PF00090,PF00090,PF00090,PF00090	PS50900,PS50092,PS50092,PS50835,PS50092,PS50092,PS50092,PS50092,PS50092,PS50092			G3DSA:2.60.40.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10	SSF82895,SSF82895,SSF82895,SSF48726,SSF82895,SSF82895,SSF82895,SSF82895									
aly270.2	Unknown		n/a										G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly270.3	Unknown	GO:0016772	CG2004-PA				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly2700.1	E3 ubiquitin-protein ligase RNF19A	GO:0005737,GO:0004842,GO:0016021,GO:0005815,GO:0016567,GO:0008270,GO:0003676,GO:0016874	CG5709-PA				SM00647,SM00647,SM00184		PF01485,PF01485,PF00097	PS50089			G3DSA:3.30.40.10	SSF57850,SSF57850,SSF57850									
aly2700.10	Dorsal-ventral patterning tolloid-like protein 1	GO:0004222,GO:0009953,GO:0001707,GO:0001568,GO:0008270,GO:0036342,GO:0035162,GO:0005575,GO:0008237,GO:0005576,GO:0003674,GO:0005509,GO:0006508,GO:0001885,GO:0008150,GO:0008233,GO:0030513,GO:0048264,GO:0035124	CG42613-PE				SM00042,SM00042,SM00042,SM00042,SM00042		PF00431,PF00431,PF00431,PF00431,PF00431	PS01180,PS01180,PS01180,PS01180,PS01180			G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290	SSF49854,SSF49854,SSF49854,SSF49854,SSF49854									
aly2700.11	Unknown		n/a																				
aly2700.12	Heterogeneous nuclear ribonucleoprotein Q	GO:0035770,GO:0008143,GO:0070934,GO:0070937,GO:0046843,GO:0001649,GO:0005737,GO:0016020,GO:0000166,GO:0097452,GO:0008380,GO:0030529,GO:0046011,GO:0071011,GO:0071013,GO:0044822,GO:0007310,GO:0022008,GO:0071346,GO:0000398,GO:0017148,GO:0003729,GO:0071204,GO:0006397	CG17838-PJ				SM00360,SM00360,SM00360	TIGR01648	PF00076,PF00076,PF00076	PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2700.13	ER membrane protein complex subunit 1	GO:0016021,GO:0072546	CG2943-PA										G3DSA:2.140.10.10,G3DSA:2.140.10.10,G3DSA:2.140.10.10	SSF50998,SSF50998,SSF50998,SSF50998,SSF50998									
aly2700.14	TELO2-interacting protein 1 homolog	GO:0005737,GO:0031932,GO:0031931,GO:0046331,GO:0005488,GO:0032006	CG16908-PA										G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371									
aly2700.15	TELO2-interacting protein 1 homolog	GO:0005737,GO:0032006,GO:0031932,GO:0031931	n/a																				
aly2700.16	Protein FAM185A	GO:0005737	CG8187-PA						PF13349														
aly2700.17	Unknown		CG13607-PA											SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2700.18	Rootletin	GO:0005737,GO:0051656,GO:0015629,GO:0035253,GO:0005813,GO:0051297,GO:0045494,GO:0005814,GO:0010457,GO:0003779,GO:0030030,GO:0019894,GO:0001917,GO:0010669,GO:0005886,GO:0033365,GO:0008104,GO:0032053,GO:0005198,GO:0007049,GO:0070062	CG6129-PD						PF15035						9~29,267~287,97~166,48~68									
aly2700.19	Unknown		n/a																				
aly2700.2	RING finger and transmembrane domain-containing protein 2	GO:0016021,GO:0008270	CG13605-PB				SM00184		PF13639	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850									
aly2700.3	Unknown	GO:0016772,GO:0022008	CG31097-PB				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly2700.4	ADP-ribosylation factor-like protein 6-interacting protein 4	GO:0016607,GO:0005730,GO:0008380,GO:0006397	CG18428-PA						PF10500						24~73								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2700.5	Thioredoxin domain-containing protein 5	GO:0006457,GO:0005783,GO:0009986,GO:0005788,GO:0003756,GO:0043277,GO:2000427,GO:0045454,GO:0034976,GO:0015035,GO:0006662,GO:0070062	CG1837-PA						PF00085,PF00085,PF00085	PS51352,PS51352		PS00194	G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10	SSF52833,SSF52833,SSF52833	380~400								
aly2700.6	Serine/threonine-protein kinase LATS1	GO:0048749,GO:0033138,GO:0060439,GO:0000082,GO:0045464,GO:0051220,GO:0007067,GO:0000922,GO:0043254,GO:0051301,GO:0005737,GO:0030833,GO:0010212,GO:0030216,GO:0007430,GO:0001708,GO:0000287,GO:0005815,GO:0043065,GO:0004674,GO:0005524,GO:0045736,GO:0042127,GO:0008285,GO:0006468,GO:0034613,GO:0000086,GO:0046621,GO:0009987,GO:0060253,GO:0019901,GO:0008360,GO:0045892,GO:0035329,GO:0042771,GO:0000819,GO:0007446,GO:0090090,GO:0048814,GO:0005515,GO:0009755,GO:0045570,GO:0072089	CG12072-PA				SM00220		PF00627,PF00069	PS50011,PS51285,PS50030		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10,G3DSA:1.10.8.10	SSF56112,SSF56112,SSF46934										
aly2700.7	Valacyclovir hydrolase	GO:0016787,GO:0070062,GO:0005739,GO:0017171	CG5377-PA						PF12695				G3DSA:3.40.50.1820	SSF53474									
aly2700.8	T-complex protein 1 subunit alpha	GO:0006457,GO:1902600,GO:0005829,GO:0005753,GO:0005832,GO:0007052,GO:0090037,GO:0051082,GO:0006909,GO:0008553,GO:0005875,GO:0005524	CG5374-PB					TIGR02340	PF00118		PR00304,PR00304,PR00304,PR00304,PR00304	PS00750,PS00751,PS00995	G3DSA:3.50.7.10,G3DSA:3.30.260.10,G3DSA:3.30.260.10,G3DSA:1.10.560.10,G3DSA:1.10.560.10	SSF54849,SSF54849,SSF48592,SSF48592,SSF52029			REACT_17015						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2700.9	Unknown		n/a																				
aly270017.1	Unknown		n/a																				
aly2701.1	Unknown		n/a																				
aly2701.2	Unknown		n/a																				
aly2701.3	Probable tubulin polyglutamylase TTLL1	GO:0005737,GO:0018095,GO:0060271,GO:0035082,GO:0005874,GO:0018166,GO:0003351,GO:0044782,GO:0016874,GO:0004835	CG32238-PA						PF03133	PS51221				SSF56059,SSF56059									
aly270117.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2706.1	Unknown	GO:0005515	CG32432-PA				SM00192,SM00192,SM00042		PF00431,PF00057	PS50068,PS01180,PS50068	PR00261,PR00261	PS01209,PS01209	G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.60.120.290	SSF49854,SSF49854,SSF57424,SSF49854									
aly27099.1	Juvenile hormone epoxide hydrolase	GO:0019439,GO:0016021,GO:0033961,GO:0005789	n/a										G3DSA:3.40.50.1820										
aly2716.1	Pro-resilin	GO:0040003,GO:0032992,GO:0005214,GO:0030023,GO:0008010,GO:0031012,GO:0005576,GO:0008061,GO:0042302	CG6305-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly2716.2	Lactoylglutathione lyase	GO:0005975,GO:0070062,GO:0004462,GO:0030316,GO:0043066,GO:0006357,GO:0006749,GO:0046872,GO:0009438,GO:0008270	CG1707-PA					TIGR00068	PF00903			PS00934,PS00935	G3DSA:3.10.180.10	SSF54593		00620+4.4.1.5		PWY-5386	UPA00619				
aly2716.3	S-antigen protein	GO:0007443,GO:0005201,GO:0005587,GO:0005581,GO:0020003,GO:0005811,GO:0007519,GO:0061327	CG16858-PA																				
aly2716.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2716.5	Probable ATP-dependent RNA helicase DHX35	GO:0005737,GO:0071011,GO:0006396,GO:0071013,GO:0004004,GO:0004386,GO:0003724,GO:0000398,GO:0003676,GO:0005524,GO:0044822,GO:0005681	CG3225-PA							PS51192			G3DSA:3.40.50.300	SSF52540									
aly2716.6	Probable ATP-dependent RNA helicase DHX35	GO:0005737,GO:0071011,GO:0006396,GO:0071013,GO:0004004,GO:0004386,GO:0003724,GO:0000398,GO:0003676,GO:0005524,GO:0044822,GO:0005681	CG3225-PA				SM00847,SM00490		PF04408,PF00271	PS51194			G3DSA:3.40.50.300	SSF52540									
aly2716.7	Unknown		n/a																				
aly2716.8	Ceramide phosphoethanolamine synthase	GO:0016780,GO:0008654,GO:0016021,GO:0016020,GO:0000139,GO:0005886,GO:0006665	CG4585-PA						PF01066														
aly27171.1	2-hydroxyacyl-CoA lyase 1	GO:0051259,GO:0001561,GO:0005782,GO:0005777,GO:0008949,GO:0000287,GO:0016830,GO:0048037,GO:0030976,GO:0044255,GO:0005102,GO:0042802,GO:0044281	CG11208-PA						PF02775				G3DSA:3.40.50.970	SSF52518									
aly2718.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2718.10	Unknown	GO:0005575,GO:0003674,GO:0008150	CG33290-PA																				
aly2718.11	MOXD1 homolog 1	GO:0004500,GO:0016715,GO:0005575,GO:0005576,GO:0005507,GO:0055114	CG5235-PA				SM00664		PF01082,PF03351	PS50836	PR00767,PR00767,PR00767		G3DSA:2.60.120.310	SSF49742									
aly2718.12	Unknown		n/a																				
aly2718.13	Unknown		n/a																				
aly2718.14	Unknown		n/a																				
aly2718.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2718.3	Neuromedin-B receptor	GO:0005737,GO:0007218,GO:0016021,GO:0005886,GO:0004930,GO:0031989,GO:0004946,GO:0008188,GO:0007186	CG14593-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly2718.4	Unknown	GO:0005575,GO:0003674,GO:0008150	CG33290-PA																				
aly2718.5	Unknown	GO:0005575,GO:0003674,GO:0008150	CG33290-PA																				
aly2718.6	Unknown	GO:0005575,GO:0003674,GO:0008150	CG33290-PA																				
aly2718.7	Unknown	GO:0005575,GO:0003674,GO:0008150	CG33290-PA																				
aly2718.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2718.9	Carboxylesterase 1E	GO:0008152,GO:0005788,GO:0052689	CG10339-PA						PF00135			PS00941	G3DSA:3.40.50.1820	SSF53474									
aly272.1	Unknown		n/a																				
aly272.10	Vascular endothelial growth factor receptor 1	GO:0000186,GO:0061327,GO:0019730,GO:0030031,GO:0030154,GO:0030335,GO:0030036,GO:0008284,GO:0007419,GO:0046777,GO:0032869,GO:0007169,GO:0007298,GO:0001525,GO:0000022,GO:0023014,GO:0038084,GO:0007435,GO:0030522,GO:0001666,GO:0048661,GO:0019838,GO:0038202,GO:0004716,GO:0048803,GO:0004714,GO:0043066,GO:0048514,GO:0005017,GO:0016477,GO:0005524,GO:0004713,GO:0048598,GO:0042386,GO:0006468,GO:0006935,GO:0007015,GO:0045087,GO:0035172,GO:0035099,GO:0006974,GO:0007516,GO:0018108,GO:0005887,GO:0005886,GO:0048010,GO:0007443,GO:0036335,GO:0043410,GO:0006940,GO:0005768,GO:0005021,GO:0008360,GO:0005515,GO:0030097,GO:0045610	CG8222-PJ				SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408		PF07714,PF00047,PF07679	PS50835,PS50835,PS50835,PS50011,PS50835		PS00107,PS00240,PS00109	G3DSA:3.30.200.20,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:1.10.510.10,G3DSA:1.10.510.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF56112,SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly272.11	Platelet-derived growth factor receptor alpha	GO:0019730,GO:2000739,GO:0008585,GO:0023019,GO:0060325,GO:0060326,GO:0007298,GO:0038202,GO:0007516,GO:0033327,GO:0016020,GO:0004714,GO:0004713,GO:0043234,GO:0035172,GO:0008360,GO:0010035,GO:0007443,GO:0005829,GO:0007204,GO:0030198,GO:0050920,GO:0009897,GO:0006468,GO:0038085,GO:0048008,GO:0035790,GO:0010863,GO:0007435,GO:0048803,GO:0010544,GO:0005017,GO:0005018,GO:0016477,GO:0005524,GO:0048705,GO:0042386,GO:0009887,GO:0048557,GO:0048701,GO:0034097,GO:0042063,GO:0042060,GO:0043410,GO:0048010,GO:0048015,GO:0072277,GO:0035099,GO:0043552,GO:0038091,GO:0048407,GO:0048146,GO:0007419,GO:0005902,GO:0009653,GO:0031226,GO:0046777,GO:0030325,GO:0005737,GO:0001701,GO:0005634,GO:0045740,GO:0032403,GO:0042803,GO:0008284,GO:0055003,GO:0009986,GO:0006974,GO:0018108,GO:0001553,GO:0061298,GO:0036335,GO:0048839,GO:0005021,GO:0005515,GO:0030097,GO:0070374,GO:0045610,GO:0030324,GO:0061327,GO:0030031,GO:0005161,GO:0030036,GO:0060021,GO:0008210,GO:0032869,GO:0055093,GO:0000022,GO:0032355,GO:0002244,GO:0043066,GO:0004672,GO:0030335,GO:0071230,GO:0045087,GO:0034614,GO:0005887,GO:0005886,GO:0007015,GO:0042475,GO:0030539,GO:0070527	CG8222-PJ										G3DSA:2.60.40.10										
aly272.12	Outer dense fiber protein 3	GO:0005643,GO:0007605,GO:0022008,GO:0005737	CG8086-PI						PF07004,PF07004,PF07004,PF07004,PF07004,PF07004,PF07004,PF07004,PF07004,PF07004,PF07004,PF07004,PF07004,PF07004,PF07004,PF07004														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly272.13	Cyclic nucleotide-binding domain-containing protein 2	GO:0030552,GO:0005829,GO:0007283	CG14693-PE				SM00100		PF00027	PS50042		PS00889	G3DSA:2.60.120.10,G3DSA:2.60.120.10,G3DSA:2.60.120.10	SSF51206,SSF51206,SSF51206									
aly272.14	Proteasome maturation protein	GO:0005737,GO:0032436,GO:0005783,GO:0008283,GO:0005829,GO:0005654,GO:0007052,GO:0043248,GO:0000502,GO:0006508,GO:0000022,GO:0005634,GO:0031090	CG9324-PA						PF05348														
aly272.15	2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase	GO:0019628,GO:0019428,GO:0005777,GO:0016831,GO:0006144	n/a					TIGR03164	PF09349				G3DSA:1.10.3330.10	SSF158694		00230+4.1.1.97		PWY-7394,PWY-5691	UPA00394				
aly272.16	Homeobox protein CDX-1	GO:0007487,GO:0035224,GO:0060349,GO:0010004,GO:0003677,GO:0005737,GO:0007389,GO:0009948,GO:0005634,GO:0006366,GO:0000980,GO:0008284,GO:0035215,GO:0002807,GO:0001205,GO:0007350,GO:0007443,GO:0007442,GO:0009952,GO:0007377,GO:0003700,GO:0007379,GO:0045944,GO:0000977	CG1759-PC				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024,PR00031,PR00031	PS00027	G3DSA:1.10.10.60	SSF46689									
aly272.17	Apoptosis inhibitor 5	GO:0005737,GO:0016020,GO:2000270,GO:0005634,GO:0006915,GO:0017134,GO:0005654,GO:0043066,GO:0005515,GO:0022008,GO:0044822,GO:0005681	CG6582-PA						PF05918				G3DSA:1.25.10.10	SSF48371,SSF48371	16~36								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly272.18	Solute carrier family 22 member 21	GO:0015879,GO:0015226,GO:0016021,GO:1902603,GO:0005777,GO:0008513,GO:0031231,GO:0022008,GO:0055085,GO:0005524	CG7084-PB										G3DSA:1.20.1250.20	SSF103473									
aly272.19	Unknown		n/a																				
aly272.2	Teneurin-m	GO:0034116,GO:0051124,GO:0042051,GO:0034110,GO:0097090,GO:0045467,GO:0050808,GO:0008045,GO:0001745,GO:0007274,GO:0030054,GO:0005737,GO:0001941,GO:0043005,GO:0043025,GO:0042802,GO:0042803,GO:0016200,GO:2000331,GO:0031005,GO:0008039,GO:0031122,GO:0045211,GO:0008360,GO:0005887,GO:0005886,GO:0007155,GO:0048499,GO:0048058,GO:0031594,GO:0040017,GO:0048790,GO:0022416,GO:0046982,GO:0005578	CG5723-PE				SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181	TIGR01643	PF07974,PF07974,PF15636	PS50026,PS50026,PS50026,PS50026		PS01186,PS00022,PS00022,PS01186,PS01186,PS01186,PS01186,PS00022,PS00022,PS01186,PS00022,PS00022,PS00022,PS01186,PS00022	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.120.10.30,G3DSA:2.120.10.30	SSF101898										
aly272.20	Mediator of RNA polymerase II transcription subunit 7	GO:0005515,GO:0005634,GO:0001104,GO:0006357,GO:0006351,GO:0006367,GO:0006366,GO:0016592	CG31390-PA						PF05983					SSF140718									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly272.21	Tyrosine-protein kinase Btk29A	GO:0044719,GO:0008258,GO:0005886,GO:0006468,GO:0018108,GO:0007300,GO:0007301,GO:0071944,GO:0030717,GO:0007169,GO:0035556,GO:0005737,GO:0007254,GO:0007435,GO:0038083,GO:0045172,GO:0007619,GO:0007476,GO:0007349,GO:0030723,GO:0004715,GO:0004713,GO:0046872,GO:0048477,GO:0005524,GO:0042127,GO:0007485,GO:0030154,GO:0045087,GO:0045177,GO:0042023,GO:0030833,GO:0030036,GO:0035277,GO:0046960,GO:0008340,GO:0031234,GO:0007424,GO:0007391	CG8049-PB				SM00233,SM00326,SM00219,SM00252		PF00779,PF00018,PF00169,PF07714,PF00017	PS50001,PS51113,PS50002,PS50003,PS50011	PR00452,PR00452,PR00452,PR00109,PR00109,PR00109,PR00109,PR00401,PR00401,PR00401,PR00401	PS00109,PS00107	G3DSA:2.30.29.30,G3DSA:2.30.30.40,G3DSA:3.30.505.10,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF50729,SSF50044,SSF55550,SSF56112									
aly272.22	CRAL-TRIO domain-containing protein C3H8.02	GO:0005737,GO:0015914,GO:0008526,GO:0071852	CG32485-PA				SM00516		PF00650	PS50191			G3DSA:3.40.525.10	SSF52087,SSF46938									
aly272.23	Unknown	GO:0016787,GO:0046872,GO:0003676	CG3819-PA				SM00892		PF01223				G3DSA:3.40.570.10	SSF54060									
aly272.24	Unknown	GO:0016787,GO:0046872,GO:0003676	CG3819-PA				SM00892		PF01223				G3DSA:3.40.570.10	SSF54060									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly272.25	Eye-specific diacylglycerol kinase	GO:0006654,GO:0016310,GO:0003951,GO:0035556,GO:0005875,GO:0019992,GO:0016020,GO:0046834,GO:0006661,GO:0046872,GO:0004143,GO:0005524,GO:0007608,GO:0007605,GO:0007601,GO:0007602,GO:0008152,GO:0007015,GO:0016059,GO:0016056,GO:0043052,GO:0007205,GO:0005515,GO:0045494	CG42667-PH				SM00046,SM00045,SM00248,SM00248		PF00781,PF00130,PF00609,PF12796	PS50088,PS50146,PS50088,PS50297			G3DSA:1.25.40.20	SSF111331,SSF48403		00561+2.7.1.107,00564+2.7.1.107	REACT_14797,REACT_604	PWY-7039					
aly272.26	Unknown		n/a																				
aly272.27	Unknown		n/a							PS50016		PS01359	G3DSA:3.30.40.10	SSF57903									
aly272.3	Transcription factor SPT20 homolog	GO:0000124,GO:0005730,GO:0006325,GO:0006914,GO:0007369,GO:0003712,GO:0070461,GO:0035948,GO:0005634	CG17689-PA						PF12090														
aly272.4	B-box type zinc finger protein ncl-1	GO:0005737,GO:0007126,GO:0090071,GO:0005622,GO:0007281,GO:0008270,GO:0007276	CG12218-PE				SM00336,SM00336,SM00502,SM00184,SM00184		PF00097,PF01436,PF01436,PF01436	PS50119,PS51125,PS51125,PS51125,PS51125,PS50119,PS51125,PS50089,PS51125		PS00518	G3DSA:2.120.10.30,G3DSA:3.30.40.10	SSF57845,SSF63829,SSF57850	243~270,272~303								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly272.5	Putative N-acetylglucosamine-6-phosphate deacetylase	GO:0005975,GO:0016810,GO:0006044,GO:0008448,GO:0005575,GO:0046872	CG17065-PB			PIRSF038994		TIGR00221	PF01979				G3DSA:2.30.40.10,G3DSA:3.20.20.140,G3DSA:2.30.40.10	SSF51338,SSF51338,SSF51556		00052+3.5.1.25,00520+3.5.1.25		PWY-6906,PWY-7395,PWY-7077					
aly272.6	Unknown		n/a																				
aly272.7	Slit homolog 3 protein	GO:0030154,GO:0007420,GO:0016020,GO:0021510,GO:0005576,GO:0005509	CG1504-PB										G3DSA:3.80.10.10	SSF52058									
aly272.8	Probable cytochrome P450 4d14	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG3540-PB						PF00067		PR00465,PR00465		G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly272.9	Cytochrome P450 4e3	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005811,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG4105-PA										G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly27293.1	Unknown		n/a						PF14529				G3DSA:3.60.10.10,G3DSA:3.60.10.10	SSF56219									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly27341.1	Unknown	GO:0003676	n/a										G3DSA:3.30.420.10	SSF53098									
aly27343.1	Unknown		n/a												5~25								
aly27343.2	Allatostatin-A receptor	GO:0004930,GO:0016021,GO:0008261,GO:0042923,GO:0007218,GO:0005887,GO:0008188,GO:0005886,GO:0007186,GO:0042562	CG2872-PB							PS50262			G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly274.1	Unknown		n/a																				
aly274.10	Bromodomain containing protein 2	GO:0007362,GO:0005737,GO:0006334,GO:0003677,GO:0007476,GO:0007283,GO:0070577,GO:0006357,GO:0045892,GO:0006351,GO:0004672,GO:0003682,GO:0005634,GO:0016568	CG2252-PG				SM00297,SM00297		PF17035,PF00439,PF00439	PS51525,PS50014,PS50014	PR00503,PR00503,PR00503,PR00503	PS00633,PS00633	G3DSA:1.20.920.10,G3DSA:1.20.920.10	SSF47370,SSF47370	516~561,731~758,1163~1205								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly274.11	Metal-response element-binding transcription factor 2	GO:0005737,GO:0035098,GO:0048863,GO:0035064,GO:0000122,GO:0003700,GO:0005634,GO:0061087,GO:0007379,GO:0050832,GO:0061086,GO:0045892,GO:0008270,GO:0005515,GO:0003677,GO:0045944,GO:0022008,GO:0003682,GO:0019827,GO:0016568	CG5109-PA				SM00249,SM00249		PF00628	PS50016		PS01359,PS01359	G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57903,SSF57903	509~529								
aly274.12	Leucine-rich repeat-containing protein 57		CG3040-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00365,SM00365,SM00365		PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly274.13	Putative 1-acyl sn-glycerol-3-phosphate acyltransferase acl-2	GO:0048149,GO:0008654,GO:0016021,GO:0016020,GO:0016024,GO:0003841,GO:0016746,GO:0008152	CG17608-PA				SM00563	TIGR00530	PF01553				G3DSA:3.40.1130.10	SSF69593		00564+2.3.1.51,00561+2.3.1.51	REACT_22258	PWY-7589,PWY-5667,PWY-5981,PWY-7417,PWY-7411,PWY-7587,PWY-6453	UPA00557				
aly274.14	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	GO:0006654,GO:0006644,GO:0005783,GO:0008654,GO:0016021,GO:0016020,GO:0001961,GO:0016024,GO:0003841,GO:0019432,GO:0006112,GO:0044281,GO:0046474,GO:0000502,GO:0044255,GO:0005789,GO:0031325,GO:0001819	CG3812-PA				SM00563		PF01553				G3DSA:3.40.1130.10	SSF69593									
aly274.15	1-acyl-sn-glycerol-3-phosphate acyltransferase beta	GO:0006654,GO:0006644,GO:0008544,GO:0005783,GO:0008654,GO:0016021,GO:0016020,GO:0001961,GO:0016024,GO:0003841,GO:0019432,GO:0044281,GO:0046474,GO:0000502,GO:0044255,GO:0005789,GO:0001819	CG3812-PA				SM00563		PF01553				G3DSA:3.40.1130.10	SSF69593									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly274.16	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	GO:0006654,GO:0006644,GO:0005783,GO:0008654,GO:0016021,GO:0016020,GO:0001961,GO:0016024,GO:0003841,GO:0019432,GO:0006112,GO:0044281,GO:0046474,GO:0000502,GO:0044255,GO:0005789,GO:0031325,GO:0001819	CG3812-PA				SM00563	TIGR00530	PF01553				G3DSA:3.40.1130.10	SSF69593		00564+2.3.1.51,00561+2.3.1.51	REACT_22258	PWY-7589,PWY-5667,PWY-5981,PWY-7417,PWY-7411,PWY-7587,PWY-6453	UPA00557				
aly274.17	Gamma-aminobutyric acid type B receptor subunit 1	GO:0005737,GO:0042734,GO:0038037,GO:0006813,GO:0038039,GO:0016021,GO:0016020,GO:0007214,GO:0006814,GO:0005391,GO:0045211,GO:0005890,GO:0030425,GO:0005887,GO:0004965,GO:0007193,GO:0046982,GO:0007186,GO:0007194,GO:0030054	CG15274-PB						PF01094,PF00003	PS50259	PR01177,PR01177,PR01177,PR01177,PR01177,PR01177,PR01177,PR01177,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176		G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300	SSF53822	897~931							
aly274.18	Unknown		n/a																				
aly274.19	FGFR1 oncogene partner	GO:0006996,GO:0034453,GO:0030335,GO:0006469,GO:0000278,GO:0000086,GO:0005813,GO:0005829,GO:0018108,GO:0008284,GO:0030292,GO:0004713,GO:0005515,GO:0030307,GO:0061099,GO:0048471,GO:0005634,GO:0019901,GO:0042803	n/a							PS50896													
aly274.2	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0055114	CG6142-PA			PIRSF000137			PF05199,PF00732			PS00623	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905,SSF54373		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly274.20	Protein sickie	GO:0007015,GO:0045087,GO:0017111,GO:0005575,GO:0007409,GO:0050829,GO:0005524	CG43720-PI				SM00033,SM00382			PS50021			G3DSA:3.40.50.300,G3DSA:1.10.418.10	SSF52540,SSF47576	1193~1220,1439~1459,1228~1269,1467~1494								
aly274.21	Unknown		n/a																				
aly274.22	Unknown		n/a																				
aly274.23	Unknown		n/a																				
aly274.24	Putative lipoyltransferase 2, mitochondrial	GO:0005737,GO:0009249,GO:0016979,GO:0006464,GO:0016415,GO:0005739,GO:0033819,GO:0009107,GO:0016874	CG9804-PA	MF_00013		PIRSF016262		TIGR00214	PF03099	PS51733		PS01313	G3DSA:3.90.1550.10	SSF55681		00785+2.3.1.181		PWY-6987,PWY-7381	UPA00538				
aly274.25	Cuticlin-1	GO:0007015,GO:0016324,GO:0007160,GO:0003674,GO:0003383,GO:0016476,GO:0060102,GO:0042302	CG17131-PA				SM00473,SM00473,SM00241		PF14295,PF00024,PF00024,PF00100	PS50948,PS50948,PS51034,PS50948			G3DSA:3.50.4.10,G3DSA:3.50.4.10	SSF57414,SSF57414									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly274.26	Odorant receptor 4	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0004984	CG17911-PA						PF02949														
aly274.27	AP-3 complex subunit mu-1	GO:0008021,GO:0006901,GO:0007040,GO:0030131,GO:0030135,GO:0030123,GO:0008565,GO:0016183,GO:0006886,GO:0006887,GO:0008089,GO:0005794,GO:0006727,GO:0030659,GO:0048490,GO:0007269,GO:0008340,GO:0022008,GO:0007220,GO:0006897,GO:0016192,GO:0046907	CG3035-PA			PIRSF005992			PF00928	PS51072	PR00314,PR00314,PR00314	PS00990,PS00991	G3DSA:2.60.40.1170,G3DSA:3.30.450.60	SSF64356,SSF49447									
aly274.28	40S ribosomal protein S5	GO:0006450,GO:0022627,GO:0019083,GO:0006614,GO:0000184,GO:0000228,GO:0005925,GO:0000022,GO:0005737,GO:0044267,GO:0070062,GO:0005730,GO:0016020,GO:0030529,GO:0003735,GO:0010467,GO:0019058,GO:0044822,GO:0007052,GO:0005840,GO:0005829,GO:0003723,GO:0016032,GO:0006415,GO:0006414,GO:0006413,GO:0006412,GO:0003729	CG8922-PD			PIRSF002122		TIGR01028	PF00177			PS00052	G3DSA:1.10.455.10	SSF47973									
aly274.29	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial (Fragment)	GO:0005811,GO:0005739,GO:0003824,GO:0006099,GO:0004776,GO:0005525,GO:0005524,GO:0045244	CG10622-PA			PIRSF001554		TIGR01016	PF08442,PF00549			PS01217	G3DSA:3.30.1490.20,G3DSA:3.30.470.20,G3DSA:3.40.50.261	SSF52210,SSF56059		00640+6.2.1.5,00660+6.2.1.5,00020+6.2.1.5,00720+6.2.1.5	REACT_1046	PWY-5913,PWY-7384,PWY-5392,PWY-6969,PWY-5537,PWY-6728,PWY-5538,PWY-5690	UPA00223				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly274.3	39S ribosomal protein L51, mitochondrial	GO:0003735,GO:0032543,GO:0006412,GO:0005762,GO:0005761	CG13098-PA						PF10244														
aly274.30	Mitochondrial-processing peptidase subunit alpha	GO:0004222,GO:0005615,GO:0005759,GO:0016485,GO:0006508,GO:0046872	CG8728-PA						PF00675,PF05193				G3DSA:3.30.830.10,G3DSA:3.30.830.10	SSF63411,SSF63411									
aly274.31	NADPH:adrenodoxin oxidoreductase, mitochondrial	GO:0005737,GO:0006744,GO:0035073,GO:0042331,GO:0042048,GO:0007552,GO:0007591,GO:0005739,GO:0004324,GO:0015039,GO:0042810,GO:0006694,GO:0007619,GO:0005759,GO:0006707,GO:0008203,GO:0055114,GO:0009055	CG12390-PA			PIRSF000362			PF07992		PR00419,PR00419,PR00419,PR00419		G3DSA:3.40.50.720,G3DSA:3.40.50.720,G3DSA:3.50.50.60	SSF51971,SSF51971									
aly274.32	Anoctamin-5	GO:0005229,GO:0031982,GO:1902476,GO:0016021,GO:0005622,GO:0006821,GO:0005886,GO:0005789	CG6938-PC						PF04547,PF16178														
aly274.33	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	GO:0030488,GO:0031515,GO:0006446,GO:0044822,GO:0046331,GO:0005634,GO:0003743	CG9596-PB						PF04189														
aly274.34	Serine/threonine-protein kinase zyg-8	GO:0005737,GO:0006468,GO:0007017,GO:0007026,GO:0005819,GO:0005813,GO:0008017,GO:0007275,GO:0004674,GO:0040001,GO:0004672,GO:0035556,GO:0005875,GO:0005524	CG17528-PC				SM00537,SM00537,SM00220		PF00069,PF03607,PF03607	PS50309,PS50011,PS50309		PS00108	G3DSA:3.10.20.230,G3DSA:3.10.20.230,G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF89837,SSF56112,SSF89837									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly274.35	Ras-related protein Rab-7a	GO:0032510,GO:0005811,GO:0042147,GO:0008333,GO:0034045,GO:0048102,GO:0033227,GO:0045202,GO:0005774,GO:0044130,GO:0030904,GO:0031982,GO:0090385,GO:0006886,GO:0005770,GO:0090383,GO:1903543,GO:0043025,GO:0022615,GO:0005525,GO:0005794,GO:0048190,GO:0035071,GO:0019076,GO:0003924,GO:0006622,GO:0032482,GO:0045335,GO:0007174,GO:2000785,GO:0008593,GO:0045022,GO:0070062,GO:0016197,GO:0042470,GO:0006897,GO:0016192,GO:0030670,GO:0005764,GO:0045732,GO:0019003,GO:0015031,GO:0048524	CG5915-PC				SM00175,SM00176,SM00174,SM00173	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly274.36	b(0,+)-type amino acid transporter 1	GO:0016021,GO:0042605,GO:0016324,GO:0003333,GO:0016020,GO:0031526,GO:0015804,GO:0005886,GO:0015175,GO:0015184,GO:0015171,GO:0015811	CG9413-PB						PF13520,PF13520														
aly274.37	Parafibromin	GO:0071222,GO:0008285,GO:0048147,GO:0010390,GO:0008587,GO:0008586,GO:0030177,GO:0045880,GO:0016593,GO:0001745,GO:0032968,GO:0007049,GO:2000134,GO:0000122,GO:0005634,GO:0008407,GO:0031648,GO:0001711,GO:0007480,GO:0008134,GO:0050680,GO:0045893,GO:0033523,GO:0043234,GO:0019827,GO:0031442,GO:0016055,GO:0045638,GO:0045944,GO:0006351,GO:0006378,GO:0000993	CG11990-PA						PF16050,PF05179														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly274.38	Unknown		n/a																				
aly274.39	Guanine nucleotide-releasing factor 2	GO:0016203,GO:0005088,GO:0043547,GO:0017034,GO:0032317,GO:0005622,GO:0005575,GO:0032854,GO:0045214,GO:0007265,GO:0043087,GO:0007525	CG42328-PH																				
aly274.4	Zinc finger protein 100	GO:0006351,GO:0003700,GO:0005634,GO:0006355,GO:0000790,GO:0008270,GO:0005515,GO:0003677,GO:0046872,GO:0043035	CG2711-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										
aly274.40	Guanine nucleotide-releasing factor 2	GO:0016203,GO:0005088,GO:0043547,GO:0017034,GO:0032317,GO:0005085,GO:0005622,GO:0005575,GO:0032854,GO:0045214,GO:0007265,GO:0007264,GO:0043087,GO:0007525	CG42328-PH				SM00147,SM00229		PF00617	PS50009,PS50212		PS00720	G3DSA:1.10.840.10,G3DSA:1.20.870.10	SSF48366									
aly274.41	Zinc metalloproteinase nas-7	GO:0004222,GO:0043050,GO:0005576,GO:0008270,GO:0006508,GO:0060465	CG15254-PA				SM00235		PF01400		PR00480,PR00480,PR00480,PR00480,PR00480		G3DSA:3.40.390.10	SSF55486									
aly274.42	Zinc metalloproteinase nas-15	GO:0006508,GO:0022008,GO:0005576,GO:0004222,GO:0008270	CG15255-PA				SM00235		PF01400		PR00480,PR00480,PR00480,PR00480,PR00480		G3DSA:3.40.390.10	SSF55486									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly274.43	E3 ubiquitin-protein ligase LRSAM1	GO:0005737,GO:0004842,GO:0016020,GO:0000164,GO:0017016,GO:0051865,GO:0046579,GO:0030163,GO:0070086,GO:0046755,GO:0045806,GO:0016874,GO:0000209,GO:0008270	CG5407-PA				SM00369,SM00369,SM00369,SM00184		PF13920,PF13855	PS50089			G3DSA:3.30.40.10,G3DSA:3.80.10.10	SSF52058,SSF57850	305~325,501~521,254~274								
aly274.44	Unknown		n/a																				
aly274.5	Surfeit locus protein 6 homolog	GO:0015232,GO:0005730,GO:0042254,GO:0008535,GO:0003676,GO:0022008	CG4510-PA						PF04935						87~107,237~257,49~83								
aly274.6	Protein arginine N-methyltransferase 5	GO:0006479,GO:0032922,GO:0042118,GO:0035243,GO:0048714,GO:0008469,GO:0035246,GO:0008276,GO:0034660,GO:0008168,GO:0007067,GO:0019918,GO:0034709,GO:0005737,GO:0000387,GO:0006355,GO:0006325,GO:0005634,GO:0003714,GO:0005654,GO:0010467,GO:0034969,GO:0043021,GO:0007088,GO:0008283,GO:1903507,GO:0045596,GO:0007315,GO:0001046,GO:0007318,GO:0030719,GO:0097421,GO:0005829,GO:0043985,GO:0018216,GO:0008298,GO:0006351,GO:0046982,GO:0044030,GO:0070372	CG3730-PA			PIRSF015894			PF05185	PS51678			G3DSA:3.40.50.150,G3DSA:3.40.50.150,G3DSA:2.70.160.11	SSF53335									
aly274.7	Ubiqui biosynthesis protein COQ4 homolog, mitochondrial	GO:0005743,GO:0031314,GO:0006744,GO:0003674,GO:0005739	CG32174-PB	MF_03111					PF05019										UPA00232				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly274.8	Unknown		n/a																				
aly274.9	High affinity copper uptake protein 1	GO:0005737,GO:0072719,GO:0005770,GO:0006878,GO:0006825,GO:0016021,GO:0035434,GO:0015088,GO:0006855,GO:0055037,GO:0002027,GO:0015679,GO:0005886,GO:0015677,GO:0005375,GO:0043025,GO:1902861	CG3977-PC						PF04145														
aly27410.1	Unknown	GO:0005575,GO:0008150,GO:0016021,GO:0003674	CG1103-PA																				
aly27473.1	Unknown		n/a																				
aly274886.1	ATP-binding cassette sub-family B member 6, mitochondrial	GO:0043190,GO:0042626,GO:0015886,GO:0015232,GO:0005743,GO:0005215,GO:0016021,GO:0006810,GO:0015086,GO:0005774,GO:0070574,GO:0005741,GO:0005794,GO:0005886,GO:0046686,GO:0071585,GO:0055085,GO:0005524,GO:0005783	CG4225-PA						PF00664	PS50929			G3DSA:1.20.1560.10	SSF90123									
aly274894.1	Probable dimethyladenosine transferase	GO:0000179,GO:0005730,GO:0000154,GO:0005575,GO:0052909,GO:0003723,GO:0022008	CG11837-PA						PF00398	PS51689			G3DSA:3.40.50.150	SSF53335	67~70								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly274937.1	Unknown		n/a						PF13857					SSF48403									
aly274988.1	Unknown		n/a																				
aly274992.1	Unknown	GO:0005615	CG14457-PB						PF06585														
aly2750.1	Low-density lipoprotein receptor (Fragment)	GO:0005794,GO:0034362,GO:0016021,GO:0006897,GO:0004252,GO:0045087,GO:0005770,GO:0005769,GO:0006869,GO:0005905,GO:0005509,GO:0005515,GO:0005886,GO:0005764,GO:0006508,GO:0009986,GO:0008203	CG31217-PA				SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00020		PF00057,PF00057,PF00057,PF00057,PF00057,PF00089	PS50923,PS50068,PS50923,PS50068,PS50068,PS50068,PS50068,PS50068,PS50240	PR00261,PR00261,PR00261,PR00261,PR00261,PR00261	PS01209,PS01209,PS01209,PS01209,PS00134,PS01209	G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.10.70.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10	SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF50494,SSF57424,SSF57424,SSF57535										
aly2750.2	Kinesin-like protein KIF3A	GO:0005737,GO:0042384,GO:0035058,GO:0030951,GO:0007605,GO:0007411,GO:0008017,GO:0007018,GO:0008089,GO:0048812,GO:0003777,GO:0005874,GO:0005929,GO:0007288,GO:0005871,GO:0072372,GO:0005524,GO:0007608	CG10642-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10	SSF52540	299~374,231~268,273~297,162~189								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2750.3	Coiled-coil domain-containing protein 186	GO:0004871	CG4925-PA												685~705,748~800,609~681,407~469,568~595,526~560,1006~1033,819~846								
aly2750.4	Protein VPRBP	GO:0005737,GO:0000122,GO:1990245,GO:1990244,GO:0035212,GO:0033151,GO:0005634,GO:0030183,GO:0005575,GO:0016567,GO:0003674,GO:0006351,GO:0016032,GO:0005730,GO:0005524	CG10080-PA										G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371										
aly2750.5	Ubiquitin-associated domain-containing protein 1	GO:0005737,GO:0016567,GO:0005515,GO:0004221	CG11025-PC				SM00165			PS50030			G3DSA:1.10.8.10	SSF46934										
aly2750.6	Unknown	GO:0000413,GO:0006457,GO:0003755	n/a						PF00160				G3DSA:2.40.100.10	SSF50891										
aly2750.7	Unknown		n/a																				
aly275023.1	Unknown	GO:0005737,GO:0045177,GO:0007426,GO:0007476,GO:0008586,GO:0019899,GO:0008595,GO:0005913,GO:0007165,GO:0005515,GO:0005886,GO:0008293,GO:0007265,GO:0001751	CG6556-PA												80~89								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275041.1	Unknown		n/a																				
aly2751.1	Metabotropic glutamate receptor	GO:0030425,GO:0008066,GO:0001642,GO:0001641,GO:0016595,GO:0004930,GO:0016021,GO:0007216,GO:0007186,GO:0038038,GO:0007528,GO:0005887,GO:0005886,GO:0008343,GO:0015485,GO:0042734,GO:0007200,GO:0072553,GO:0045121,GO:0051966,GO:0017085,GO:0007196	CG30361-PG						PF07562,PF01094,PF00003	PS50259	PR00593,PR00593,PR00593,PR00593,PR00593,PR00248,PR00248,PR00248,PR00248,PR00248,PR00248,PR00248,PR00248,PR00248,PR00248,PR00248,PR00248,PR00248	PS00981	G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300	SSF53822	585~605		REACT_14797							
aly275103.1	Unknown		n/a																				
aly275119.1	Unknown	GO:0046331	CG5953-PA				SM00595,SM00717		PF10545	PS51029,PS50090			G3DSA:1.10.10.60										
aly275123.1	Splicing factor 3A subunit 3	GO:0051726,GO:0071011,GO:0005634,GO:0009566,GO:0000398,GO:0051533,GO:0007052,GO:0008270,GO:0003676,GO:0005686,GO:0007067,GO:0071013,GO:0005681,GO:0003723	CG2925-PA						PF11931	PS50171													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275128.1	Oocyte zinc finger protein XlCOF22	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG30443-PA				SM00355,SM00355,SM00355,SM00355		PF13912,PF13912	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly275148.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473	201~221								
aly275151.1	Unknown		n/a																				
aly275183.1	Unknown		n/a																				
aly275184.1	2-phosphoxylose phosphatase 1	GO:0005794,GO:0016791,GO:0016311,GO:0050650,GO:0000139,GO:0003993,GO:0016021,GO:0006024,GO:0010909	CG15385-PA						PF00328			PS00616	G3DSA:3.40.50.1240,G3DSA:3.40.50.1240,G3DSA:3.40.50.1240	SSF53254,SSF53254,SSF53254	643~643								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275184.2	X-ray repair cross-complementing protein 5	GO:0008022,GO:0000784,GO:0003677,GO:0043564,GO:0006303,GO:0006302,GO:0005730,GO:0005634,GO:0016020,GO:0050769,GO:0005654,GO:0042162,GO:0003691,GO:0044822,GO:0005524,GO:0070419,GO:0005737,GO:0008283,GO:0004003,GO:0017116,GO:0017117,GO:0045892,GO:0005886,GO:0060218,GO:0051575,GO:0006310,GO:0044212,GO:0031625,GO:0000723,GO:0006351,GO:0003684	CG18801-PA				SM00559		PF08785,PF03731,PF02735				G3DSA:1.25.40.240,G3DSA:1.10.1600.10,G3DSA:2.40.290.10,G3DSA:3.40.50.410	SSF53300,SSF100939,SSF101420			REACT_216,REACT_6185						
aly275184.3	Unknown		n/a																				
aly275184.4	Unknown		CG15125-PB																				
aly275184.5	Tudor and KH domain-containing protein	GO:0043186,GO:0043046,GO:0030154,GO:0009566,GO:0071546,GO:0005739,GO:0007283,GO:0010467,GO:0003723,GO:0005515,GO:0034587,GO:0071547,GO:0007140,GO:0031047	CG7082-PA				SM00322,SM00322,SM00333		PF00567,PF00013,PF00013	PS50084,PS50084,PS50304			G3DSA:2.30.30.140,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10	SSF54791,SSF54791,SSF63748									
aly2752.1	Unknown		n/a							PS50081			G3DSA:3.30.60.20	SSF57889									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2752.10	Unknown		n/a																				
aly2752.2	Nuclear receptor coactivator 2	GO:0048675,GO:0032922,GO:0015721,GO:0003713,GO:0010906,GO:0007165,GO:0004871,GO:0008230,GO:0007298,GO:0044255,GO:0005737,GO:0000122,GO:0006325,GO:0005634,GO:0004402,GO:0005654,GO:0035258,GO:0035257,GO:0060250,GO:0030375,GO:0030374,GO:0032870,GO:0045475,GO:0008206,GO:0007264,GO:0016922,GO:0006355,GO:0045944,GO:0006351,GO:0046983,GO:0003682,GO:0044281	CG13109-PG				SM00353		PF14598	PS50888			G3DSA:3.30.450.20,G3DSA:3.30.450.20	SSF47459	100~120									
aly2752.3	Pyruvate kinase	GO:0030955,GO:0000287,GO:0043186,GO:0016310,GO:0005829,GO:0005811,GO:0007525,GO:0007520,GO:0004743,GO:0006096,GO:0005524	CG7070-PA						PF00224,PF02887		PR01050,PR01050		G3DSA:2.40.33.10,G3DSA:3.40.1380.20,G3DSA:3.20.20.60,G3DSA:3.20.20.60	SSF51621,SSF51621,SSF50800,SSF52935		00230+2.7.1.40,00010+2.7.1.40,00620+2.7.1.40	REACT_474	PWY-1042,PWY-2221,PWY-6901,PWY-7218,PWY-7383,PWY-6886,PWY-5723,PWY-6142,PWY-5484,PWY-7003	UPA00109				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2752.4	Serine-protein kinase ATM	GO:0071044,GO:0007507,GO:0071480,GO:0033151,GO:0016310,GO:0034605,GO:0030889,GO:0008340,GO:0018105,GO:0005488,GO:1990164,GO:0003677,GO:0042159,GO:0046777,GO:0000723,GO:0043065,GO:0006348,GO:0010212,GO:0006302,GO:0043525,GO:0000724,GO:0016023,GO:0000706,GO:0005654,GO:0004674,GO:0004677,GO:0004672,GO:0032403,GO:0005524,GO:0048599,GO:0006468,GO:0007165,GO:0047485,GO:0006281,GO:0016303,GO:0035174,GO:0035173,GO:0007050,GO:0006975,GO:0051402,GO:0006977,GO:0036092,GO:0008630,GO:0031572,GO:0043517,GO:0001756,GO:0007420,GO:0001666,GO:0006974,GO:0072434,GO:0051276,GO:0000075,GO:1900034,GO:0090399,GO:0007131,GO:0030717,GO:0016233,GO:0007094,GO:0007095,GO:0046983,GO:0002331,GO:0005819,GO:0045494,GO:0007093	CG6535-PB				SM00146		PF11640,PF00454	PS50290,PS51189		PS00915,PS00916	G3DSA:1.10.1070.11,G3DSA:1.10.1070.11,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:3.30.1010.10	SSF48371,SSF48371,SSF56112,SSF56112										
aly2752.5	B9 domain-containing protein 2	GO:0005737,GO:0036064,GO:0036038,GO:0042384,GO:0005813,GO:0005634,GO:0043015	CG42730-PA						PF07162	PS51381													
aly2752.6	Tectonic-1	GO:0005737,GO:0035869,GO:0008589,GO:0001701,GO:0005615,GO:0060271,GO:0021537,GO:0005856,GO:0036038,GO:0021523,GO:0003674,GO:0021904,GO:0001841,GO:0016020,GO:0021956	CG42731-PA						PF07773,PF07773														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2752.7	Cullin-3	GO:0048208,GO:0007291,GO:0031208,GO:0001745,GO:0000209,GO:0005737,GO:0006888,GO:0006513,GO:0043161,GO:0005634,GO:0007476,GO:0042787,GO:0032467,GO:0006919,GO:0007283,GO:0045187,GO:0030162,GO:0030431,GO:0007409,GO:0035324,GO:0031463,GO:0004842,GO:0031625,GO:0007423,GO:0040016,GO:0007229,GO:0000152,GO:0000139,GO:0016567,GO:0048813,GO:0006511,GO:0019005,GO:0017145,GO:0045475	CG42616-PF				SM00884,SM00182		PF00888,PF10557	PS50069		PS01256	G3DSA:1.10.10.10,G3DSA:1.20.1310.10,G3DSA:1.20.1310.10,G3DSA:1.10.10.10,G3DSA:4.10.1030.10,G3DSA:1.20.1310.10,G3DSA:1.20.1310.10	SSF46785,SSF74788,SSF75632					UPA00143				
aly2752.8	Bcl-2-related ovarian killer protein	GO:0016239,GO:0005783,GO:0035234,GO:0016021,GO:0006915,GO:0000139,GO:0012501,GO:0043066,GO:0009267,GO:0005789,GO:0042981,GO:0043068	CG8238-PA				SM00337		PF00452	PS50062		PS01258	G3DSA:1.10.437.10	SSF56854									
aly2752.9	Unknown		n/a																				
aly275206.1	Unknown		n/a																				
aly275206.10	Mitochondrial genome maintenance exonuclease 1	GO:0006264,GO:0000002,GO:0043504,GO:0008297,GO:0005739	n/a	MF_03030					PF12705														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275206.11	Connectin	GO:0016200,GO:0007156,GO:0009986,GO:0044295,GO:0031594,GO:0005515,GO:0005886,GO:0007155,GO:0007413,GO:0031225	CG7503-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00365,SM00365,SM00365,SM00365		PF13855,PF13855,PF00560	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly275206.2	Unknown		n/a						PF15868														
aly275206.3	Plexin A3	GO:0048675,GO:0005886,GO:0060272,GO:0016021,GO:0016020,GO:0048696,GO:0016199,GO:0005622,GO:0071889,GO:0008046,GO:0007165,GO:0005515,GO:0008045,GO:0007411,GO:2000305,GO:0048755,GO:0017154,GO:0008201,GO:0042803	CG11081-PA										G3DSA:3.30.1680.10	SSF103575									
aly275206.4	Unknown		n/a						PF15430														
aly275206.5	Probable 4-coumarate--CoA ligase 3	GO:0016207,GO:0009062,GO:0046627,GO:0003824,GO:0019433,GO:0004467,GO:0071616,GO:0008152,GO:0009698,GO:0005524	CG9009-PA						PF00501,PF13193			PS00455	G3DSA:3.30.300.30,G3DSA:3.40.50.980,G3DSA:3.40.50.980,G3DSA:2.30.38.10	SSF56801									
aly275206.6	Probable 4-coumarate--CoA ligase 4	GO:0016207,GO:0046627,GO:0009062,GO:0019433,GO:0004467,GO:0071616,GO:0009698,GO:0005524	CG9009-PA						PF13193,PF00501,PF00501			PS00455	G3DSA:3.40.50.980,G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.30.300.30	SSF56801									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275206.7	4-coumarate--CoA ligase 2	GO:0016207,GO:0046627,GO:0009062,GO:0019433,GO:0004467,GO:0071616,GO:0009698,GO:0005524	CG9009-PA						PF13193,PF00501			PS00455	G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:3.30.300.30,G3DSA:3.40.50.980	SSF56801										
aly275206.8	4-coumarate--CoA ligase-like 7	GO:0031408,GO:0009695,GO:0004321,GO:0005777,GO:0046627,GO:0009062,GO:0019433,GO:0004467,GO:0071616,GO:0016874,GO:0005524	CG9009-PA						PF00501,PF13193			PS00455	G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.30.300.30	SSF56801										
aly275206.9	Probable 4-coumarate--CoA ligase 3	GO:0016207,GO:0046627,GO:0009062,GO:0019433,GO:0004467,GO:0071616,GO:0009698,GO:0005524	CG9009-PA						PF00501,PF13193			PS00455	G3DSA:3.40.50.980,G3DSA:3.30.300.30,G3DSA:2.30.38.10,G3DSA:3.40.50.980	SSF56801										
aly275207.1	Putative uncharacterized transposon-derived protein F52C9.6		n/a																				
aly275208.1	Transcription factor egl-13	GO:0040025,GO:0003700,GO:0005634,GO:0006355,GO:0045823,GO:0006351,GO:0003677,GO:0045026,GO:0009653,GO:0001708	CG11153-PB				SM00398		PF00505	PS50118			G3DSA:1.10.30.10	SSF47095	233~253,200~220								
aly275208.2	Hermansky-Pudlak syndrome 5 protein homolog	GO:0005737,GO:0031084,GO:0031409,GO:0050896,GO:0007601,GO:0048072,GO:0006622,GO:0006726,GO:0060967,GO:0003674,GO:0006727,GO:0005515	CG9770-PA							PS50089			G3DSA:3.30.40.10,G3DSA:2.130.10.10	SSF50978,SSF57850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275208.3	Hemicentin-1	GO:0016319,GO:0005938,GO:0005604,GO:0070062,GO:0007601,GO:0050896,GO:0008406,GO:0008038,GO:0007419,GO:0008046,GO:0048036,GO:0005886,GO:0007411,GO:0030424,GO:0030054,GO:0005509	CG5423-PA				SM00408,SM00408,SM00408,SM00409,SM00409,SM00409		PF07679,PF07679	PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly275209.1	Unknown	GO:0005737,GO:0016319,GO:0051018,GO:0016021,GO:0007528,GO:0042675,GO:0008104,GO:0043025,GO:0007614,GO:0008355	CG44835-PQ																				
aly275209.10	Transmembrane protein 131 homolog	GO:0005575,GO:0003674,GO:0016021,GO:0008150,GO:0012505	CG8370-PA						PF12371				G3DSA:2.60.40.360		374~394								
aly275209.11	Thioredoxin-like protein 4A	GO:0008380,GO:0030532,GO:0071011,GO:0000398,GO:0005682,GO:0007052,GO:0005681,GO:0022008,GO:0007067,GO:0051301,GO:0006397	CG3058-PA			PIRSF017199			PF02966				G3DSA:3.40.30.10	SSF52833									
aly275209.12	Lutropin-choriogonadotropic hormone receptor	GO:0004930,GO:0005887,GO:0007564,GO:0016500,GO:0016021,GO:0008188,GO:0043950,GO:0007218,GO:0001837,GO:0005515,GO:0005886,GO:0004964,GO:0042700,GO:0007186	CG8930-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF13855,PF00001	PS51450,PS51450,PS51450,PS51450,PS51450,PS50262,PS51450,PS51450,PS51450,PS51450	PR00373,PR00373,PR00373,PR00373,PR00373,PR00373,PR00373,PR00373,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:1.20.1070.10	SSF52058,SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275209.13	Leucine-rich repeat-containing G-protein coupled receptor 4	GO:0032922,GO:0048565,GO:0005887,GO:0090263,GO:0072282,GO:0008188,GO:0030282,GO:0001649,GO:2001013,GO:0004930,GO:0072224,GO:0016021,GO:0072202,GO:0007186,GO:0045087,GO:0034122,GO:0007218,GO:0090190,GO:0007283,GO:0045892,GO:0045893,GO:0061290,GO:0005886,GO:0036335,GO:0050710,GO:0007564,GO:0030539,GO:0001837,GO:0004888,GO:0046849,GO:0016500,GO:0001942	CG8930-PA						PF13855	PS51257			G3DSA:3.80.10.10	SSF52058										
aly275209.14	Unknown		n/a																				
aly275209.2	Septin-2	GO:0000910,GO:0031105,GO:0005819,GO:0005940,GO:0008152,GO:0007067,GO:0045172,GO:0007444,GO:0003924,GO:0007349,GO:0000281,GO:0051726,GO:0005515,GO:0007295,GO:0006184,GO:0022008,GO:0042803,GO:0005875,GO:0005525	CG4173-PA			PIRSF006698			PF00735	PS51719			G3DSA:3.40.50.300	SSF52540	344~403,322~342									
aly275209.3	Growth arrest-specific protein 2	GO:0005737,GO:0005881,GO:0016020,GO:0015629,GO:0030713,GO:0006915,GO:0030707,GO:0045746,GO:0007050,GO:0005856,GO:0008360	CG3973-PA				SM00033,SM00243		PF02187,PF00307	PS51460,PS50021			G3DSA:3.30.920.20,G3DSA:1.10.418.10	SSF47576,SSF143575										
aly275209.4	Eukaryotic translation initiation factor 2D	GO:0005737,GO:0022627,GO:0005634,GO:0032790,GO:0005654,GO:0002192,GO:0001731,GO:0006413,GO:0003743	CG31426-PA						PF01253	PS50296			G3DSA:3.30.780.10	SSF55159	226~237									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275209.5	Probable serine/threonine-protein kinase nek2	GO:0005737,GO:0006468,GO:0007017,GO:0005813,GO:0005634,GO:0004702,GO:0030496,GO:0004674,GO:0045335,GO:0007098,GO:0004672,GO:0007059,GO:0007067,GO:0007088,GO:0005524	CG17256-PA				SM00220		PF00069	PS50011			G3DSA:3.30.200.20	SSF56112									
aly275209.6	Kinesin-like protein Klp68D	GO:0005737,GO:0007608,GO:0030951,GO:0008017,GO:0007018,GO:0008089,GO:0008152,GO:0005875,GO:0005524,GO:0016887,GO:0005871,GO:0005873,GO:0005874,GO:0003774,GO:0003777	CG7293-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10	SSF52540,SSF52540	379~399,434~454,532~559								
aly275209.7	Down syndrome critical region protein 3 homolog	GO:0008565,GO:0006886,GO:0005634	CG4074-PA						PF03643					SSF81296									
aly275209.8	Unknown		n/a																				
aly275209.9	Protein cereblon homolog	GO:0004176,GO:0006508	CG3925-PA				SM00464		PF02190					SSF88697,SSF88697									
aly275210.1	Probable G-protein coupled receptor 158	GO:0004930,GO:0007186,GO:0016021,GO:0005886	CG43795-PA						PF00003	PS50259	PR00248,PR00248,PR00248				696~716		REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275210.2	General transcription factor II-I repeat domain-containing protein 2	GO:0006355,GO:0005634,GO:0006351,GO:0003677	n/a						PF14291														
aly275210.3	Unknown		n/a																				
aly275211.1	Unknown	GO:0005214,GO:0040003,GO:0005578	CG14534-PA				SM00690		PF03103														
aly275211.10	Tyrosine-protein kinase Abl	GO:0019897,GO:0021785,GO:0007169,GO:0005911,GO:0030154,GO:0018108,GO:0030424,GO:0008064,GO:0007419,GO:0007303,GO:0001764,GO:0016199,GO:0003382,GO:0008045,GO:0005927,GO:0042981,GO:0032880,GO:0005737,GO:0002009,GO:0038083,GO:0046827,GO:0042127,GO:0045179,GO:0004715,GO:0004713,GO:0007417,GO:0005524,GO:0048749,GO:0006468,GO:0072499,GO:0045087,GO:0008360,GO:0010977,GO:0005912,GO:0007409,GO:0007268,GO:0007611,GO:0031234,GO:0007370,GO:0010592,GO:0005829,GO:0031647,GO:0007411,GO:0007391,GO:0003402,GO:0048813,GO:0045886,GO:0005515,GO:0005102,GO:0005938	CG4032-PF										G3DSA:2.30.30.40										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275211.11	Unknown		n/a																				
aly275211.12	Tyrosine-protein kinase Abl	GO:0019897,GO:0021785,GO:0007169,GO:0005911,GO:0030154,GO:0018108,GO:0030424,GO:0008064,GO:0007419,GO:0007303,GO:0001764,GO:0016199,GO:0003382,GO:0008045,GO:0005927,GO:0042981,GO:0032880,GO:0005737,GO:0002009,GO:0038083,GO:0046827,GO:0042127,GO:0045179,GO:0004715,GO:0004713,GO:0007417,GO:0005524,GO:0048749,GO:0006468,GO:0072499,GO:0045087,GO:0008360,GO:0010977,GO:0005912,GO:0007409,GO:0007268,GO:0007611,GO:0031234,GO:0007370,GO:0010592,GO:0005829,GO:0031647,GO:0007411,GO:0007391,GO:0003402,GO:0048813,GO:0045886,GO:0005515,GO:0005102,GO:0005938	CG4032-PF																				
aly275211.13	Alpha-tubulin N-acetyltransferase 1	GO:0005737,GO:0048666,GO:0070507,GO:0048149,GO:0071929,GO:0019799,GO:0030424,GO:0005575,GO:0005819,GO:0003674,GO:0005905,GO:0005925,GO:0005874	CG3967-PC	MF_03130					PF05301	PS51730			G3DSA:3.40.630.30,G3DSA:3.40.630.30										
aly275211.14	Adenylate cyclase type 5	GO:0046872,GO:0016021,GO:0045121,GO:0016849,GO:0004016,GO:0072372,GO:0005886,GO:0035556,GO:0009190,GO:0005768,GO:0006171,GO:0005524,GO:0008294	CG43373-PC				SM00044,SM00044		PF16214,PF06327,PF00211,PF00211	PS50125,PS50125		PS00452	G3DSA:3.30.70.1230,G3DSA:3.30.70.1230	SSF55073,SSF55073	676~696,363~383	00230+4.6.1.1	REACT_14797,REACT_15295,REACT_11061,REACT_1505						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275211.15	Unknown		n/a																				
aly275211.16	Unknown	GO:0035556,GO:0009190,GO:0016021,GO:0004016	CG43373-PC																				
aly275211.2	Frequenin-1	GO:0031284,GO:0008021,GO:0016192,GO:0016020,GO:0005623,GO:0007528,GO:0046928,GO:0005509,GO:0007269,GO:0007268,GO:0008048	CG5907-PA				SM00054,SM00054,SM00054		PF00036,PF13499	PS50222,PS50222,PS50222	PR00450,PR00450,PR00450,PR00450,PR00450,PR00450	PS00018,PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473										
aly275211.3	[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1, mitochondrial	GO:0005737,GO:0004741,GO:0046872,GO:0006470,GO:0005634,GO:0004722,GO:0004721,GO:0003824,GO:0005739,GO:0035970,GO:0005759,GO:0006090	CG12151-PA				SM00332		PF00481	PS51746		PS01032	G3DSA:3.60.40.10,G3DSA:3.60.40.10	SSF81606,SSF81606,SSF81606										
aly275211.4	Vesicle-associated membrane protein/synaptobrevin-binding protein	GO:0043005,GO:0008021,GO:0005811,GO:0045202,GO:0005615,GO:0005789,GO:0016021,GO:0016082,GO:0008088,GO:0005198,GO:0007528,GO:0070972,GO:0046488,GO:0060074,GO:0007269,GO:0005886,GO:0050829,GO:0031122,GO:0030054,GO:0005783	CG5014-PB			PIRSF019693			PF00635	PS50202			G3DSA:2.60.40.360	SSF49354	194~228		REACT_22258						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275211.5	BTB/POZ domain-containing protein 8	GO:0005654,GO:0005515	CG13917-PA				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695									
aly275211.6	MAGUK p55 subfamily member 7	GO:0008582,GO:0016020,GO:0004385,GO:0005923,GO:0048812,GO:0005912,GO:0005886,GO:0071212	CG30021-PA				SM00326,SM00228,SM00569,SM00569,SM00072		PF07653,PF00595,PF00625,PF02828,PF02828	PS50002,PS51022,PS50052,PS50106,PS51022		PS00856	G3DSA:3.30.63.10,G3DSA:2.30.30.40,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:2.30.42.10	SSF50156,SSF101288,SSF52540,SSF50044		00230+2.7.4.8		PWY-7221					
aly275211.7	Unknown		n/a																				
aly275211.8	Unknown		n/a																				
aly275211.9	Anion exchange protein 2	GO:0015701,GO:0015301,GO:1902476,GO:0016021,GO:0016020,GO:0016323,GO:0051453,GO:0006820,GO:0006821,GO:0005887,GO:0005452,GO:0005925,GO:0015108	CG8177-PG					TIGR00834	PF00955,PF07565		PR01231,PR01231,PR01231,PR01231,PR01231,PR01231,PR01231,PR01231	PS00219	G3DSA:3.40.1100.10,G3DSA:3.40.1100.10,G3DSA:1.10.287.570	SSF55804,SSF55804	450~470		REACT_15518						
aly275215.1	Unknown		CG12811-PA						PF16033														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275215.10	NADPH-dependent D-xylose reductase II,III	GO:0008106,GO:0042843,GO:0035220,GO:0022416,GO:0055114,GO:0016491	CG2767-PA			PIRSF000097			PF00248		PR00069,PR00069,PR00069,PR00069	PS00063,PS00798	G3DSA:3.20.20.100	SSF51430									
aly275215.11	Elongation of very long chain fatty acids protein 4	GO:0008020,GO:0009922,GO:0009584,GO:0005783,GO:0016021,GO:0030497,GO:0005575,GO:0019432,GO:0016740,GO:0030176,GO:0035338,GO:0044281,GO:0044255,GO:0042761,GO:0019367,GO:0006633	CG5278-PA						PF01151			PS01188				00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598						
aly275215.12	HSPB1-associated protein 1	GO:0005575,GO:0008150,GO:0003674,GO:0005737	CG43320-PA				SM00558		PF13621	PS51184			G3DSA:2.60.120.650	SSF51197									
aly275215.13	Single-strand selective monofunctional uracil DNA glycosylase	GO:0006284,GO:0000702,GO:0043231,GO:0005730,GO:0006281,GO:0019104,GO:0003697,GO:0005654,GO:0004844,GO:0017065	CG5285-PA						PF03167				G3DSA:3.40.470.10	SSF52141									
aly275215.14	tRNA-specific adenosine deaminase 2	GO:0002100,GO:0004131,GO:0008270,GO:0008251	CG5292-PA						PF00383	PS51747			G3DSA:3.40.140.10	SSF53927									
aly275215.15	Protein HEXIM1	GO:0005737,GO:0007507,GO:0000122,GO:0005634,GO:0097322,GO:0005654,GO:0004861,GO:0045892,GO:0045736,GO:1901798,GO:0017069,GO:0006351	CG3508-PB						PF15313		PR02094,PR02094,PR02094				161~181,252~272									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275215.16	Dynein beta chain, ciliary	GO:0005737,GO:0042623,GO:0007605,GO:0007018,GO:0005858,GO:0005875,GO:0030030,GO:0005524,GO:0016887,GO:0031514,GO:0030286,GO:0005874,GO:0003774,GO:0003777	CG3723-PC						PF08385						328~348,350~419								
aly275215.17	Unknown		n/a																				
aly275215.2	Ankyrin repeat, PH and SEC7 domain containing protein secG	GO:0005764,GO:0031589,GO:0006935,GO:0005829,GO:0030036,GO:0005086,GO:0031154,GO:0043327,GO:0005515	CG42534-PC				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796,PF12796	PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50297,PS50088,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403									
aly275215.3	Dynein beta chain, ciliary	GO:0005737,GO:0042623,GO:0007605,GO:0007018,GO:0005858,GO:0005875,GO:0030030,GO:0005524,GO:0016887,GO:0031514,GO:0030286,GO:0005874,GO:0003774,GO:0003777	CG3723-PC						PF08385,PF12775,PF12777,PF07728,PF12781,PF12780,PF12774,PF08393,PF03028,PF03028				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540,SSF52540	2847~2888,1136~1156,1290~1310,136~156,889~909,614~634,3834~3834								
aly275215.4	DNA replication licensing factor Mcm5	GO:0003682,GO:0007126,GO:0042555,GO:0003688,GO:0000712,GO:0032508,GO:0006270,GO:0030261,GO:0042023,GO:0005656,GO:0006267,GO:0006260,GO:0003677,GO:0003678,GO:0043138,GO:0005634,GO:0005524	CG4082-PA				SM00350		PF14551,PF00493	PS50051	PR01657,PR01657,PR01657,PR01657,PR01657,PR01661,PR01661,PR01661,PR01661	PS00847	G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:3.40.50.300,G3DSA:3.30.1640.10	SSF50249,SSF52540	314~319		REACT_152,REACT_383,REACT_1538						
aly275215.5	Alcohol dehydrogenase [NADP(+)]	GO:0008106,GO:0022416,GO:0035220,GO:0055114,GO:0016491	CG2767-PA			PIRSF000097			PF00248		PR00069,PR00069,PR00069,PR00069,PR00069	PS00798,PS00062,PS00063	G3DSA:3.20.20.100	SSF51430									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275215.6	N-alpha-acetyltransferase 40	GO:0006909,GO:0008080	CG7593-PA												4~24								
aly275215.7	UDP-glucuronosyltransferase 2B19	GO:0015020,GO:0016021,GO:0002121,GO:0008152,GO:0005789	CG17323-PA						PF00201				G3DSA:3.40.50.2000	SSF53756									
aly275215.8	N-alpha-acetyltransferase 40	GO:0006909,GO:0008080	CG7593-PA						PF00583	PS51186			G3DSA:3.40.630.30	SSF55729									
aly275215.9	Homeobox protein Nkx-6.3	GO:0043565,GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003677	CG15696-PA				SM00389		PF00046	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689									
aly275216.1	Phosphoenolpyruvate carboxykinase [GTP]	GO:0004613,GO:0046872,GO:0006094,GO:0005739,GO:0005525	CG17725-PA	MF_00452		PIRSF001348			PF00821			PS00505	G3DSA:3.90.228.20,G3DSA:3.90.228.20,G3DSA:3.40.449.10	SSF68923,SSF53795	625~634	00620+4.1.1.32,00010+4.1.1.32,00020+4.1.1.32	REACT_474	PWY-7383	UPA00138				
aly275216.2	Unknown	GO:0005179,GO:0005576	n/a									PS00256											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275216.3	Actin-binding protein anillin	GO:0008104,GO:0017022,GO:0000281,GO:0007279,GO:0007009,GO:0070938,GO:0007067,GO:0008356,GO:0045035,GO:0005737,GO:0045172,GO:0005634,GO:0007349,GO:0003779,GO:0043063,GO:0032465,GO:0048477,GO:0051297,GO:0031106,GO:0008017,GO:0032154,GO:0051015,GO:0035323,GO:0022008,GO:0000915,GO:0000910,GO:0007112,GO:0005826,GO:0007423,GO:0032189,GO:0051533,GO:0005515,GO:0030726	CG2092-PB						PF00169,PF08174				G3DSA:2.30.29.30	SSF50729	552~579								
aly275216.4	Unknown	GO:0005576,GO:0008150,GO:0030414	CG30197-PA							PS51390			G3DSA:4.10.75.10	SSF57256									
aly275216.5	Actin-binding protein anillin	GO:0008104,GO:0017022,GO:0000281,GO:0007279,GO:0007009,GO:0070938,GO:0007067,GO:0008356,GO:0045035,GO:0005737,GO:0045172,GO:0005634,GO:0007349,GO:0003779,GO:0043063,GO:0032465,GO:0048477,GO:0051297,GO:0031106,GO:0008017,GO:0032154,GO:0051015,GO:0035323,GO:0022008,GO:0000915,GO:0000910,GO:0007112,GO:0005826,GO:0007423,GO:0032189,GO:0051533,GO:0005515,GO:0030726	CG2092-PB						PF16018														
aly275216.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275218.1	Unknown		n/a																				
aly275222.1	Unknown		n/a																				
aly275223.1	Probable arginine--tRNA ligase, mitochondrial	GO:0006420,GO:0005759,GO:0004814,GO:0005739,GO:0005524	CG10092-PA						PF00750				G3DSA:3.40.50.620	SSF52374		00970+6.1.1.19	REACT_71						
aly275233.1	Histone-lysine N-methyltransferase eggless	GO:0018024,GO:0035220,GO:0002165,GO:0046974,GO:0008270,GO:0051567,GO:0005737,GO:0005634,GO:0040029,GO:0016571,GO:0045814,GO:0048477,GO:0010385,GO:0045892,GO:0044026,GO:0048132,GO:0051038,GO:0060968,GO:0005700,GO:0010369,GO:0006351,GO:0005515	CG30426-PA																				
aly275305.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275305.2	Unknown		n/a																				
aly275305.3	Unknown		n/a																				
aly275312.1	Hemicentin-2	GO:0035206,GO:0007498,GO:0030017,GO:0005875,GO:0030054,GO:0007062,GO:0007517,GO:0007519,GO:0003779,GO:0030018,GO:0005509,GO:0016203,GO:0008307,GO:0005604,GO:0045214,GO:0005938,GO:0000794,GO:0007520,GO:0040011,GO:0004687,GO:0050896,GO:0005576,GO:0005515,GO:0007076	CG1915-PP				SM00409,SM00409		PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726										
aly27553.1	Unknown	GO:0000723,GO:0003678,GO:0006281	n/a						PF05970														
aly27556.1	Unknown		n/a						PF13843														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly275771.1	DNA ligase 1	GO:0005737,GO:0006310,GO:0005739,GO:0071897,GO:0006281,GO:0006273,GO:0005634,GO:0051103,GO:1903469,GO:0051301,GO:0006266,GO:0043596,GO:0006260,GO:0003910,GO:1903461,GO:0003677,GO:0005524	CG5602-PA						PF04679	PS50160			G3DSA:2.40.50.140	SSF50249			REACT_216						
aly2758.1	NADH dehydrogenase [ubiqui] 1 alpha subcomplex assembly factor 5	GO:0005575,GO:0008168,GO:0031314,GO:0008152,GO:0032981	CG8067-PA						PF13489				G3DSA:3.40.50.150	SSF53335									
aly2758.2	Small integral membrane protein 12	GO:0016021	CG34228-PA						PF15990														
aly2758.3	Zinc finger protein 155	GO:0003700,GO:0005634,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG11902-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly2758.4	Unknown		n/a												64~84								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2758.5	Serine/threonine-protein kinase BRSK1	GO:0008021,GO:0018105,GO:0007269,GO:0000086,GO:0009411,GO:0030010,GO:0035556,GO:0030054,GO:0005737,GO:0031572,GO:0006487,GO:0005813,GO:0005634,GO:0000287,GO:0005654,GO:0004674,GO:0004672,GO:0005524,GO:0006468,GO:0051298,GO:0030182,GO:0006974,GO:0007409,GO:0007528,GO:0048812,GO:0050321,GO:0043015,GO:0019901	CG6114-PA						PF00069	PS50011		PS00107	G3DSA:3.30.200.20	SSF56112										
aly276.1	Unknown		n/a						PF12937	PS50181			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047,SSF81383	171~191								
aly276.2	Alpha-ketoglutarate-dependent dioxygenase alkB homolog 7, mitochondrial	GO:0006631,GO:0051213,GO:0006974,GO:1902445,GO:0010883,GO:0005759,GO:0046872	CG14130-PA										G3DSA:2.60.120.590	SSF51197									
aly276.3	Zinc finger protein 62	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG6654-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13894,PF12874	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60	SSF57667,SSF57667									
aly276.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276042.1	Coagulation factor XI	GO:0004252,GO:0007596,GO:0008201,GO:0005576,GO:0006508	CG4927-PC						PF00089				G3DSA:2.40.10.10	SSF50494									
aly276269.1	Unknown		CG43693-PG						PF01490														
aly2763.1	Unknown		n/a																				
aly276378.1	Caspase-8	GO:0004175,GO:0006963,GO:0006964,GO:0007291,GO:0050829,GO:0005737,GO:0002230,GO:0006508,GO:0043069,GO:0045089,GO:0006919,GO:0045087,GO:0006915,GO:0006952,GO:0006955,GO:0016485,GO:0061057,GO:0008656,GO:0004197,GO:0005515,GO:0048935,GO:0016505	CG7486-PE				SM00115		PF00656	PS50208,PS50207	PR00376,PR00376,PR00376,PR00376		G3DSA:3.40.50.1460	SSF52129	545~550								
aly276378.10	Estrogen sulfotransferase	GO:0005737,GO:0005829,GO:0051923,GO:0008146,GO:0006805,GO:0008210,GO:0004304,GO:0005496,GO:0050294	CG6704-PA						PF00685				G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276378.11	Sulfotransferase 1C4	GO:0005829,GO:0051923,GO:0008146,GO:0006805,GO:0044281,GO:0050427	CG6704-PA						PF00685				G3DSA:3.40.50.300	SSF52540									
aly276378.12	Sulfotransferase family cytosolic 1B member 1	GO:0005737,GO:0005829,GO:0051923,GO:0008146,GO:0006805,GO:0008202	CG6704-PA						PF00685				G3DSA:3.40.50.300	SSF52540									
aly276378.13	Protein phosphatase 1E	GO:0043234,GO:0006469,GO:0005730,GO:0006470,GO:0005634,GO:0004722,GO:0005739,GO:0003824,GO:0035690,GO:0035970,GO:0051496,GO:0046872	CG10376-PA				SM00332		PF00481	PS51746		PS01032	G3DSA:3.60.40.10	SSF81606									
aly276378.14	Fatty acid-binding protein, heart	GO:0005737,GO:0050543,GO:0006631,GO:0015909,GO:0070062,GO:0006635,GO:0070538,GO:0007616,GO:0005215,GO:0005829,GO:0006810,GO:0042493,GO:0005324,GO:0016528,GO:0070542,GO:0005504,GO:0032868,GO:0005875,GO:0005615	CG6783-PC						PF00061				G3DSA:2.40.128.20	SSF50814									
aly276378.15	ADP-ribosylation factor-like protein 6-interacting protein 1	GO:0005737,GO:0005784,GO:0006613,GO:0016021,GO:0016020,GO:0005887,GO:0005829	CG10326-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276378.16	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase	GO:0033857,GO:0000832,GO:0000827,GO:0005829,GO:0003993,GO:0006020,GO:0052723,GO:0052724,GO:0005524	CG14616-PK						PF00328			PS00616	G3DSA:3.40.50.1240,G3DSA:3.40.50.1240,G3DSA:3.40.50.1240	SSF53254,SSF53254,SSF53254										
aly276378.17	Probable tRNA (uracil-O(2)-)-methyltransferase	GO:0005737,GO:0008033,GO:0005575,GO:0008150,GO:0008168,GO:0046872	CG9386-PA						PF07757				G3DSA:3.40.50.150	SSF53335				PWY-6829						
aly276378.18	Peroxisomal targeting signal 1 receptor	GO:0008022,GO:0007031,GO:0005782,GO:0016560,GO:0000268,GO:0016558,GO:0005052,GO:0005829,GO:0005777,GO:0051262,GO:0072347,GO:0005778,GO:0005515,GO:0016561,GO:0015031,GO:0006625,GO:0005622	CG14815-PA				SM00028,SM00028,SM00028,SM00028,SM00028		PF00515,PF13414	PS50005,PS50005,PS50005,PS50293,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452										
aly276378.19	UPF0545 protein C22orf39 homolog		CG15908-PA						PF11326														
aly276378.2	Ribonuclease P/MRP protein subunit POP5	GO:0008033,GO:0005730,GO:0005634,GO:0004526,GO:0046331,GO:0022008	CG14057-PA			PIRSF023803			PF01900					SSF160350										
aly276378.20	Putative aldehyde dehydrogenase family 7 member A1 homolog	GO:0006081,GO:0004029,GO:0008152,GO:0055114,GO:0016491	CG9629-PA						PF00171			PS00687	G3DSA:3.40.309.10,G3DSA:3.40.605.10	SSF53720										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276378.21	Methyltransferase-like protein 5	GO:0008168,GO:0009007,GO:0032259,GO:0003676	CG9666-PA									PS00092	G3DSA:3.40.50.150	SSF53335									
aly276378.22	SOSS complex subunit C homolog B		CG42374-PA						PF15925														
aly276378.23	Longitudinals lacking protein like	GO:0006351,GO:0001700,GO:0007435,GO:0031519,GO:0006357,GO:0003700,GO:0006342,GO:0005634,GO:0000794,GO:0005700,GO:0016458,GO:0007426,GO:0031208,GO:0045893,GO:0005515,GO:0003677,GO:0045892,GO:0035167,GO:0016568,GO:0042803	CG5738-PB				SM00225,SM01025		PF10523,PF00651	PS51457,PS50097			G3DSA:3.30.710.10	SSF54695										
aly276378.24	Ribosome maturation protein SBDS	GO:0005737,GO:0042273,GO:0005819,GO:0005730,GO:0005634,GO:0030687,GO:0005654,GO:0006364,GO:0003723	CG8549-PA						PF09377					SSF109728									
aly276378.25	Gametogenetin-binding protein 2-like	GO:0005575,GO:0008150,GO:0003674	CG2182-PA												580~600,382~413								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276378.26	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	GO:0006633,GO:0005737,GO:0006637,GO:0005739,GO:0004315,GO:0051790,GO:0051792	CG12170-PA			PIRSF000447	SM00825	TIGR03150	PF00109,PF02801			PS00606	G3DSA:3.40.47.10,G3DSA:3.40.47.10	SSF53901,SSF53901					UPA00094				
aly276378.27	Unknown		n/a																				
aly276378.28	Unknown		n/a																				
aly276378.3	Probable peptide chain release factor C12orf65, mitochondrial	GO:0006415,GO:0003747,GO:0005739	CG30100-PA						PF00472				G3DSA:3.30.160.20	SSF75620									
aly276378.4	FGGY carbohydrate kinase domain containing protein	GO:0005737,GO:0005975,GO:0016773,GO:0016301,GO:0070050,GO:0046835	CG11594-PA			PIRSF000538		TIGR01315	PF00370,PF02782				G3DSA:3.30.420.40,G3DSA:3.30.420.40	SSF53067,SSF53067		00561+2.7.1.30		PWY-4261	UPA00618				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276378.5	E3 ubiquitin-protein ligase BRE1B	GO:0006909,GO:0010390,GO:0019898,GO:0033503,GO:0033523,GO:0043679,GO:1900364,GO:1902916,GO:0005654,GO:0003730,GO:0043005,GO:1901800,GO:0032403,GO:0017075,GO:0016570,GO:2001168,GO:0004842,GO:0043434,GO:0016874,GO:0043234,GO:0031624,GO:0007422,GO:0005829,GO:0006511,GO:0008270	CG10542-PA				SM00184		PF13920	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850	807~827,667~687,443~491,401~428,376~396,295~339,609~629,574~605,730~750,772~799,226~281,526~560									
aly276378.6	Unknown		n/a												631~658								
aly276378.7	Unknown		n/a																				
aly276378.8	Unknown		n/a																				
aly276378.9	Sulfotransferase family cytosolic 1B member 1	GO:0005737,GO:0005829,GO:0051923,GO:0008146,GO:0008202	CG16733-PA						PF00685				G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly27642.1	Unknown	GO:0006030,GO:0016810,GO:0005576,GO:0005975,GO:0008061	CG17905-PA																				
aly276451.1	Exosome complex exonuclease RRP44	GO:0071027,GO:0005085,GO:0090305,GO:0000288,GO:0043547,GO:0005634,GO:0016020,GO:0005654,GO:0010467,GO:0006364,GO:0005652,GO:0006402,GO:0010468,GO:0071034,GO:0022008,GO:0043928,GO:0090503,GO:0000178,GO:0016075,GO:0004519,GO:0005829,GO:0000176,GO:0000177,GO:0000175,GO:0003723,GO:0006397	CG6413-PA											SSF50249									
aly276475.1	Protein CLP1 homolog	GO:0031124,GO:0005849,GO:0000214,GO:0003674,GO:0006388,GO:0022008,GO:0005524	CG5970-PA						PF06807														
aly276551.1	Antichymotrypsin-1	GO:0010951,GO:0045861,GO:0030162,GO:0005615,GO:0004867	CG12172-PA						PF00079				G3DSA:3.30.497.10	SSF56574									
aly276558.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276558.10	Unknown		n/a																				
aly276558.11	Unknown		n/a																				
aly276558.12	Cilia- and flagella-associated protein 20	GO:0048666,GO:0036064,GO:0007517,GO:0070062,GO:0060271,GO:0006355,GO:0003700,GO:0005634,GO:0044822,GO:0000398,GO:0060296,GO:0071011,GO:0048813,GO:0002000253,GO:0005814,GO:2000147,GO:0005929,GO:0005874,GO:0071013,GO:0018095	CG5343-PA						PF05018	PS51257													
aly276558.13	Cilia- and flagella-associated protein 20	GO:0048666,GO:0036064,GO:0007517,GO:0070062,GO:0060271,GO:0006355,GO:0003700,GO:0005634,GO:0044822,GO:0000398,GO:0060296,GO:0071011,GO:0048813,GO:0002000253,GO:0005814,GO:2000147,GO:0005929,GO:0005874,GO:0071013,GO:0018095	CG5343-PA						PF05018														
aly276558.14	Semaphorin-1A	GO:0031987,GO:0045792,GO:0030215,GO:0048854,GO:0016021,GO:0005886,GO:0048813,GO:0008039,GO:0001964,GO:0016199,GO:0005515,GO:0008045,GO:0007411,GO:2000305,GO:0008201,GO:0007416,GO:0004872	CG18405-PG				SM00630		PF01403	PS51004			G3DSA:2.130.10.10	SSF101912									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276558.15	cAMP-dependent protein kinase type II regulatory subunit	GO:0005737,GO:0030552,GO:0006468,GO:0008603,GO:0007623,GO:0007622,GO:0048149,GO:0005886,GO:0045475,GO:0005515,GO:0005952,GO:0007411,GO:0001932	CG15862-PA				SM00100,SM00100		PF04182,PF00027,PF00027	PS50042,PS50042	PR00103,PR00103,PR00103,PR00103	PS00889,PS00889,PS00888,PS00888	G3DSA:2.60.120.10,G3DSA:2.60.120.10,G3DSA:1.20.890.10	SSF51206,SSF51206,SSF47391									
aly276558.16	Cyclin-related protein FAM58A	GO:0005575,GO:0000079,GO:0043410,GO:0019901,GO:0006355,GO:0003674,GO:0048133,GO:0030295,GO:0007179	CG44010-PB						PF00134				G3DSA:1.10.472.10,G3DSA:1.10.472.10	SSF47954,SSF47954									
aly276558.17	Guanine nucleotide-binding protein G(o) subunit alpha	GO:0050916,GO:0007419,GO:0045886,GO:0007165,GO:0004871,GO:0042595,GO:0001664,GO:0008356,GO:0005834,GO:0019991,GO:0007188,GO:0060857,GO:0046872,GO:0007186,GO:0005525,GO:0031683,GO:0003924,GO:0005886,GO:0006184,GO:0001737,GO:0031234,GO:0007507,GO:0016055,GO:0030866,GO:0061343	CG2204-PB				SM00275		PF00503		PR00318,PR00318,PR00318,PR00318,PR00318,PR00441,PR00441,PR00441,PR00441,PR00441		G3DSA:1.10.400.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF47895,SSF52540,SSF52540			REACT_14797,REACT_15295						
aly276558.18	Unknown		n/a																				
aly276558.19	X-ray repair cross-complementing protein 5	GO:0043564,GO:0000723,GO:0006351,GO:0006303,GO:0006302,GO:0006281,GO:0042162,GO:0005634,GO:0003677,GO:0051575,GO:0005654,GO:0004677,GO:0045892,GO:0006310,GO:0004003,GO:0046982,GO:0005694,GO:0003684,GO:0005524,GO:0070419	CG5247-PA			PIRSF003033	SM00559	TIGR00578	PF02735,PF03731,PF03730				G3DSA:1.10.720.30,G3DSA:1.10.1600.10,G3DSA:2.40.290.10,G3DSA:3.40.50.410,G3DSA:4.10.970.10	SSF100939,SSF53300			REACT_216,REACT_6185						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276558.2	Unknown		n/a																				
aly276558.20	TM2 domain-containing protein almondex	GO:0007219,GO:0001713,GO:0007220,GO:0044214,GO:0007498,GO:0007398,GO:0045747,GO:0046331,GO:0003674	CG12127-PA						PF05154														
aly276558.21	Unknown		n/a						PF08914				G3DSA:1.10.10.60	SSF46689	750~775,861~881								
aly276558.22	DNA replication complex GINS protein PSF3	GO:0000811,GO:0005654,GO:0046331,GO:0006260,GO:0022008,GO:0043138	CG2222-PA						PF05916					SSF160059,SSF158573									
aly276558.23	Cyclin-dependent-like kinase 5	GO:0007409,GO:0008582,GO:0031175,GO:0030426,GO:0030425,GO:0030424,GO:0031594,GO:0043525,GO:0008045,GO:0004693,GO:0007049,GO:0000278,GO:0005737,GO:0030549,GO:0048511,GO:0005634,GO:0016020,GO:0004674,GO:0051301,GO:0004672,GO:0043125,GO:0016533,GO:0043025,GO:0005524,GO:2000273,GO:0006468,GO:0030332,GO:0030182,GO:0030027,GO:0016301,GO:0007629,GO:0005176,GO:0035011,GO:0045211,GO:0014069,GO:0061001,GO:0007269,GO:0008340,GO:0051642,GO:0008344,GO:0043204,GO:0070059,GO:0030054,GO:0050321	CG8203-PA				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276558.24	Peptidyl-prolyl cis-trans isomerase FKBP8	GO:0006457,GO:0021904,GO:0005789,GO:0030176,GO:0035264,GO:0035556,GO:0005737,GO:0000413,GO:0001708,GO:0016020,GO:0005528,GO:0043066,GO:0003755,GO:0046872,GO:0010468,GO:0042802,GO:0016032,GO:0006915,GO:0031966,GO:0030513,GO:0061077,GO:0018208,GO:0007224,GO:0005515,GO:0043010	CG5482-PA				SM00028,SM00028,SM00028		PF03704,PF00254	PS50005,PS50005,PS50293,PS50059,PS50005			G3DSA:1.25.40.10,G3DSA:3.10.50.40	SSF54534,SSF48452									
aly276558.25	GPI ethanolamine phosphate transferase 2	GO:0044267,GO:0016020,GO:0005783,GO:0016780,GO:0043687,GO:0051267,GO:0005789,GO:0006501,GO:0003824,GO:0030176,GO:0008152,GO:0006506,GO:0016254	CG2144-PA										G3DSA:3.40.720.10	SSF53649									
aly276558.26	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA						PF00011	PS01031	PR00299,PR00299,PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly276558.27	Protein dead ringer	GO:0070491,GO:0007517,GO:0007435,GO:0009952,GO:0045924,GO:0000122,GO:0003700,GO:0005634,GO:0007431,GO:0042063,GO:0006351,GO:0048813,GO:0000976,GO:0045893,GO:0003677,GO:0007411,GO:0008049,GO:0048477,GO:0009880	CG5403-PB				SM01014,SM00501		PF01388	PS51011			G3DSA:1.10.150.60	SSF46774									
aly276558.28	Unknown		n/a												141~182,115~135								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276558.29	High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A	GO:0046058,GO:0070062,GO:0006355,GO:0004114,GO:0004115,GO:0000156,GO:0004871,GO:0007498,GO:0009187,GO:0007165,GO:0006198,GO:0000160,GO:0046872,GO:0005829	CG45019-PO				SM00471		PF00233		PR00387,PR00387,PR00387,PR00387,PR00387		G3DSA:3.40.50.2300,G3DSA:1.10.1300.10	SSF109604									
aly276558.3	Unknown		n/a																				
aly276558.30	Collagen type IV alpha-3-binding protein	GO:0005794,GO:0035620,GO:0035621,GO:0005783,GO:0005829,GO:0004674,GO:0097001,GO:0035627,GO:0006665,GO:0070273	CG7207-PA				SM00233,SM00234		PF00169,PF01852	PS50003,PS50848			G3DSA:2.30.29.30,G3DSA:3.30.530.20	SSF50729,SSF55961	238~265								
aly276558.31	RNA polymerase II subunit A C-terminal domain phosphatase	GO:0005737,GO:0010458,GO:0005819,GO:0015629,GO:0030496,GO:0005813,GO:0005634,GO:0006366,GO:0008420,GO:0005700,GO:0000922,GO:0005654,GO:0010467,GO:0016032,GO:0006470,GO:0003899,GO:0022008,GO:0051233,GO:0050434,GO:0051301,GO:0006368	CG12252-PA				SM00292,SM00577	TIGR02250	PF00533,PF03031	PS50969,PS50172			G3DSA:3.40.50.10190,G3DSA:2.40.50.100,G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF56784,SSF51230,SSF52113	592~612								
aly276558.32	28S ribosomal protein S17, mitochondrial	GO:0005840,GO:0019843,GO:0003735,GO:0005743,GO:0005763,GO:0006412	CG4326-PA						PF00366				G3DSA:2.40.50.140	SSF50249									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276558.33	Peroxisomal membrane protein 11B	GO:0043234,GO:0005779,GO:0007031,GO:0070062,GO:0016559,GO:0051260,GO:0016020,GO:0005777,GO:0005739,GO:0005778,GO:0007165,GO:0044375,GO:0042803	CG8315-PA						PF05648														
aly276558.34	Putative RNA-binding protein 15	GO:0048749,GO:0007221,GO:0016032,GO:0071011,GO:0031965,GO:0044822,GO:0001569,GO:0035222,GO:0045638,GO:0000398,GO:0000166,GO:0005654,GO:0030177,GO:0003676,GO:0060674,GO:0048536,GO:0060412,GO:0022008,GO:0003729	CG2910-PB				SM00360,SM00360,SM00360		PF14259,PF00076,PF07744	PS50102,PS50917,PS50102			G3DSA:2.40.290.10,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF100939,SSF54928,SSF54928										
aly276558.35	Neuralized-like protein 2	GO:0030239,GO:0030891,GO:0016567,GO:0045214,GO:0005927,GO:0035556	CG3894-PC				SM00588		PF07177,PF07525	PS51065,PS50225				SSF158235					UPA00143				
aly276558.36	Leukotriene A 4 hydrolase	GO:0005737,GO:0004177,GO:0005840,GO:0019370,GO:0044822,GO:0004301,GO:0043171,GO:0003735,GO:0008270,GO:0005762,GO:0004463,GO:0006508,GO:0005654,GO:0006412,GO:0008237,GO:0070062	CG10602-PE						PF01433,PF09127		PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF48371,SSF55486,SSF63737		00590+3.3.2.6			UPA00878				
aly276558.37	39S ribosomal protein L13, mitochondrial	GO:0003735,GO:0005739,GO:0005840,GO:0005762,GO:0006412	CG10603-PA	MF_01366		PIRSF002181			PF00572				G3DSA:3.90.1180.10	SSF52161									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276558.38	Sorting nexin-2	GO:1990459,GO:0019898,GO:0010008,GO:0005737,GO:0070062,GO:0006886,GO:0016020,GO:0061357,GO:1990460,GO:0031901,GO:0043234,GO:0005154,GO:0030027,GO:0005158,GO:0042147,GO:0072673,GO:0034498,GO:0051259,GO:0006897,GO:0043231,GO:0035091,GO:0016050,GO:0030904,GO:0005768	CG2774-PA						PF09325						123~143									
aly276558.39	Sorting nexin-2	GO:1990459,GO:0019898,GO:0010008,GO:0005737,GO:0070062,GO:0006886,GO:0016020,GO:0061357,GO:1990460,GO:0031901,GO:0043234,GO:0005154,GO:0030027,GO:0005158,GO:0042147,GO:0072673,GO:0034498,GO:0051259,GO:0006897,GO:0043231,GO:0035091,GO:0016050,GO:0030904,GO:0005768	CG2774-PA				SM00312		PF00787	PS50195			G3DSA:3.30.1520.10	SSF64268										
aly276558.4	Midasin	GO:0005737,GO:0045111,GO:0006461,GO:0016887,GO:0005730,GO:0005634,GO:0016020,GO:0051082,GO:0008152,GO:0005524	CG13185-PD				SM00382,SM00382,SM00382,SM00382,SM00382		PF07728,PF07728,PF07728,PF07728,PF07728,PF07728,PF07728				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540,SSF52540,SSF52540,SSF52540	3626~3646,219~239,3388~3415,2673~2693,2070~2090								
aly276558.40	Protein PRRC1	GO:0005794	n/a						PF01931				G3DSA:3.90.950.10	SSF52972	234~254								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276558.41	Unknown		n/a																				
aly276558.42	Unknown		n/a																				
aly276558.43	Probable cytochrome P450 49a1	GO:0004497,GO:0016705,GO:0020037,GO:0016020,GO:0005739,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG18377-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00465,PR00465,PR00465,PR00465,PR00465	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly276558.44	Unknown		n/a																				
aly276558.5	Midasin	GO:0005737,GO:0045111,GO:0006461,GO:0016887,GO:0005730,GO:0005634,GO:0016020,GO:0051082,GO:0008152,GO:0005524	CG13185-PD				SM00327		PF00092	PS50234			G3DSA:3.40.50.410	SSF53300									
aly276558.6	Pleckstrin homology domain-containing family F member 2	GO:0007032,GO:0005770,GO:0006897,GO:0005783,GO:0035091,GO:0008333,GO:0048812,GO:0015031,GO:0030133,GO:0046872,GO:0005769,GO:0031901	CG14782-PA				SM00064,SM00233		PF01363,PF00169	PS50003,PS50178			G3DSA:3.30.40.10,G3DSA:2.30.29.30	SSF57903,SSF50729									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276558.7	Ribonuclease kappa	GO:0005575,GO:0090502,GO:0016021,GO:0004521,GO:0009303	CG40127-PB																				
aly276558.8	Ribonuclease kappa	GO:0005575,GO:0090502,GO:0016021,GO:0004521,GO:0009303	CG40127-PB																				
aly276558.9	Testis-specific serine/threonine-protein kinase 4	GO:0005737,GO:0006468,GO:0000287,GO:0031514,GO:0030154,GO:0032793,GO:0004674,GO:0007283,GO:0048812,GO:0001669,GO:0004672,GO:0035556,GO:0007275,GO:0005524,GO:0009966	CG9222-PA				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly276560.1	Protein phosphatase 1 regulatory subunit 15A	GO:0032515,GO:0005783,GO:1902310,GO:0032516,GO:0005789,GO:0060734,GO:0010628,GO:0033138,GO:1903573,GO:0005737,GO:0070972,GO:0016020,GO:0000164,GO:0005739,GO:0045943,GO:1990441,GO:0005794,GO:0070262,GO:0019888,GO:0006915,GO:0019901,GO:0035308,GO:0019903,GO:0008157,GO:1903912,GO:0036496,GO:0030968,GO:0005741,GO:0034976	CG3825-PA						PF10488						690~722								
aly276560.2	Unknown		CG2837-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276561.1	Unknown		n/a																				
aly276561.2	T-complex protein 1 subunit gamma	GO:0005737,GO:0006457,GO:0007430,GO:0042623,GO:0060439,GO:0051082,GO:0007052,GO:0090307,GO:0005832,GO:0005875,GO:0005524	CG8977-PD						PF00118,PF00118		PR00304,PR00304,PR00304	PS00750,PS00995,PS00751	G3DSA:3.50.7.10,G3DSA:1.10.560.10,G3DSA:1.10.560.10	SSF54849,SSF54849,SSF52029,SSF48592,SSF48592	296~316		REACT_17015						
aly276561.3	Unknown		CG15478-PA																				
aly276561.4	Unknown		n/a																				
aly276561.5	Centrosome-associated zinc finger protein CP190	GO:0031937,GO:0090202,GO:0031208,GO:0003677,GO:0005874,GO:0005875,GO:0005737,GO:0005813,GO:0005634,GO:0051493,GO:0046872,GO:0010468,GO:0008017,GO:0007017,GO:0005704,GO:0035191,GO:0005700,GO:0006351,GO:0005515,GO:0003682,GO:0016568,GO:0043035	CG6384-PA				SM00225,SM00355,SM00355,SM00355,SM00355,SM00355		PF00651	PS50157,PS50097,PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.710.10	SSF54695,SSF57667	1238~1262								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276561.6	Ubiquitin-conjugating enzyme E2 J2	GO:0005737,GO:0006986,GO:0005783,GO:0016874,GO:0016021,GO:0061630,GO:0000151,GO:0005789,GO:1903955,GO:0031625,GO:0030433,GO:0061631,GO:0004842,GO:0000209,GO:0005524	CG5823-PB				SM00212		PF00179	PS50127			G3DSA:3.10.110.10	SSF54495	160~183								
aly276561.7	Unknown		n/a												29~49,137~157								
aly276630.1	Unknown	GO:0050975,GO:0072347,GO:0007623,GO:0043679,GO:0005245,GO:0006811,GO:0016020,GO:0008344,GO:0042752,GO:0055085,GO:0048512,GO:0005261,GO:0022008,GO:0043025,GO:0005216	CG1517-PF																				
aly276633.1	Eukaryotic peptide chain release factor subunit 1	GO:0005737,GO:0008079,GO:0043022,GO:0016149,GO:0035071,GO:0007224,GO:0005829,GO:0006605,GO:0048102,GO:0018444,GO:0006415,GO:0003747,GO:0044822,GO:0006449	CG5605-PG					TIGR03676	PF03463,PF03465,PF03464				G3DSA:3.30.420.60,G3DSA:3.30.960.10,G3DSA:3.30.1330.30	SSF53137,SSF55315,SSF55481									
aly276633.2	StAR-related lipid transfer protein 7, mitochondrial	GO:1903955,GO:0008525,GO:0008289,GO:0005739	CG6565-PA						PF01852	PS50848			G3DSA:3.30.530.20,G3DSA:3.30.530.20	SSF55961,SSF55961									
aly276633.3	Unknown		n/a												43~63								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276633.4	Unknown		n/a																				
aly276633.5	Longitudinals lacking protein, isoforms H/M/V	GO:0045476,GO:0019730,GO:0035167,GO:0045467,GO:0003677,GO:0007411,GO:0002121,GO:0031987,GO:0005634,GO:0044719,GO:0008406,GO:0005654,GO:0001964,GO:0045893,GO:0007409,GO:0022008,GO:0007526,GO:0003700,GO:0048854,GO:0007464,GO:0016199,GO:0006355,GO:0048813,GO:0006351,GO:0005515	CG3726-PB				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695,SSF46689										
aly276634.1	DNA transposase THAP9	GO:0006310,GO:0004803,GO:0006313,GO:0043565,GO:0015074,GO:0016740,GO:0046872	n/a						PF12017														
aly276634.2	Neuferricin	GO:0020037,GO:0007399,GO:0005575,GO:0005576,GO:0003674,GO:0008150	CG12056-PA						PF00173				G3DSA:3.10.120.10	SSF55856	159~179								
aly276634.3	Protein tantalus	GO:0005737,GO:0007423,GO:0005634,GO:0003674,GO:0003677,GO:0005694	CG6586-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276634.4	Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type	GO:0030322,GO:0005635,GO:0016529,GO:0005783,GO:0006874,GO:0016021,GO:0005811,GO:0051282,GO:0006816,GO:0007629,GO:0000166,GO:0033017,GO:0046872,GO:0060047,GO:1901896,GO:0005515,GO:0005388,GO:0005789,GO:0007274,GO:0005524	CG3725-PE				SM00831	TIGR01494,TIGR01494,TIGR01116	PF00122,PF00689,PF00690,PF08282,PF13246		PR00119,PR00119,PR00119,PR00119,PR00119,PR00119	PS00154	G3DSA:3.40.1110.10,G3DSA:2.70.150.10,G3DSA:2.70.150.10,G3DSA:1.20.1110.10,G3DSA:1.20.1110.10	SSF56784,SSF81660,SSF81653,SSF81665,SSF81665,SSF81665										
aly276634.5	Poly(A)-specific ribonuclease PARN-like domain-containing protein 1	GO:0016021,GO:0005634,GO:0003676	n/a						PF04857				G3DSA:3.30.420.10,G3DSA:3.30.420.10,G3DSA:3.30.1370.50	SSF53098,SSF53098									
aly276634.6	Laccase-2	GO:0040003,GO:0052716,GO:0046274,GO:0005576,GO:0005507,GO:0055114	CG42345-PA						PF07732,PF00394,PF07731				G3DSA:2.60.40.420,G3DSA:2.60.40.420,G3DSA:2.60.40.420	SSF49503,SSF49503,SSF49503									
aly276635.1	Unknown	GO:0003677	n/a						PF05225					SSF46689	193~213								
aly276635.2	Unknown		n/a						PF13843														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276636.1	SID1 transmembrane family member 1	GO:0016021,GO:0033227,GO:0051033	n/a						PF13965,PF13965														
aly276636.2	GTPase-activating protein CdGAPr	GO:0043547,GO:0005096,GO:0005622,GO:0005575,GO:0007165,GO:0005100,GO:0007266,GO:0031290	CG10538-PA												624~644								
aly276637.1	Plasma membrane calcium-transporting ATPase 3	GO:0005794,GO:1903561,GO:0006874,GO:0016021,GO:0007596,GO:0070588,GO:0034220,GO:0006810,GO:0005886,GO:0005388,GO:0046872,GO:0055085,GO:0005524	CG42314-PS					TIGR01517,TIGR01494,TIGR01494,TIGR01494	PF12710,PF12424,PF00122,PF00122,PF00689		PR00119,PR00119,PR00119,PR00119,PR00119,PR00119	PS00154	G3DSA:1.20.1110.10,G3DSA:1.20.1110.10,G3DSA:1.20.1110.10	SSF81665,SSF81665,SSF81665,SSF56784,SSF56784,SSF81653,SSF81660									
aly276637.2	Unknown		n/a												1094~1110								
aly276637.3	Protein ref(2)P	GO:0005737,GO:0030382,GO:0005634,GO:0019058,GO:0008270,GO:0003677,GO:0007005,GO:0006351	CG10360-PA				SM00692,SM00291,SM00980		PF00569,PF05485	PS50950,PS50135		PS01357		SSF57850,SSF57716									
aly276637.4	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA						PF00011	PS01031	PR00299,PR00299,PR00299,PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276637.5	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA			PIRSF036514			PF00011	PS01031	PR00299,PR00299,PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly276637.6	Tyrosine-protein phosphatase 69D	GO:0016021,GO:0007409,GO:0004728,GO:0006470,GO:0004725,GO:0008045,GO:0035335,GO:0030424,GO:0005001,GO:0048813,GO:0046331,GO:0005515,GO:0005886,GO:0007155,GO:0007411,GO:0007414,GO:0007415,GO:0097155	CG10975-PA				SM00194,SM00194,SM00404,SM00404,SM00409,SM00409,SM00060,SM00060,SM00060		PF07679,PF00102,PF00102,PF00041,PF00041	PS50835,PS50853,PS50055,PS50056,PS50853,PS50853,PS50835,PS50056,PS50055	PR00700,PR00700,PR00700,PR00700,PR00700,PR00700	PS00383,PS00383	G3DSA:2.60.40.10,G3DSA:3.90.190.10,G3DSA:3.90.190.10,G3DSA:2.60.40.10,G3DSA:3.90.190.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF49265,SSF48726,SSF48726,SSF52799,SSF52799,SSF52799										
aly276637.7	Unknown		n/a												64~87,14~41								
aly276637.8	Unknown		n/a																				
aly276638.1	Unknown		n/a																				
aly276638.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276639.1	Unknown	GO:0015074,GO:0006313,GO:0003677	n/a						PF01498,PF13518				G3DSA:1.10.10.10,G3DSA:1.10.10.60	SSF46689									
aly276639.2	Unknown	GO:0003676	n/a						PF03184														
aly276639.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276640.1	Copper-transporting ATPase 1	GO:0060003,GO:0043085,GO:0005783,GO:0048085,GO:0007595,GO:0005886,GO:0048812,GO:0051353,GO:0048066,GO:0000302,GO:0002082,GO:0002164,GO:0043524,GO:0001836,GO:0007626,GO:0006825,GO:0010043,GO:0010041,GO:0010273,GO:0042421,GO:0006568,GO:0021702,GO:0032767,GO:0005737,GO:0016020,GO:0001701,GO:0051542,GO:0016532,GO:0016021,GO:0005770,GO:0048813,GO:0000166,GO:0030198,GO:0007005,GO:0043005,GO:0030141,GO:0015677,GO:0021954,GO:0005375,GO:0005507,GO:0043025,GO:0010468,GO:0005524,GO:0048554,GO:0005794,GO:0004008,GO:0048471,GO:0006878,GO:0042428,GO:0048553,GO:0030140,GO:0046034,GO:0006584,GO:0016323,GO:0042417,GO:0034220,GO:0048251,GO:0051216,GO:0030001,GO:0055065,GO:0042093,GO:0021860,GO:0031069,GO:0006570,GO:0043473,GO:0046872,GO:0055085,GO:0018205,GO:0005829,GO:0005802,GO:0042415,GO:0015679,GO:0031526,GO:0001974,GO:0030199,GO:0042414,GO:0043588,GO:0048286,GO:0019430,GO:0001568	CG1886-PB					TIGR01494	PF00122,PF00403	PS50846	PR00942,PR00942,PR00942,PR00942,PR00943,PR00943,PR00943		G3DSA:2.70.150.10,G3DSA:3.30.70.100	SSF55008,SSF81653									
aly276665.1	Unknown		n/a																				
aly276665.10	Transmembrane protein 201	GO:0016021	CG7744-PA						PF09779														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276665.11	Tetratricopeptide repeat protein 27	GO:0022008,GO:0005515	CG5290-PA				SM00028,SM00028,SM00028,SM00028		PF13414,PF07719	PS50293,PS50005,PS50005,PS50005			G3DSA:1.25.40.10	SSF48452									
aly276665.12	Rabenosyn-5	GO:0008103,GO:0048227,GO:0045324,GO:0010009,GO:0035088,GO:0070062,GO:0001737,GO:0046872,GO:0031901,GO:0017137,GO:0005886,GO:0000011,GO:0030100,GO:0034058,GO:0006896,GO:0006897,GO:0043231,GO:0006895,GO:0031267,GO:0005515,GO:0015031,GO:0045451,GO:0005768,GO:0005769	CG8506-PA				SM00064		PF01363,PF11464	PS50157,PS50178		PS00028	G3DSA:3.30.40.10	SSF57903,SSF140125	344~371,404~431								
aly276665.13	WD repeat-containing protein 78	GO:0042623,GO:0007018,GO:0005875,GO:0002244,GO:0005515,GO:0005868,GO:0030286,GO:0003774	CG13930-PA				SM00320,SM00320,SM00320,SM00320,SM00320			PS50294,PS50082			G3DSA:2.130.10.10	SSF50978									
aly276665.14	Unknown		CG7991-PB							PS50002			G3DSA:2.30.30.40	SSF50044									
aly276665.15	THO complex subunit 6	GO:0009408,GO:0003674,GO:0006406,GO:0000347,GO:0008283	CG5632-PA				SM00320,SM00320		PF00400	PS50082,PS50294		PS00678	G3DSA:2.130.10.10	SSF50978,SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276665.16	Serine/arginine repetitive matrix protein 2	GO:0016607,GO:0071011,GO:0071013,GO:0044822,GO:0000398,GO:0015030,GO:0008380,GO:0006397	CG7971-PF						PF08312						883~906								
aly276665.17	Unknown		n/a																				
aly276665.18	Peroxisomal membrane protein 2	GO:0043234,GO:0016021,GO:0005778,GO:0005829,GO:0005739	CG7970-PA						PF04117														
aly276665.19	Unknown		n/a																				
aly276665.2	Unknown		n/a																				
aly276665.20	Thioredoxin domain-containing protein 17	GO:0033209,GO:0070062,GO:0005829,GO:0047134,GO:0006726,GO:0009055,GO:0004601,GO:0055114,GO:0015036	CG11024-PA						PF06110				G3DSA:3.40.30.10	SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276665.21	SEC14-like protein 2	GO:0005737,GO:0005215,GO:0016021,GO:0006810,GO:0008289,GO:0005622,GO:0006355,GO:0006351,GO:0005634	CG13893-PA				SM00516		PF00650	PS50866,PS50191			G3DSA:3.40.525.10	SSF52087,SSF46938,SSF101576									
aly276665.22	Armadillo repeat-containing protein 4	GO:0005737,GO:0005856,GO:0021591,GO:0007368,GO:0005654,GO:0036158,GO:0070986,GO:0005575,GO:0007291,GO:0003674,GO:0005488,GO:0003356,GO:0003341,GO:0005634,GO:0005930,GO:0097546	CG5155-PA				SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185		PF00514	PS50176,PS50176,PS50176			G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371									
aly276665.23	DNA-directed RNA polymerase II subunit GRINL1A	GO:0003899,GO:0016591	CG3773-PA						PF15328		PR02085,PR02085												
aly276665.24	Probable RNA binding protein 18	GO:0003729,GO:0003723,GO:0003676,GO:0000166	CG14414-PE						PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly276665.25	RNA polymerase I-specific transcription initiation factor RRN3	GO:0007000,GO:0005736,GO:0001701,GO:0048872,GO:0008283,GO:0006361,GO:0007028,GO:0005634,GO:0005730,GO:0010467,GO:0042254,GO:0005654,GO:0006360,GO:0006356,GO:2000142,GO:0010976,GO:1902254,GO:0045893	CG3278-PA						PF05327,PF05327														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276665.26	Guanine nucleotide-binding protein subunit alpha homolog	GO:0007166,GO:0031752,GO:0003384,GO:0010004,GO:0004871,GO:0006184,GO:0005737,GO:0005834,GO:0007369,GO:0007188,GO:0016476,GO:0046872,GO:0007186,GO:0005525,GO:0031683,GO:0003924,GO:0008360,GO:0008152,GO:0007266,GO:0031234,GO:0007370,GO:0007374,GO:0031526,GO:0019001,GO:0070252	CG17678-PA				SM00275		PF00503		PR00440,PR00440,PR00440,PR00440,PR00318,PR00318,PR00318,PR00318,PR00318		G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.400.10	SSF47895,SSF52540,SSF52540			REACT_14797,REACT_604							
aly276665.27	Unknown		n/a																				
aly276665.3	DNA-directed RNA polymerase III subunit RPC9	GO:0004930,GO:0051607,GO:0048812,GO:0045087,GO:0001635,GO:0007218,GO:0000166,GO:0045745,GO:0009360,GO:0006351,GO:0001669,GO:0005666,GO:0003899,GO:0005886,GO:0006384,GO:0006383	CG4875-PB				SM00657		PF03874				G3DSA:1.10.150.80	SSF47819										
aly276665.4	Glutamine synthetase 1, mitochondrial	GO:0015930,GO:0006909,GO:0004356,GO:0005811,GO:0006541,GO:0005739,GO:0006542,GO:0006807,GO:0005524,GO:0007005	CG2718-PC						PF03951,PF00120			PS00180	G3DSA:3.30.590.10,G3DSA:3.10.20.70	SSF55931,SSF54368		00330+6.3.1.2,00630+6.3.1.2,00250+6.3.1.2,00910+6.3.1.2	REACT_13	PWY-6964,PWY-6963,PWY-5675,PWY-381,PWY-6549					
aly276665.5	Glutamine synthetase 1, mitochondrial	GO:0015930,GO:0006909,GO:0004356,GO:0005811,GO:0006541,GO:0005739,GO:0006542,GO:0005524,GO:0007005	CG2718-PC						PF00120,PF03951			PS00180	G3DSA:3.30.590.10,G3DSA:3.10.20.70	SSF55931,SSF54368		00330+6.3.1.2,00630+6.3.1.2,00250+6.3.1.2,00910+6.3.1.2	REACT_13	PWY-6964,PWY-6963,PWY-5675,PWY-381,PWY-6549					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276665.6	Plasminogen activator inhibitor 1 RNA-binding protein	GO:0005737,GO:0016020,GO:0070062,GO:0043488,GO:0005634,GO:0070828,GO:0005703,GO:0005700,GO:0003730,GO:0005886,GO:0016246,GO:0048471,GO:0016442,GO:0042981,GO:0044822,GO:0003729	CG4170-PD						PF16174,PF04774						26~46								
aly276665.7	E3 ubiquitin-protein ligase HECW2	GO:0005737,GO:0016874,GO:0042787,GO:0004842,GO:0005515	CG42797-PD				SM00119,SM00456,SM00456		PF00632,PF16562,PF00397	PS50020,PS50020,PS50237		PS01159,PS01159	G3DSA:3.30.2160.10,G3DSA:2.20.70.10,G3DSA:2.20.70.10	SSF51045,SSF56204,SSF51045	53~73				UPA00143				
aly276665.8	Unknown		n/a												34~54								
aly276665.9	Unknown		n/a																				
aly276668.1	Unknown		n/a																				
aly276670.1	Serine protease 30	GO:0004252,GO:0006814,GO:0017080,GO:0005576,GO:0005886,GO:0006508,GO:0008236,GO:0031225	CG40160-PA				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276670.2	Serine protease 30	GO:0004252,GO:0006814,GO:0017080,GO:0005576,GO:0005886,GO:0006508,GO:0008236,GO:0031225	CG5390-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly276674.1	Unknown		n/a												140~174								
aly276676.1	Rootletin	GO:0005737,GO:0051656,GO:0015629,GO:0035253,GO:0005813,GO:0051297,GO:0045494,GO:0005814,GO:0010457,GO:0003779,GO:0030030,GO:0019894,GO:0001917,GO:0010669,GO:0005886,GO:0033365,GO:0008104,GO:0032053,GO:0005198,GO:0007049,GO:0070062	CG6129-PD										G3DSA:1.20.5.50	SSF57997,SSF57997	939~959,733~753,761~781,328~383,1059~1093,76~96,396~445,476~506,10~68,973~1007,111~320,511~675,690~710,789~931									
aly276676.2	Ras-related protein Rap-1b	GO:0016020,GO:0034333,GO:0007165,GO:0046328,GO:0030054,GO:0022409,GO:0005811,GO:0016476,GO:0005525,GO:0006930,GO:0042067,GO:0003924,GO:0031252,GO:0008360,GO:0032486,GO:0005886,GO:0007155,GO:0006184,GO:0007264,GO:0001752,GO:0035099,GO:0030718,GO:0030713,GO:0007391,GO:0019003,GO:0005515,GO:0005829	CG1956-PA				SM00173,SM00174,SM00175,SM00176	TIGR00231	PF00071	PS51421	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540	86~106		REACT_11044						
aly276678.1	Unknown	GO:0001104,GO:0016592,GO:0006357	n/a						PF09606														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276689.1	Copper-transporting ATPase 1	GO:0048085,GO:0007595,GO:0005886,GO:0051353,GO:0048066,GO:0002082,GO:0002164,GO:0043524,GO:0001836,GO:0042428,GO:0006825,GO:0010043,GO:0046688,GO:0010273,GO:0010041,GO:0021702,GO:0042421,GO:0005737,GO:0001701,GO:0051542,GO:0016532,GO:0016021,GO:0005770,GO:0048813,GO:0000166,GO:0007626,GO:0043005,GO:0030141,GO:0015677,GO:0005375,GO:0005507,GO:0043025,GO:0010468,GO:0005524,GO:0048554,GO:0005794,GO:0004008,GO:0006878,GO:0048553,GO:0030140,GO:0046034,GO:0006568,GO:0048471,GO:0016323,GO:0042417,GO:0048251,GO:0051216,GO:0030001,GO:0055065,GO:0042093,GO:0021860,GO:0031069,GO:0006570,GO:0043473,GO:0046872,GO:0018205,GO:0005802,GO:0015679,GO:0031526,GO:0001974,GO:0030199,GO:0042414,GO:0048286,GO:0019430,GO:0001568	CG1886-PB						PF00403	PS50846	PR00942,PR00942,PR00942		G3DSA:3.30.70.100	SSF55008									
aly276703.1	Protein son of sevenless	GO:0005088,GO:0003677,GO:0046579,GO:0035022,GO:0035023,GO:0005737,GO:2000134,GO:0043547,GO:0045500,GO:0007480,GO:0008595,GO:0008360,GO:0007265,GO:0007264,GO:0031234,GO:0030676,GO:0007015,GO:0007426,GO:0007399,GO:0005829,GO:0016199,GO:0005515,GO:0008293,GO:0046982	CG7793-PA								PR00620,PR00620,PR00620		G3DSA:1.10.20.10	SSF47113									
aly276746.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276754.1	Unknown	GO:0004222,GO:0008586,GO:0007415,GO:0010629,GO:0005509,GO:0008045,GO:0016485,GO:0007411,GO:0006508,GO:0008270	CG6863-PB												20~47,163~183								
aly276758.1	Unknown	GO:0005575,GO:0004177,GO:0008270,GO:0008237,GO:0006508	CG4467-PB																				
aly276758.2	RuvB-like helicase 2	GO:0035102,GO:0031011,GO:0030111,GO:0035267,GO:0003678,GO:0005875,GO:0000123,GO:0043486,GO:0005634,GO:0003714,GO:0016573,GO:0043141,GO:0005524,GO:0042127,GO:0035072,GO:0006281,GO:0022008,GO:0010629,GO:0007480,GO:0006351,GO:0006342,GO:0007095	CG9750-PB				SM00382		PF06068				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.8.60	SSF52540										
aly276758.3	Oxysterol-binding protein-related protein 8	GO:0046628,GO:0030336,GO:0015485,GO:0006869,GO:0008142,GO:0016020,GO:0031965,GO:0010891,GO:0090204,GO:0045444,GO:0051897	CG42668-PM						PF01237			PS01013		SSF144000	576~596								
aly276759.1	Transient receptor potential cation channel trpm	GO:0098655,GO:0070838,GO:0097682,GO:0043052,GO:0005261,GO:0034703,GO:0016049,GO:0046873,GO:0055069,GO:0010960,GO:0055085,GO:0007005	CG44240-PE																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276759.2	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly276759.3	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly276759.4	Transient receptor potential cation channel trpm	GO:0098655,GO:0070838,GO:0097682,GO:0043052,GO:0005261,GO:0034703,GO:0016049,GO:0046873,GO:0055069,GO:0010960,GO:0055085,GO:0007005	CG44240-PE																				
aly276759.5	Unknown		CG5180-PB				SM00595		PF10545	PS51029													
aly276759.6	Unknown		CG5180-PB																				
aly276760.1	Furin-like protease 2	GO:0004252,GO:0051048,GO:0016021,GO:0005886,GO:0016485,GO:0006508	CG18734-PB				SM00261,SM00261,SM00261,SM00261,SM00261,SM00261,SM00261,SM00261,SM00261		PF14843,PF00082,PF01483		PR00723,PR00723,PR00723	PS00136,PS00138,PS00137	G3DSA:2.60.120.260,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:3.40.50.200	SSF57184,SSF52743,SSF57184,SSF57184,SSF49785										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276764.1	Unknown		CG9896-PA																				
aly276765.1	Unknown		n/a																				
aly276778.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly276790.1	Trafficking protein particle complex subunit 6B	GO:0005794,GO:0006888,GO:0005783,GO:0003674,GO:0030008,GO:0016192	CG6196-PA						PF04051				G3DSA:3.30.1380.20	SSF111126									
aly276791.1	MAP/microtubule affinity-regulating kinase 3	GO:0008360,GO:0051124,GO:0019730,GO:0009994,GO:0005886,GO:0031594,GO:0030111,GO:0000226,GO:0007294,GO:0009798,GO:0007298,GO:0007276,GO:0030709,GO:0070062,GO:0045172,GO:0009948,GO:0030707,GO:0004674,GO:0004672,GO:0045451,GO:0005524,GO:0006468,GO:0016325,GO:0016323,GO:0007317,GO:0045185,GO:0051663,GO:0005938,GO:0061174,GO:0001737,GO:0007318,GO:0007015,GO:0090176,GO:0045169,GO:0007314,GO:0050321	CG8201-PX				SM00220		PF02149,PF00069	PS50030,PS50032,PS50011		PS00107,PS00108	G3DSA:1.10.8.10,G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:3.30.310.80	SSF56112,SSF103243									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276791.2	Zinc finger protein 512B	GO:0006355,GO:0005634,GO:0046872,GO:0006351,GO:0003677	CG30101-PA																				
aly276791.3	Unknown		n/a																				
aly276791.4	Unknown		n/a												96~116								
aly276792.1	Non-structural maintenance of chromosomes element 1 homolog	GO:0006301,GO:0000724,GO:0005634,GO:0006281,GO:0030915,GO:0016567,GO:0008270,GO:2001022,GO:0004842	CG11329-PA						PF07574						2~22								
aly276794.1	Unknown	GO:0008028,GO:0016021,GO:0055085	CG8028-PC										G3DSA:1.20.1250.20	SSF103473									
aly276794.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276799.1	NADH dehydrogenase [ubiqui] iron-sulfur protein 6, mitochondrial	GO:0070584,GO:0006631,GO:0010259,GO:0006936,GO:0061458,GO:0008137,GO:0072358,GO:0005747,GO:0035264,GO:0022904	CG8680-PA						PF10276				G3DSA:2.60.260.40										
aly276809.1	Putative adenosylhomocysteinase 3	GO:0004013,GO:0006730,GO:0005783	CG9977-PA						PF05221				G3DSA:3.40.50.1480	SSF52283		00270+3.3.1.1		PWY-5041	UPA00314				
aly276811.1	Unknown		n/a												2~47								
aly276813.1	Probable deoxyhypusine synthase	GO:0050983,GO:0034038,GO:0008612	CG8005-PA					TIGR00321	PF01916				G3DSA:3.40.910.10	SSF52467					UPA00354				
aly276822.1	Juvenile hormone epoxide hydrolase	GO:0008096,GO:0043231,GO:0033961,GO:0016021,GO:0005789,GO:0004301,GO:0019439,GO:0006719	CG15102-PA										G3DSA:3.40.50.1820										
aly276830.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276834.1	Unknown		n/a																				
aly276848.1	Unknown		n/a							PS51304			G3DSA:2.60.120.200										
aly276856.1	Golgin subfamily A member 7	GO:0005795,GO:0018230,GO:0070062,GO:0031228,GO:0050821,GO:0043001,GO:0002178	CG5447-PB																				
aly276859.1	Unknown		n/a												508~528								
aly276863.1	Unknown	GO:0016021,GO:0055085,GO:0008513	CG42269-PE																				
aly276876.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276879.1	Unknown		n/a																				
aly276882.1	Lysosomal acid phosphatase	GO:0043202,GO:0001501,GO:0070062,GO:0005765,GO:0016311,GO:0031410,GO:0016021,GO:0016020,GO:0004721,GO:0005764,GO:0048102,GO:0043005,GO:0007040,GO:0010033,GO:0003993	CG6656-PA						PF00328				G3DSA:3.40.50.1240	SSF53254									
aly276882.10	Transient receptor potential cation channel subfamily V member 5	GO:0016324,GO:0050974,GO:0005261,GO:0005262,GO:0007605,GO:0006812,GO:0006816,GO:0051262,GO:0048060,GO:0009270,GO:0034703,GO:0005887,GO:0001964,GO:0010996,GO:0055085	CG5842-PB				SM00248,SM00248,SM00248,SM00248,SM00248		PF00520	PS50297,PS50088,PS50088			G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403									
aly276882.11	Transient receptor potential cation channel subfamily V member 5	GO:0016324,GO:0050974,GO:0005261,GO:0060402,GO:0005262,GO:0007605,GO:0006812,GO:0006816,GO:0051262,GO:0005622,GO:0048060,GO:0009270,GO:0034703,GO:0005887,GO:0001964,GO:0010996,GO:0055085	CG5842-PB				SM00248,SM00248,SM00248,SM00248,SM00248		PF00520	PS50297,PS50088,PS50088			G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276882.12	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0005737,GO:0030728,GO:0070062,GO:0055114,GO:0004022,GO:0016323,GO:0003824,GO:0045786,GO:0007179,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									
aly276882.13	Unknown		n/a																				
aly276882.14	Unknown	GO:0008601,GO:0046331,GO:0005509	CG4733-PB																				
aly276882.15	Unknown		n/a																				
aly276882.16	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276882.17	Unknown		n/a																				
aly276882.2	Retinol dehydrogenase 11	GO:0016062,GO:0004745,GO:0016021,GO:0052650,GO:0007603,GO:0005789,GO:0001917,GO:0008152,GO:0042572,GO:0005622,GO:0042574,GO:0001523,GO:0016491	CG2064-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735	50~70								
aly276882.3	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246	n/a				SM00034		PF00059	PS50041			G3DSA:3.10.100.10	SSF56436,SSF56436									
aly276882.4	Solute carrier family 25 member 51	GO:0016021,GO:0006810,GO:0005740,GO:0005739,GO:0005743,GO:0022857	CG7943-PB						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly276882.5	Integrator complex subunit 4	GO:0016180,GO:0034472,GO:0005634,GO:0032039,GO:0003674,GO:0022008	CG12113-PA										G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371									
aly276882.6	Steroid receptor RNA activator 1	GO:0005737,GO:2000273,GO:0006915,GO:0008283,GO:0042981,GO:0005634,GO:0030154,GO:0003713,GO:0030374,GO:0006355,GO:0006351,GO:0030529,GO:0016922	n/a						PF07304														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276882.7	Stromal cell-derived factor 2	GO:0035269,GO:0016020,GO:0004169,GO:0005615,GO:0006486	CG11999-PA				SM00472,SM00472,SM00472		PF02815	PS50919,PS50919,PS50919			G3DSA:2.80.10.50	SSF82109									
aly276882.8	Serine/threonine-protein kinase polo	GO:0008104,GO:0006909,GO:0035046,GO:0035044,GO:0007147,GO:0007067,GO:0005874,GO:0007060,GO:0007140,GO:0007344,GO:0030954,GO:0005813,GO:0030726,GO:0000940,GO:0005814,GO:0000922,GO:0004674,GO:0004672,GO:0005635,GO:0005524,GO:0005737,GO:0006468,GO:0000278,GO:0051297,GO:0034613,GO:0048600,GO:0035050,GO:1990023,GO:0007052,GO:0005819,GO:0007058,GO:0007406,GO:0022008,GO:0051315,GO:0000776,GO:0000910,GO:0007112,GO:0000915,GO:0005828,GO:0030496,GO:0051257,GO:0007143,GO:0005515	CG12306-PA				SM00220		PF00069,PF00659,PF00659	PS50011,PS50078,PS50078		PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:3.30.1120.30,G3DSA:3.30.1120.30	SSF56112,SSF82615,SSF82615									
aly276882.9	Pancreatic triacylglycerol lipase (Fragment)	GO:0004806,GO:0007476,GO:0016042,GO:0005575,GO:0005576,GO:0046872,GO:0016298	CG5966-PA						PF00151		PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly276890.1	Unknown		n/a												220~240								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276890.10	PHD finger protein 14	GO:0008285,GO:0000122,GO:0072201,GO:0005634,GO:0046331,GO:0008270,GO:0048286,GO:2000791,GO:2000584	CG15439-PA				SM00184,SM00184,SM00184,SM00184,SM00249,SM00249,SM00249,SM00249		PF13832,PF00628,PF00628,PF00628,PF00628	PS50016,PS50016,PS50016,PS50016		PS01359,PS01359,PS01359	G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57903,SSF57903,SSF57903,SSF57903	425~452								
aly276890.11	Unknown	GO:0016020,GO:0016199,GO:0005622,GO:0071889,GO:0008046,GO:0005515,GO:0008045,GO:0007411,GO:2000305,GO:0017154,GO:0008201	CG11081-PA						PF01437														
aly276890.12	Aquaporin-4	GO:0005737,GO:0009992,GO:0070295,GO:0005887,GO:0009897,GO:0007605,GO:0016021,GO:0071346,GO:0006833,GO:0016323,GO:0015250,GO:0034220,GO:0015267,GO:0003014,GO:0015254,GO:0005911,GO:0015793,GO:0030104,GO:0005886,GO:0055085	CG17664-PC						PF00230		PR00783,PR00783,PR00783,PR00783,PR00783	PS00221	G3DSA:1.20.1080.10	SSF81338									
aly276890.13	Venom allergen 5	GO:0008150,GO:0005576,GO:0003674	CG8483-PA				SM00198		PF00188				G3DSA:3.40.33.10	SSF55797									
aly276890.14	Fasciclin-1	GO:0050839,GO:0016338,GO:0008038,GO:0007158,GO:0005886,GO:0007155,GO:0007411,GO:0007156,GO:0031225	CG6588-PD				SM00554,SM00554,SM00554,SM00554		PF02469,PF02469,PF02469,PF02469	PS50213,PS50213,PS50213,PS50213			G3DSA:2.30.180.10,G3DSA:2.30.180.10,G3DSA:2.30.180.10,G3DSA:2.30.180.10	SSF82153,SSF82153,SSF82153,SSF82153									
aly276890.15	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276890.16	Unknown	GO:0005488	n/a										G3DSA:1.25.10.10	SSF48371									
aly276890.2	Protein FAM76A		CG4452-PA						PF16046						216~236,280~311								
aly276890.3	Venom allergen 5	GO:0008150,GO:0005576,GO:0003674	CG8483-PA				SM00198		PF00188		PR00838,PR00838,PR00838,PR00837,PR00837,PR00837	PS01009	G3DSA:3.40.33.10	SSF55797									
aly276890.4	Venom allergen 3	GO:0008150,GO:0005576,GO:0003674	CG8483-PA				SM00198		PF00188				G3DSA:3.40.33.10	SSF55797									
aly276890.5	Putative serine protease K12H4.7	GO:0006508,GO:0045087,GO:0008236	CG3734-PA						PF05577				G3DSA:3.40.50.1820	SSF53474,SSF53474									
aly276890.6	S-adenosylmethionine synthase	GO:0004478,GO:0006556,GO:0006730,GO:0035220,GO:0022416,GO:0046872,GO:0005829,GO:0005524	CG2674-PE						PF02772,PF02773,PF00438			PS00377,PS00376	G3DSA:3.30.300.10,G3DSA:3.30.300.10,G3DSA:3.30.300.10	SSF55973,SSF55973,SSF55973		00270+2.5.1.6	REACT_13433	PWY-5912,PWY-5041	UPA00315				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276890.7	Calcitonin gene-related peptide type 1 receptor	GO:0004930,GO:0048512,GO:0042332,GO:0005887,GO:0010579,GO:0007186,GO:0016021,GO:0016020,GO:0007218,GO:0042745,GO:0045475,GO:0043005,GO:0008188,GO:0007623,GO:0005886,GO:0043025,GO:0042749,GO:0004948	CG13758-PB						PF02793,PF00002	PS50227,PS50261	PR00249,PR00249,PR00249,PR00249,PR00249,PR00249	PS00650		SSF111418									
aly276890.8	Putative defense protein 3	GO:0045087,GO:0042832,GO:0042742,GO:0005576	CG14515-PA						PF02014	PS51019													
aly276890.9	Tubulin-specific chaperone D	GO:0005737,GO:0007023,GO:0006457,GO:0043547,GO:0034333,GO:0070830,GO:0010812,GO:0005096,GO:0005575,GO:0048487,GO:0005912,GO:0016328,GO:0005923,GO:0031115	CG7261-PA						PF12612				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371									
aly276891.1	Dynein heavy chain-like protein PF11_0240	GO:0005737,GO:0016887,GO:0007018,GO:0003774,GO:0003777,GO:0008152,GO:0030286,GO:0005874,GO:0005875,GO:0005524	CG44085-PO												627~661,520~565,570~621								
aly276891.2	Unknown		n/a																				
aly276892.1	Alkylglycerol monooxygenase	GO:0006633,GO:0005783,GO:0006643,GO:0016021,GO:0050479,GO:0005789,GO:0046485,GO:0005506,GO:0055114,GO:0016491	n/a						PF04116														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276892.2	Alkylglycerol monooxygenase	GO:0006633,GO:0005783,GO:0006643,GO:0016021,GO:0050479,GO:0005789,GO:0046485,GO:0005506,GO:0055114,GO:0016491	n/a						PF04116														
aly276893.1	Collagen-like protein 6	GO:0005581,GO:2001046,GO:0008045,GO:0030246,GO:0005198,GO:0014732,GO:0019012,GO:0071711,GO:0007155,GO:0031012,GO:0014899,GO:0007005	CG42543-PR						PF06482,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391				G3DSA:3.10.100.10	SSF56436									
aly276893.2	Unknown		n/a																				
aly276893.3	Collagen alpha 3(VI) chain	GO:0005201,GO:0005587,GO:0005581,GO:0007391,GO:0005604,GO:0004867,GO:0007155,GO:0005578,GO:0035848	CG4145-PC						PF01391,PF01391														
aly276893.4	Unknown		n/a											SSF49899									
aly276896.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276897.1	Unknown		CG13408-PA																				
aly276897.2	Unknown		n/a																				
aly276897.3	Unknown		n/a																				
aly276898.1	IQ and AAA domain-containing protein 1-like	GO:0005524	CG14183-PA										G3DSA:3.40.50.300	SSF52540									
aly276898.2	Unknown	GO:0005524	CG14183-PA																				
aly276918.1	Neural/ectodermal development factor IMP-L2	GO:0046628,GO:0005615,GO:0046627,GO:0005576,GO:0007155,GO:0008340,GO:0005520	CG15009-PC				SM00409,SM00409,SM00408,SM00408		PF07679,PF13895	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276918.2	Unknown		n/a																				
aly276919.1	Unknown		n/a																				
aly276922.1	Protein I'm not dead yet	GO:0071422,GO:0015744,GO:0006848,GO:1901475,GO:0006814,GO:0015137,GO:0050833,GO:0016323,GO:0015746,GO:0005887,GO:0005886,GO:0015141,GO:0008340,GO:0015142,GO:0055085,GO:0010889	CG3979-PB						PF00939			PS01271					REACT_20633,REACT_15518						
aly276922.2	Solute carrier family 13 member 3	GO:0015142,GO:0070062,GO:0005215,GO:0016021,GO:0016020,GO:0015137,GO:0015362,GO:0006835,GO:0015183,GO:0005886,GO:0015141,GO:0008340,GO:0006814,GO:0055085,GO:0010889	CG3979-PB						PF00939								REACT_20633,REACT_15518						
aly276922.3	Alpha-tocopherol transfer protein-like	GO:0005215,GO:0016020,GO:0005622	CG11550-PA						PF00650	PS50191			G3DSA:3.40.525.10	SSF52087,SSF46938									
aly276927.1	Potassium voltage-gated channel protein Shal	GO:0043204,GO:0071805,GO:0006813,GO:0016021,GO:0005886,GO:0051260,GO:0008076,GO:0030425,GO:0005249,GO:0007268,GO:0005250,GO:0005251,GO:0055085	CG9262-PB						PF11879				G3DSA:1.10.287.70	SSF81324									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly276928.1	Ubiquitin-related modifier 1 homolog	GO:0005737,GO:0004252,GO:0005829,GO:0032447,GO:0005576,GO:0034227,GO:0006508,GO:0002098	CG33276-PB	MF_03048		PIRSF037379			PF09138				G3DSA:3.10.20.30	SSF54285					UPA00988				
aly276986.1	Unknown		n/a																				
aly277.1	Cytochrome P450 6j1	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG8345-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly277.2	Neuroligin-4, Y-linked	GO:0042043,GO:0071625,GO:0035176,GO:0009986,GO:0007612,GO:0052689,GO:0097110,GO:0045211,GO:0050808,GO:0030054,GO:0045202,GO:0005887,GO:0004872,GO:0014069,GO:0007158,GO:0050839,GO:0051932,GO:0007416,GO:0030431	CG34139-PD						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly277095.1	Unknown		n/a																				
aly2774.1	Unknown	GO:0007155,GO:0007156,GO:0042802,GO:0005887,GO:0005886	CG31190-PE							PS50835			G3DSA:2.60.40.10	SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2774.10	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098	PS50292	PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									
aly2774.11	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098	PS50292	PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10	SSF48113									
aly2774.12	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098,PF03098	PS50292	PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									
aly2774.13	Probable sulfite oxidase, mitochondrial	GO:0020037,GO:0030151,GO:0042128,GO:0008482,GO:0006790,GO:0030163,GO:0005758,GO:0055114,GO:0009055	CG7280-PA						PF00174,PF00173,PF03404	PS50255	PR00407,PR00407,PR00407,PR00407,PR00407,PR00407,PR00407	PS00191	G3DSA:3.10.120.10,G3DSA:2.60.40.650,G3DSA:3.90.420.10	SSF55856,SSF81296,SSF56524									
aly2774.14	Gamma-butyrobetaine dioxygenase	GO:0005737,GO:0008336,GO:0008270,GO:0045329,GO:0005506,GO:0055114	CG5321-PB						PF06155,PF02668				G3DSA:3.60.130.10	SSF51197			REACT_13		UPA00118				
aly2774.15	Mitotic spindle assembly checkpoint protein MAD2B	GO:0005737,GO:0008432,GO:0001558,GO:0033138,GO:0006302,GO:0006351,GO:0051726,GO:0005819,GO:0051349,GO:0016035,GO:0042177,GO:0045893,GO:0007067,GO:0042772,GO:0005634,GO:0051301,GO:0060564	CG2948-PA						PF02301	PS50815			G3DSA:3.30.900.10	SSF56019									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2774.16	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 1	GO:0016021,GO:0005739,GO:0031966,GO:0003674,GO:0005747,GO:0008150,GO:0055114	CG34439-PB						PF15879														
aly2774.17	Tripeptidyl-peptidase 2	GO:0005737,GO:0004252,GO:0005615,GO:0004177,GO:0008240,GO:0051260,GO:0005739,GO:0008238,GO:0006508	CG3991-PD						PF00082,PF12580		PR00723,PR00723,PR00723	PS00138	G3DSA:3.40.50.200,G3DSA:3.40.50.200	SSF52743,SSF52743	767~771,1168~195								
aly2774.18	Unknown		n/a																				
aly2774.19	Unknown		n/a																				
aly2774.2	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0005515,GO:0048812,GO:0005887,GO:0005886,GO:0007155,GO:0007156,GO:0042802	CG31190-PE				SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00406,SM00406,SM00406,SM00406		PF13895,PF07679,PF07679,PF07679,PF07679,PF07679,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041	PS50853,PS50835,PS50835,PS50835,PS50835,PS50835,PS50853,PS50853,PS50853,PS50853,PS50853,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF49265,SSF49265,SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2774.20	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA						PF00011	PS01031	PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly2774.21	Unknown		n/a						PF14846						453~487,311~331,419~439,256~283,183~217								
aly2774.22	Alpha-crystallin A chain	GO:0006497,GO:0005212,GO:0009790,GO:0010998,GO:0009408,GO:0046872,GO:0010506	CG4533-PA						PF00011	PS01031	PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly2774.23	Unknown		n/a																				
aly2774.24	Unknown		n/a																				
aly2774.3	Gamma-2-syntrophin	GO:0005737,GO:0005856,GO:0097109,GO:0042383,GO:0042052,GO:0008092,GO:0008582,GO:0016013,GO:0008307,GO:0030165,GO:0001654,GO:0005515	CG4905-PE				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50729,SSF50729,SSF50156									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2774.4	Atrial natriuretic peptide-converting enzyme	GO:0004252,GO:0003050,GO:0005887,GO:0030182,GO:0005044,GO:0009986,GO:0016020,GO:0005576,GO:0008217,GO:0005515,GO:0007565,GO:0006508,GO:0035813,GO:0016486	CG2105-PB				SM00063,SM00192,SM00192,SM00020		PF01392,PF00057,PF00057,PF00089	PS50287,PS50068,PS50068,PS50240,PS50038	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:4.10.400.10,G3DSA:3.10.250.10,G3DSA:2.40.10.10,G3DSA:1.10.2000.10,G3DSA:2.40.10.10,G3DSA:4.10.400.10	SSF63501,SSF57424,SSF50494,SSF56487,SSF57424	894~900									
aly2774.5	Unknown		n/a																				
aly2774.6	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098	PS50292	PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									
aly2774.7	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098	PS50292			G3DSA:1.10.640.10	SSF48113									
aly2774.8	Chorion peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0005576,GO:0042744,GO:0007306,GO:0042743,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098	PS50292			G3DSA:1.10.640.10	SSF48113	54~74								
aly2774.9	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098	PS50292			G3DSA:1.10.640.10	SSF48113									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly27742.1	Unknown	GO:0005575,GO:0003674,GO:0008150	CG9395-PC						PF01697														
aly277490.1	Unknown		n/a												75~111,9~36,44~72								
aly277714.1	Unknown		n/a																				
aly278.1	Bombyxin A-1 homolog	GO:0005179,GO:0060180,GO:0008286,GO:0005615,GO:0005158,GO:0005576	CG14167-PA			PIRSF018431	SM00078		PF00049		PR00276,PR00276	PS00262	G3DSA:1.10.100.10	SSF56994									
aly278.2	Protein kinase C	GO:0006468,GO:0035206,GO:0019992,GO:0005622,GO:0004674,GO:0004698,GO:0008270,GO:0035556,GO:0004697,GO:0005524	CG6622-PB							PS50081	PR00008,PR00008		G3DSA:3.30.60.20	SSF57889									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly278.3	Rac GTPase-activating protein 1	GO:0048487,GO:0030111,GO:0090307,GO:0001669,GO:0004871,GO:0008272,GO:0035556,GO:0005547,GO:0007405,GO:0030178,GO:0032507,GO:0005819,GO:0070062,GO:0019992,GO:0005634,GO:0001709,GO:0000281,GO:0097149,GO:0031234,GO:0005654,GO:0048471,GO:0046872,GO:0048666,GO:0051298,GO:0055028,GO:0008283,GO:0008017,GO:0034613,GO:0005096,GO:0032154,GO:0032467,GO:0019901,GO:0043014,GO:0007052,GO:0072686,GO:0051988,GO:0007266,GO:0022008,GO:0051233,GO:0007525,GO:0043547,GO:0000910,GO:0000915,GO:0009790,GO:0030496,GO:0007283,GO:0051256,GO:0048813,GO:0005100,GO:0043015,GO:0070507	CG13345-PA				SM00324,SM00109		PF00620	PS50081,PS50238			G3DSA:3.30.60.20,G3DSA:1.10.555.10	SSF57889,SSF48350	53~80		REACT_11044						
aly278.4	Glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase 1	GO:0016267,GO:0006486,GO:0016263,GO:0016021,GO:0016020,GO:0009247,GO:0021551,GO:0016757,GO:0046872,GO:0048531	CG9520-PB						PF02434														
aly278.5	Unknown		n/a						PF08357														
aly278.6	Unknown	GO:0007031,GO:0006625,GO:0005777,GO:0005778,GO:0003674,GO:0016560	CG4289-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly278.7	Calpain-7	GO:0005737,GO:0010634,GO:0007632,GO:0004175,GO:0070062,GO:0007399,GO:0005622,GO:0005654,GO:0008270,GO:0097264,GO:0006508,GO:0004198,GO:0090541	CG1391-PB				SM00720,SM00230,SM00745,SM00745		PF04212,PF04212,PF00648,PF01067	PS50203	PR00704,PR00704,PR00704,PR00704,PR00704		G3DSA:1.20.58.280,G3DSA:1.20.58.280,G3DSA:2.60.120.380,G3DSA:2.60.120.380,G3DSA:3.90.70.10,G3DSA:3.90.70.10	SSF49758,SSF54001,SSF49758,SSF116846,SSF116846	49~76									
aly278042.1	Unknown		n/a																				
aly2781.1	Uncharacterized WD repeat-containing protein alr3466	GO:0005875	CG10132-PA				SM00320,SM00320,SM00320,SM00320			PS50294		PS00678	G3DSA:2.130.10.10	SSF50998	202~222,313~333								
aly2781.2	Cytochrome c oxidase subunit 6C	GO:0004129,GO:0016021,GO:0005811,GO:0006123,GO:0044237,GO:0005751,GO:0005743,GO:0010467,GO:0005739,GO:0006367,GO:0022904,GO:0006091,GO:0044281	CG14028-PA						PF02937				G3DSA:4.10.93.10	SSF81415									
aly2781.3	Protein SON	GO:0000910,GO:0016607,GO:0051726,GO:0044822,GO:0043484,GO:0005654,GO:0043066,GO:0000226,GO:0003723,GO:0003676,GO:0003677,GO:0008380,GO:0006397	n/a																				
aly2781.4	Unknown	GO:0005751,GO:0004129,GO:0005811,GO:0006123	CG14028-PA						PF02937				G3DSA:4.10.93.10	SSF81415									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2781.5	Coiled-coil domain-containing protein 102A	GO:0016459	CG31638-PA												67~122,192~212,237~271,32~52								
aly2781.6	Unknown		n/a						PF09808														
aly2781.7	Cytochrome c oxidase subunit 5B, mitochondrial	GO:0004129,GO:0005811,GO:0006123,GO:0005739,GO:0005751,GO:0005743,GO:0046872	CG11015-PA						PF01215	PS51359			G3DSA:2.60.11.10	SSF57802									
aly2781.8	Unknown		CG14321-PA						PF16029														
aly2784.1	Unknown		n/a																				
aly278595.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly27894.1	Mediator of RNA polymerase II transcription subunit 15	GO:0001104,GO:0016592,GO:0006357,GO:0006367,GO:0006366	CG4184-PA						PF09606														
aly279.1	Putative BEN domain-containing protein B1		n/a						PF10523	PS51457													
aly279.2	Putative BEN domain-containing protein B1		n/a						PF10523	PS51457													
aly279.3	Unknown		n/a						PF03372				G3DSA:3.60.10.10	SSF56219									
aly2790.1	Zinc finger and SCAN domain-containing protein 22	GO:0003700,GO:0005634,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly2790.10	Zinc finger protein 26	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872	CG6254-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2790.11	Zinc finger protein 91	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0070895,GO:0007476,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178,GO:0008270	CG14938-PA				SM00355,SM00355		PF13912,PF13912,PF13912,PF13912,PF13912	PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667	2238~2238								
aly2790.12	Zinc finger protein 273	GO:0051726,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG11247-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF12756,PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667									
aly2790.13	Zinc finger and SCAN domain-containing protein 22	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0007476,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF12874,PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly2790.2	Zinc finger protein 425 (Fragment)	GO:0005737,GO:0005634,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776,PF13912,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57716									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2790.3	Zinc finger protein 2	GO:0051726,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG11247-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868,SM00868		PF13912,PF07776,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	178~198								
aly2790.4	Zinc finger protein 324A	GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG6654-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776	PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028		SSF57667,SSF57667	174~194								
aly2790.5	Gastrula zinc finger protein XlCGF26.1 (Fragment)	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG2129-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF13912,PF13912,PF12756	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.40.10,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly2790.6	Gastrula zinc finger protein XlCGF57.1 (Fragment)	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG15269-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly2790.7	Zinc finger and SCAN domain-containing protein 2	GO:0051726,GO:0003700,GO:0005634,GO:0030154,GO:0007283,GO:0006351,GO:0003676,GO:0003677,GO:0046872,GO:0007275	CG11247-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2790.8	Zinc finger protein Xfin	GO:0005737,GO:0006355,GO:0046872,GO:0003723,GO:0003676	CG12299-PA				SM00355,SM00355		PF12756	PS50157,PS50157,PS50157,PS50157,PS51008,PS50157,PS50157,PS50157,PS50157,PS51008,PS50157,PS50157,PS50157,PS50157,PS51008		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly2790.9	Zinc finger protein 559	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG5245-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667								
aly279231.1	Unknown		n/a																				
aly2793.1	Dopamine receptor 2	GO:0001588,GO:0001306,GO:0004935,GO:0007212,GO:0008226,GO:0016021,GO:0004952,GO:0005887,GO:0005886,GO:0007191,GO:0030285,GO:0007186,GO:0008227,GO:1903223	CG18741-PC						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly2793.2	Unknown	GO:0016772	CG13813-PA				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2799.1	Lipoma HMGIC fusion partner-like 2 protein	GO:0016021,GO:0007163,GO:0060857,GO:0005918	CG3770-PA						PF10242														
aly2799.2	Lipoma HMGIC fusion partner-like 2 protein	GO:0016021,GO:0007163,GO:0060857,GO:0005918	CG3770-PA																				
aly2799.3	Cullin-1	GO:1990452,GO:0009887,GO:0031625,GO:0008283,GO:0006915,GO:0031146,GO:0016322,GO:0046627,GO:0006513,GO:0006511,GO:0019005,GO:0031461,GO:0032007,GO:0007095,GO:0000152	CG1877-PC				SM00884,SM00182		PF10557,PF00888	PS50069		PS01256	G3DSA:1.20.1310.10,G3DSA:1.10.10.10,G3DSA:1.20.1310.10,G3DSA:1.20.1310.10,G3DSA:1.10.10.10,G3DSA:1.20.1310.10,G3DSA:4.10.1030.10	SSF74788,SSF75632,SSF46785	267~287				UPA00143				
aly2799.4	Luciferin 4-monooxygenase	GO:0046872,GO:0006637,GO:0045289,GO:0004321,GO:0005777,GO:0004467,GO:0046949,GO:0001676,GO:0008218,GO:0047077,GO:0005524	CG6178-PA						PF13193,PF00501			PS00455	G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.30.300.30,G3DSA:3.40.50.980	SSF56801									
aly2799.5	LIM and SH3 domain protein F42H10.3	GO:0070864,GO:0045856,GO:0015629,GO:0003779,GO:0007279,GO:0007283,GO:0007291,GO:0008270,GO:0055120,GO:0005925,GO:0030054	CG3849-PB				SM00227,SM00227,SM00326		PF00880,PF00880,PF14604	PS51216,PS51216,PS50002	PR00499,PR00499,PR00499,PR00452,PR00452,PR00452,PR00452		G3DSA:2.30.30.40	SSF50044									
aly2802.1	Glutathione S-transferase 1	GO:0005737,GO:0004364,GO:0006749	CG17531-PA						PF13410,PF13417	PS50405,PS50404			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF47616,SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2802.2	Lachesin	GO:0007606,GO:0005575,GO:0004714,GO:0003674,GO:0005515,GO:0005886,GO:0007155,GO:0007169,GO:0031225	CG12191-PA				SM00408,SM00408,SM00409,SM00409,SM00406,SM00406		PF00047,PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly2802.3	Unknown	GO:0016021,GO:0046331,GO:0055085	CG3690-PA						PF00083				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473,SSF103473									
aly280232.1	Protein rhomboid	GO:0004252,GO:0035202,GO:0016337,GO:0048149,GO:0038005,GO:0035225,GO:0008586,GO:0007611,GO:0010629,GO:0001763,GO:0007438,GO:0035311,GO:0008236,GO:0007436,GO:0045177,GO:0007479,GO:0007432,GO:0048865,GO:0007431,GO:0016021,GO:0007476,GO:0000281,GO:0007474,GO:0045742,GO:0005509,GO:0006508,GO:0008355,GO:0061331,GO:0005794,GO:0035160,GO:0007173,GO:0030707,GO:0007409,GO:0005886,GO:0042058,GO:0007424,GO:0007420,GO:0007422,GO:0000139,GO:0046845	CG33166-PB						PF01694				G3DSA:1.20.1540.10	SSF144091									
aly28025.1	Protein singed wings 2	GO:0035075,GO:0035073,GO:0005622,GO:0005575,GO:0003674,GO:0035556	CG14485-PA										G3DSA:3.80.10.10	SSF52058									
aly28025.2	Pogo transposable element with KRAB domain	GO:0006355,GO:0005634,GO:0007275,GO:0003677	n/a						PF03184,PF05225	PS50960			G3DSA:3.30.40.10	SSF46689,SSF57903									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly280735.1	Unknown		n/a						PF03372					SSF56219									
aly280823.1	Unknown		n/a																				
aly28086.1	E3 ubiquitin-protein ligase UBR1	GO:0005737,GO:0016874,GO:0061630,GO:0000151,GO:0016567,GO:0008270,GO:0004842,GO:0071596,GO:0030163	CG9086-PA																				
aly281.1	Unknown		n/a																				
aly281.10	Transaldolase	GO:0005737,GO:0004801,GO:0005975,GO:0070062,GO:0005829,GO:0019682,GO:0030246,GO:0003824,GO:0006098,GO:0048029,GO:0009052,GO:0005634,GO:0006002,GO:0043231	CG2827-PA					TIGR00874	PF00923			PS00958,PS01054	G3DSA:3.20.20.70	SSF51569		00030+2.2.1.2		PWY-5723,PWY-1861	UPA00115				
aly281.11	Heat shock 70 kDa protein 4L	GO:0005737,GO:0006986,GO:0006457,GO:0005829,GO:0051087,GO:0005634,GO:0005524	CG6603-PI						PF00012		PR00301,PR00301,PR00301,PR00301,PR00301,PR00301	PS01036	G3DSA:3.30.30.30,G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:2.60.34.10,G3DSA:2.60.34.10,G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:1.20.1270.10,G3DSA:3.90.640.10	SSF100934,SSF100934,SSF100920,SSF100920,SSF53067,SSF53067	498~518,610~634									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly281.12	Ethanolamine kinase	GO:0004103,GO:0016319,GO:0055059,GO:0007420,GO:0007638,GO:0016310,GO:0006657,GO:0009612,GO:0005737,GO:0006646,GO:0007616,GO:0008306,GO:0004305,GO:0046337,GO:0046959,GO:0046474,GO:0001666,GO:0005524	CG3525-PC						PF01633				G3DSA:3.90.1200.10,G3DSA:3.10.450.110	SSF56112										
aly281.13	Cytochrome b-c1 complex subunit 8	GO:0021539,GO:0005743,GO:0005811,GO:0008121,GO:0006122,GO:0005739,GO:0021860,GO:0021766,GO:0005750,GO:0021854,GO:0030901,GO:0021548,GO:0070469,GO:0048039,GO:0021680,GO:0021794	CG7580-PA						PF02939				G3DSA:1.20.5.210	SSF81508										
aly281.14	UDP-N-acetylglucosamine transporter	GO:0005794,GO:0005797,GO:0015788,GO:0005351,GO:0015782,GO:0016021,GO:1990569,GO:0015789,GO:0015785,GO:0000139,GO:0005463,GO:0005462,GO:0005461,GO:0005459,GO:0005464,GO:0006047,GO:0005456,GO:0055085,GO:0015757	CG2675-PB			PIRSF005799		TIGR00803	PF04142					SSF103481			REACT_15518							
aly281.15	39S ribosomal protein L22, mitochondrial	GO:0003735,GO:0005739,GO:0005840,GO:0005762,GO:0006412	CG4742-PA						PF00237				G3DSA:3.90.470.10	SSF54843										
aly281.16	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	GO:0005737,GO:0016791,GO:0005634,GO:0008420,GO:0004721,GO:0070940,GO:0006397	CG14216-PA						PF04722														
aly281.17	28S ribosomal protein S27, mitochondrial	GO:0003700,GO:0005743,GO:0005634,GO:0005840	CG4882-PA						PF10037						377~397,354~374								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly281.18	Coiled-coil domain-containing protein 22 homolog	GO:0005575,GO:0003674,GO:0008150	CG9951-PA						PF05667,PF05667						385~412,204~238,334~361,292~312								
aly281.19	DEAD-box helicase Dbp80	GO:0005737,GO:0008026,GO:0044614,GO:0031965,GO:0004004,GO:0004386,GO:0003723,GO:0003676,GO:0015031,GO:0051028,GO:0005524	CG17023-PE				SM00487,SM00490		PF00270,PF00271	PS51192,PS51195,PS51194			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540										
aly281.2	Cilia- and flagella-associated protein 99	GO:0042995	n/a												288~308,411~460,374~401,492~548,554~574								
aly281.20	ER membrane protein complex subunit 10	GO:0016021,GO:0072546	CG32441-PC																				
aly281.21	Uncharacterized oxidoreductase YrbE	GO:0055114,GO:0016491	CG3609-PA						PF01408,PF02894				G3DSA:3.30.360.10,G3DSA:3.40.50.720	SSF51735,SSF55347									
aly281.22	Delta-sarcoglycan	GO:0005737,GO:0005856,GO:0007016,GO:0042383,GO:0007498,GO:0016021,GO:0016012,GO:0008307,GO:0060047,GO:0045214,GO:0043034	CG14808-PA						PF04790														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly281.23	Zeta-sarcoglycan	GO:0005737,GO:0048738,GO:0007016,GO:0042383,GO:0055001,GO:0007498,GO:0016021,GO:0005856,GO:0007517,GO:0046716,GO:0016012,GO:0061024,GO:0008307,GO:0060047,GO:0045214,GO:0043034	CG14808-PA						PF04790														
aly281.24	Unknown		n/a												149~169								
aly281.25	Unknown		CG8236-PA																				
aly281.26	Solute carrier family 22 member 13	GO:0090416,GO:0070062,GO:0016324,GO:0005215,GO:0016021,GO:0008513,GO:0022857,GO:2001142,GO:0015747,GO:0055085	CG7458-PA						PF07690	PS50850		PS00216,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly281.27	Unknown		n/a																				
aly281.28	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly281.29	Otopetrin-1	GO:0016021,GO:0005615,GO:0031214	CG42265-PD						PF03189														
aly281.3	Paired box protein Pax-6	GO:0007469,GO:0048749,GO:0007435,GO:0000122,GO:0003700,GO:0005634,GO:0043565,GO:0007477,GO:0006355,GO:0035214,GO:0001654,GO:0000977,GO:0005667,GO:0001745,GO:0007275,GO:0006351	CG10488-PA				SM00351,SM00389		PF00292,PF00046	PS50071,PS51057		PS00027	G3DSA:1.10.10.10,G3DSA:1.10.10.60	SSF46689,SSF46689									
aly281.30	Unknown		n/a						PF03564														
aly281.4	Serine/threonine-protein phosphatase rdgC	GO:0005622,GO:0016059,GO:0006470,GO:0043052,GO:0019722,GO:0004723,GO:0030145,GO:0004721,GO:0004722,GO:0007601,GO:0050906,GO:0005516,GO:0005506,GO:0007602,GO:0045494,GO:0005509	CG44746-PF			PIRSF000912	SM00156,SM00054,SM00054,SM00054		PF00149,PF00612,PF13499	PS50222,PS50096,PS50222,PS50222	PR00114,PR00114,PR00114,PR00114,PR00114,PR00114,PR00114	PS00018,PS00125,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:3.60.21.10	SSF56300,SSF47473	672~699									
aly281.5	CCR4-NOT transcription complex subunit 7	GO:0008284,GO:0000932,GO:0030014,GO:0003676,GO:0005737,GO:0007517,GO:0000289,GO:0005634,GO:0016020,GO:1900153,GO:0006402,GO:0046872,GO:0006351,GO:0048666,GO:0008285,GO:0033962,GO:0061014,GO:0060213,GO:0031047,GO:0022008,GO:0043928,GO:0090503,GO:0000290,GO:0004535,GO:0004532,GO:0010629,GO:0000175,GO:0006357,GO:0045944,GO:0003723,GO:0005515,GO:0017148,GO:0006417,GO:0007095	CG5684-PE						PF04857				G3DSA:3.30.420.10	SSF53098									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly281.6	Chromatin-remodeling complex ATPase chain Iswi	GO:0035060,GO:0035063,GO:0042752,GO:0016589,GO:0031491,GO:0016887,GO:0003677,GO:0003678,GO:0016590,GO:0007517,GO:0042766,GO:0008623,GO:0006325,GO:0005634,GO:0043044,GO:0000166,GO:0032508,GO:0005524,GO:0035076,GO:0005667,GO:0008134,GO:0004386,GO:0031213,GO:0000790,GO:0045892,GO:0045893,GO:0016584,GO:0008094,GO:0070615,GO:0006338,GO:0006334,GO:0006333,GO:0005700,GO:0006355,GO:0048813,GO:0006357,GO:0045944,GO:0006351,GO:0005515,GO:0003682	CG8625-PA				SM00487,SM00717,SM00717,SM00490		PF00271,PF09111,PF00176,PF09110,PF13892	PS51192,PS51194,PS51293			G3DSA:1.10.10.60,G3DSA:1.10.10.60,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF46689,SSF46689,SSF52540,SSF52540,SSF101224	765~796,950~984,628~648,264~284								
aly281.7	FAST kinase domain-containing protein 5	GO:0045333,GO:0004672	CG2124-PA																				
aly281.8	Harmonin	GO:0032420,GO:0000086,GO:0032029,GO:0005903,GO:0045202,GO:0030507,GO:0005737,GO:0045177,GO:0050885,GO:0005856,GO:0007605,GO:0050957,GO:0051017,GO:0050953,GO:0060122,GO:0005886,GO:0001750,GO:0030046,GO:0042472,GO:0005829,GO:0042491,GO:0001917,GO:0005515,GO:0045494	CG5921-PD				SM00228,SM00228		PF00595,PF00595	PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156										
aly281.9	Sodium- and chloride-dependent glycine transporter 2	GO:0006810,GO:0005328,GO:0060012,GO:0016021,GO:0015375,GO:0055085,GO:0007268,GO:0005886,GO:0036233,GO:0006836,GO:0005326	CG5549-PB						PF00209	PS50267	PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176	PS00610		SSF161070,SSF161070										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2811.1	A disintegrin and metalloprotease with thrombospondin motifs 7	GO:0044267,GO:0036066,GO:0004222,GO:0032331,GO:0071356,GO:0009986,GO:0051603,GO:0042059,GO:0031012,GO:0098779,GO:0008237,GO:0006493,GO:0008270,GO:0071347,GO:0006508,GO:0043687,GO:0005578,GO:0005788,GO:0071773	CG4096-PB				SM00209,SM00209		PF05986,PF00090,PF00090,PF01421,PF01562	PS50092,PS50215	PR01857,PR01857,PR01857,PR01705,PR01705,PR01705		G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:3.40.390.10	SSF82895,SSF55486,SSF82895									
aly2811.10	Unknown		n/a																				
aly2811.2	G kinase-anchoring protein 1	GO:0005794,GO:0007165	n/a								PR02083,PR02083,PR02083,PR02083,PR02083				260~294,210~244								
aly2811.3	Leucine-rich repeat protein 1	GO:0005737,GO:0046331,GO:0005634,GO:0019898,GO:0016567,GO:0005576,GO:0005515,GO:0007265,GO:0022008	CG6098-PA				SM00369,SM00369,SM00369,SM00369		PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058	411~411								
aly2811.4	Elongator complex protein 1	GO:0005737,GO:0006351,GO:0030335,GO:0008023,GO:0045859,GO:0033588,GO:0006952,GO:0006357,GO:0007165,GO:0016246,GO:0008607	CG10535-PC			PIRSF017233			PF04762	PS50293,PS50005			G3DSA:1.25.40.10,G3DSA:2.130.10.10	SSF48452,SSF69322,SSF69322	871~891								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2811.5	28S ribosomal protein S30, mitochondrial	GO:0005840,GO:0044822,GO:0005739,GO:0006412,GO:0003735,GO:0005743,GO:0005763,GO:0005875	CG8470-PA						PF07147														
aly2811.6	Eukaryotic translation initiation factor 2 subunit 2	GO:0000049,GO:0005850,GO:0005829,GO:0034976,GO:0016199,GO:0046872,GO:0007052,GO:0001677,GO:0000022,GO:0005525,GO:0006413,GO:0005875,GO:0003743	CG4153-PA				SM00653		PF01873				G3DSA:3.30.30.50	SSF75689,SSF100966									
aly2811.7	Beta-ureidopropionase	GO:0005737,GO:0006208,GO:0006207,GO:0016810,GO:0019483,GO:0003837,GO:0006807,GO:0046872	CG3027-PA						PF00795	PS50263			G3DSA:3.60.110.10	SSF56317									
aly2811.8	Microfibrillar-associated protein 1	GO:0043234,GO:0071011,GO:0071013,GO:0044822,GO:0000398,GO:0030198,GO:0005515,GO:0001527,GO:0022008,GO:0010389,GO:0005576	CG1017-PA						PF06991						214~246,127~163,284~318								
aly2811.9	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0006631,GO:0006629,GO:0017105,GO:0016717,GO:0042811,GO:0046872,GO:0016021,GO:0055114	CG9747-PA						PF00487		PR00075,PR00075,PR00075,PR00075,PR00075,PR00075,PR00075												
aly2813.1	Esterase FE4	GO:0005575,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2813.2	Probable glutamate receptor	GO:0009593,GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0045211,GO:0030054,GO:0004970	CG15324-PA										G3DSA:3.40.190.10	SSF53850,SSF53850									
aly2813.3	Unknown		n/a																				
aly2818.1	ATP-binding cassette sub-family A member 3	GO:0043190,GO:0042626,GO:0006810,GO:0005615,GO:0006869,GO:0097208,GO:0005215,GO:0016021,GO:0016020,GO:0042493,GO:0097233,GO:0016887,GO:0005886,GO:0055085,GO:0005524	CG6052-PA				SM00382		PF00005,PF00005,PF12698,PF12698	PS50893,PS50893		PS00211	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									
aly2818.2	Mitochondrial fission process protein 1	GO:0000266,GO:0016021,GO:0006915,GO:0005739,GO:0005743,GO:0007006	CG7772-PA						PF10558														
aly2818.3	Prestin	GO:0042391,GO:0015701,GO:0042493,GO:0015724,GO:0008271,GO:0051262,GO:0008272,GO:0034766,GO:0030507,GO:0005737,GO:0015085,GO:0090102,GO:0097066,GO:0016021,GO:0015499,GO:0015106,GO:0010996,GO:0015755,GO:1902074,GO:0016328,GO:0007605,GO:1902476,GO:0045793,GO:0016323,GO:0008360,GO:0005886,GO:0009751,GO:0002931,GO:0019531,GO:0019532,GO:0070588,GO:0015116,GO:0035864,GO:2000147,GO:0005452,GO:0015381	CG5485-PA						PF01740,PF00916	PS50801			G3DSA:3.30.750.24	SSF52091									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2818.4	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6457-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2818.5	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG8172-PF				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly28207.1	Probable nuclear hormone receptor HR3	GO:0016319,GO:0043565,GO:0006351,GO:0005515,GO:0000122,GO:0003700,GO:0005634,GO:0007552,GO:0003707,GO:0006355,GO:0045944,GO:0008270,GO:0043401,GO:0040034,GO:0004887,GO:0004879,GO:0000977	CG33183-PE										G3DSA:1.10.565.10	SSF48508			REACT_71						
aly28237.1	Unknown		n/a																				
aly28248.1	ATP-binding cassette sub-family G member 4	GO:0043190,GO:0042626,GO:0006641,GO:0005215,GO:0016021,GO:0016020,GO:0017127,GO:0033344,GO:0016887,GO:0005886,GO:0046982,GO:0055085,GO:0005524,GO:0042803	CG17646-PB						PF01061														
aly2828.1	Chloride channel protein 2	GO:0015629,GO:0030554,GO:0016020,GO:0034707,GO:0006821,GO:0005247,GO:0005254,GO:0055085	CG31116-PD						PF00654		PR00762,PR00762,PR00762		G3DSA:1.10.3080.10	SSF81340	32~52								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2828.10	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG4797-PB						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473			REACT_15518						
aly2828.11	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0022857,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly2828.12	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850		PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly2828.13	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly2828.14	Unknown		n/a																				
aly2828.15	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2828.2	Glycine receptor subunit alpha-2	GO:0030534,GO:0007218,GO:0034707,GO:0005230,GO:1902476,GO:0006811,GO:0009636,GO:0045472,GO:0045211,GO:0006821,GO:0043052,GO:0019183,GO:0019182,GO:0005887,GO:0007268,GO:0022824,GO:0016934,GO:0016021,GO:0030054,GO:0016594	CG7411-PA						PF02932,PF02931		PR00253,PR00253,PR00253,PR00253,PR00252,PR00252,PR00252	PS00236	G3DSA:1.20.58.390,G3DSA:2.70.170.10	SSF63712,SSF90112									
aly2828.3	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0005215,GO:0016021,GO:0005886,GO:0055085	CG4797-PB						PF00083	PS50850	PR00171,PR00171,PR00171	PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	206~226		REACT_15518						
aly2828.4	Lysine-specific demethylase 7A	GO:0006351,GO:0033522,GO:0006355,GO:0007379,GO:0034721,GO:0005634,GO:0030901,GO:0070544,GO:0016706,GO:0051864,GO:0071557,GO:0034647,GO:0008270,GO:0033169,GO:0003677,GO:0032454,GO:0035575,GO:0071558,GO:0035574,GO:0031519	CG11033-PB										G3DSA:3.30.40.10	SSF51197									
aly2828.5	Histone lysine demethylase PHF8	GO:0035064,GO:0034721,GO:0000082,GO:0034647,GO:0008270,GO:0003677,GO:0035574,GO:0035575,GO:0033522,GO:0005730,GO:0006325,GO:0005634,GO:0032452,GO:0005654,GO:0071557,GO:0033169,GO:0005506,GO:0071558,GO:0000278,GO:0031965,GO:0045893,GO:0031519,GO:0007420,GO:0007379,GO:0070544,GO:0016706,GO:0051864,GO:0045943,GO:0032454,GO:0006351,GO:0061188,GO:0003682	CG11033-PB				SM00558		PF02373	PS51184			G3DSA:2.60.120.650	SSF51197									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2828.6	Facilitated trehalose transporter Tret1-2 homolog	GO:0005355,GO:0035428,GO:0015992,GO:0016021,GO:0016020,GO:0046323,GO:0005887,GO:0005886,GO:0005351,GO:0055085	CG4797-PB						PF00083	PS50850	PR00171,PR00171,PR00171	PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473			REACT_15518						
aly2828.7	Unknown		n/a												294~314								
aly2828.8	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0022857,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	136~156								
aly2828.9	Facilitated trehalose transporter Tret1	GO:0022891,GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG4797-PB						PF00083	PS50850	PR00171,PR00171,PR00171	PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473			REACT_15518						
aly282962.1	Unknown		n/a																				
aly283.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly283.2	General transcription factor IIH subunit 1	GO:0001113,GO:0005634,GO:0006289,GO:0006355,GO:0000439,GO:0009411,GO:0006367,GO:0005675,GO:0000990,GO:0001111	CG8151-PB				SM00751,SM00751		PF08567,PF03909	PS50858,PS50858			G3DSA:2.30.29.30	SSF140383,SSF50729,SSF140383									
aly283.3	Transcription initiation factor TFIID subunit 3	GO:0008134,GO:0006355,GO:0006357,GO:0031208,GO:0008270,GO:0005515,GO:0005669,GO:0045944,GO:0003682,GO:0002039,GO:0005634,GO:0006351	CG2009-PA				SM00249,SM00576		PF07524,PF00628	PS50016		PS01359	G3DSA:3.30.40.10	SSF57903	882~925,561~600								
aly283.4	AFG3-like protein 2	GO:0016265,GO:0042552,GO:0004222,GO:0005783,GO:0048747,GO:0016021,GO:0060013,GO:0034982,GO:0005739,GO:0007528,GO:0005743,GO:0008053,GO:0046331,GO:0008270,GO:0016887,GO:0042407,GO:0006508,GO:0021675,GO:0007409,GO:0005524,GO:0040014	CG6512-PA	MF_01458			SM00382	TIGR01241	PF06480,PF00004,PF01434			PS00674	G3DSA:3.40.50.300,G3DSA:1.10.8.60	SSF140990,SSF52540									
aly283.5	Serine/threonine-protein kinase 40	GO:0005737,GO:0006468,GO:0035264,GO:0005977,GO:0060425,GO:0003016,GO:0005654,GO:0004674,GO:0043066,GO:0048286,GO:0010468,GO:0005524,GO:0043408	CG43143-PI				SM00220		PF00069	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly283.6	Syntaxin-12	GO:0006906,GO:0050821,GO:0005484,GO:0007067,GO:0031201,GO:0007140,GO:0010008,GO:0070062,GO:0016021,GO:0000281,GO:0007143,GO:0016081,GO:0000149,GO:0048278,GO:0045335,GO:0012505,GO:0007269,GO:0005886,GO:0031083,GO:0007110,GO:0016192,GO:0045121,GO:0000139,GO:0033344,GO:0005515,GO:0006886	CG11278-PA				SM00397,SM00503		PF05739,PF14523	PS50192		PS00914	G3DSA:1.20.58.70	SSF47661			REACT_11184						
aly283.7	Fibroblast growth factor receptor homolog 1	GO:0007492,GO:0007493,GO:0021782,GO:0007498,GO:0061320,GO:0018108,GO:0007419,GO:0010002,GO:0010001,GO:0050829,GO:0008543,GO:0008354,GO:0007417,GO:0007517,GO:0007431,GO:0016021,GO:0007369,GO:0008406,GO:0004713,GO:0016477,GO:0005524,GO:0008284,GO:0006468,GO:0008078,GO:0045089,GO:0007507,GO:0048747,GO:0007280,GO:0008360,GO:0005886,GO:0007522,GO:0007523,GO:0007525,GO:0008347,GO:0007506,GO:0001710,GO:0007500,GO:0007509,GO:0005007,GO:0048542	CG7223-PB				SM00409,SM00409,SM00409,SM00409,SM00219,SM00408,SM00408,SM00408,SM00408		PF00047,PF07714,PF07679,PF07679,PF07679	PS50835,PS50011,PS50835,PS50835,PS50835	PR00109,PR00109,PR00109,PR00109,PR00109	PS00107,PS00109	G3DSA:1.10.510.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.30.200.20,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF56112,SSF48726,SSF48726									
aly283.8	Glutathione-specific gamma-glutamylcyclotransferase 1	GO:0007219,GO:0070059,GO:0005829,GO:0005802,GO:0045746,GO:0006986,GO:0016746,GO:0022008,GO:0010955,GO:0005112	CG10365-PC						PF04752				G3DSA:3.10.490.10	SSF110857	11~31								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly283.9	StAR-related lipid transfer protein 13	GO:0007494,GO:0008258,GO:0008586,GO:0035024,GO:0007165,GO:0007274,GO:0007049,GO:0005811,GO:0031966,GO:0033109,GO:0005096,GO:0008289,GO:0035160,GO:0007173,GO:0005938,GO:0035277,GO:0007266,GO:0016323,GO:0007443,GO:0007424,GO:0007427,GO:0007391,GO:0005622,GO:0048814,GO:0005100	CG31319-PA				SM00324,SM00234		PF01852,PF00620	PS50238,PS50848			G3DSA:3.30.530.20,G3DSA:1.10.555.10	SSF55961,SSF48350,SSF47769	236~256,156~176		REACT_11044						
aly2835.1	Mitogen-activated protein kinase kinase kinase 13-B	GO:0034332,GO:0042059,GO:0006099,GO:0045886,GO:0007154,GO:0007169,GO:0046777,GO:0005737,GO:0007254,GO:0007435,GO:0016020,GO:0007476,GO:0004715,GO:0004713,GO:0004672,GO:0046529,GO:0048749,GO:0006468,GO:0051092,GO:0051017,GO:0018108,GO:0043277,GO:0090136,GO:0007424,GO:0007395,GO:0007391,GO:0005524,GO:0004709,GO:0005912	CG44128-PB						PF07714,PF07714	PS50011			G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10	SSF56112,SSF56112									
aly2835.2	Centrosomal protein of 120 kDa	GO:0005737,GO:0005694,GO:0005815	CG11908-PA						PF12416														
aly2837.1	Dolichol kinase	GO:0030176,GO:0004168,GO:0043048	CG8311-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2837.2	Aldehyde dehydrogenase, mitochondrial	GO:0005737,GO:0008774,GO:0004029,GO:0006117,GO:0005811,GO:0005739,GO:0045471,GO:0006068,GO:0008152,GO:0005759,GO:0006090,GO:0055114,GO:0016491	CG3752-PA						PF00171			PS00070,PS00687	G3DSA:3.40.605.10,G3DSA:3.40.309.10	SSF53720									
aly2837.3	Unknown		n/a																				
aly2841.1	Protein argonaute-2	GO:0033227,GO:0030423,GO:0030422,GO:0035087,GO:0048102,GO:0003676,GO:0070868,GO:0009047,GO:0005737,GO:0007367,GO:0004521,GO:0007349,GO:0016246,GO:0046872,GO:0070578,GO:0016032,GO:0035071,GO:0045071,GO:0090502,GO:0051607,GO:0007279,GO:0035195,GO:0005829,GO:0035197,GO:0035190,GO:0005515,GO:0016442,GO:0006413,GO:0003743	CG7439-PC				SM00950		PF02171	PS50822			G3DSA:3.30.420.10	SSF53098	34~54								
aly2841.2	Unknown		CG13606-PD																				
aly284141.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly28416.1	39S ribosomal protein L52, mitochondrial	GO:0003735,GO:0006412,GO:0005762	CG1577-PA												28~48								
aly284279.1	Sodium/potassium-transporting ATPase subunit alpha-4	GO:0007630,GO:0042391,GO:0051124,GO:0060439,GO:0007268,GO:0005890,GO:0050905,GO:0030641,GO:0001700,GO:0005634,GO:0019991,GO:0009612,GO:0005391,GO:0035158,GO:0035725,GO:0005886,GO:0006812,GO:0046872,GO:0015672,GO:0005524,GO:0007626,GO:0035152,GO:0007605,GO:0035159,GO:0030317,GO:0008324,GO:0016323,GO:0007283,GO:0008360,GO:0009266,GO:0008340,GO:0001894,GO:0006814,GO:0006813,GO:0008344,GO:0005918,GO:0009566,GO:0006754	CG5670-PA					TIGR01494	PF00689,PF00702		PR00121,PR00121,PR00121,PR00121,PR00121,PR00119,PR00119,PR00119,PR00119,PR00119	PS00154	G3DSA:1.20.1110.10,G3DSA:3.40.1110.10	SSF81665,SSF81665,SSF56784,SSF56784,SSF81660									
aly2844.1	Tetratricopeptide repeat protein 25	GO:0005575,GO:0003674,GO:0008150,GO:0005515	CG12993-PA										G3DSA:1.25.40.10										
aly2844.10	Unknown		CG30089-PA																				
aly2844.11	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2844.12	Unknown		n/a																				
aly2844.2	Dynein intermediate chain 3, ciliary	GO:0005737,GO:0042623,GO:0007605,GO:0005929,GO:0007018,GO:0005875,GO:0005515,GO:0005868,GO:0030286,GO:0005874,GO:0003774	CG6053-PC				SM00320,SM00320,SM00320,SM00320,SM00320			PS50294			G3DSA:2.130.10.10	SSF50978										
aly2844.3	Unknown		n/a																				
aly2844.4	Alpha-(1,3)-fucosyltransferase 6	GO:0018392,GO:0005797,GO:0006486,GO:0007399,GO:0036071,GO:0016021,GO:0016020,GO:0008417,GO:0000138,GO:0033932,GO:0005886,GO:0017060,GO:0032580,GO:0046920	CG6869-PA						PF00852,PF17039					SSF53756					UPA00378				
aly2844.5	Unknown		CG7730-PB						PF16013														
aly2844.6	Unknown	GO:0009306,GO:0005829,GO:0005811,GO:0007611,GO:0007616,GO:0003674,GO:0008355	CG8588-PF						PF16013														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2844.7	Unknown		n/a												196~216								
aly2844.8	EF-hand calcium-binding domain-containing protein 5	GO:0005201,GO:0031012,GO:0005576,GO:0008061,GO:0006030,GO:0005509	CG4090-PB				SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00494		PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607	PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625								
aly2844.9	28 kDa heat- and acid-stable phosphoprotein	GO:0044822,GO:0007165,GO:0008283	CG4438-PA						PF10252						146~169,113~133								
aly284490.1	Unknown		n/a																				
aly284610.1	ATP-dependent RNA helicase DDX18	GO:0016020,GO:0016049,GO:0005730,GO:0005634,GO:0008283,GO:0004004,GO:0003724,GO:0003676,GO:0010501,GO:0044822,GO:0005524	CG6375-PB				SM00490		PF00271,PF13959	PS51194			G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2847.1	Circadian clock-controlled protein	GO:0007623,GO:0005615	CG5867-PA				SM00700		PF06585														
aly2847.2	Phosphatidylinositol glycan anchor biosynthesis class U protein	GO:0044267,GO:0046425,GO:0016021,GO:0016020,GO:0005789,GO:0006501,GO:0042765,GO:0030176,GO:0005886,GO:0006506,GO:0042996,GO:0043687,GO:0016255	CG13089-PA						PF06728										UPA00196				
aly2847.3	RING-box protein 2	GO:0008270,GO:0051775,GO:0043224,GO:0005737,GO:0045116,GO:0080008,GO:0004842,GO:0005634,GO:0019788,GO:0005654,GO:0042787,GO:0005507,GO:0031146,GO:0031462,GO:0031463,GO:0061630,GO:0031466,GO:0031467,GO:0097602,GO:0016567,GO:0019005,GO:0005515	CG8998-PA				SM00184		PF12678	PS50089			G3DSA:3.30.40.10	SSF57850					UPA00143				
aly2847.4	Unknown	GO:0008745,GO:0009253	CG9380-PG																				
aly2847.5	Gamma-interferon-inducible lysosomal thiol reductase	GO:0005764,GO:0042590,GO:0005576,GO:0016667	CG41378-PB						PF03227				G3DSA:3.40.30.10	SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2847.6	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0016020,GO:0008643,GO:0022857,GO:0005886,GO:0055085	CG30035-PA					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171,PR00171,PR00171	PS00216,PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						
aly2847.7	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00217,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473	216~236		REACT_15518						
aly284940.1	Unknown		n/a										G3DSA:3.30.40.10	SSF57903	86~106								
aly2850.1	Rabphilin-3A	GO:0008021,GO:0019898,GO:0045202,GO:0030054,GO:0008565,GO:0016021,GO:0005543,GO:0005544,GO:0005546,GO:0017158,GO:0005509,GO:0043005,GO:0032403,GO:0030141,GO:0017137,GO:0030276,GO:0007269,GO:0005886,GO:0042301,GO:0007420,GO:0043234,GO:0008430,GO:0030672,GO:0016192,GO:0016079,GO:0005829,GO:0048791,GO:0005515,GO:0019905,GO:0070679,GO:0006886,GO:0048488,GO:0008270	CG11556-PA				SM00239		PF00168,PF00168	PS50004			G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2850.10	Transcription initiation protein SPT3 homolog	GO:0000124,GO:0006366,GO:0002230,GO:0043966,GO:0000123,GO:0006357,GO:0003700,GO:0005634,GO:0005654,GO:0003713,GO:0033276,GO:0030914,GO:0098779,GO:0006355,GO:0006325,GO:0045893,GO:0006367,GO:0003677,GO:0005669,GO:0046982,GO:0016578	CG3169-PA						PF02269				G3DSA:1.10.20.10	SSF47113									
aly2850.2	SH3 and PX domain-containing protein 2B	GO:0005737,GO:0007507,GO:0042169,GO:0002102,GO:0080025,GO:0010314,GO:0071800,GO:0030154,GO:0032266,GO:0060348,GO:0006801,GO:0001501,GO:0045600,GO:0001654,GO:0072657,GO:0005515,GO:0060612,GO:0042995,GO:0022617,GO:0030054,GO:0070273	CG10933-PA				SM00326,SM00326,SM00326		PF14604,PF00018,PF00018	PS50002,PS50002,PS50002			G3DSA:2.30.30.40,G3DSA:2.30.30.40,G3DSA:2.30.30.40	SSF50044,SSF50044,SSF50044									
aly2850.3	28S ribosomal protein S15, mitochondrial	GO:0040008,GO:0005739,GO:0006412,GO:0003735,GO:0005763,GO:0032543	CG4207-PA						PF00312				G3DSA:1.10.287.10	SSF47060	236~256		REACT_71						
aly2850.4	Vacuole membrane protein 1	GO:0007030,GO:0005783,GO:0009306,GO:0016021,GO:0033116,GO:0005774,GO:0003674,GO:0005886	CG32675-PA				SM00513			PS50800			G3DSA:1.10.720.30										
aly2850.5	DNA cross-link repair 1A protein	GO:0005654,GO:0016787,GO:0000715,GO:0006281	CG10018-PA						PF07522				G3DSA:3.60.15.10	SSF56281									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2850.6	N-acetylglucosamine-6-sulfatase	GO:0030203,GO:0006044,GO:0008449,GO:0005764,GO:0003824,GO:0008152,GO:0046872	CG18278-PA			PIRSF036666			PF00884			PS00523,PS00149	G3DSA:3.40.720.10,G3DSA:3.40.720.10,G3DSA:3.40.720.10	SSF53649,SSF53649		00531+3.1.6.14							
aly2850.7	Trypsin, alkaline C	GO:0004252,GO:0005615,GO:0006508	CG11836-PI				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly2850.8	Unknown	GO:0051259,GO:0006457,GO:0051087,GO:0005739,GO:0003674,GO:0008150	CG34246-PA						PF07743				G3DSA:1.20.1280.20	SSF47144	33~66								
aly2850.9	Iron-sulfur cluster co-chaperone protein HscB, mitochondrial	GO:0051259,GO:0005737,GO:0006457,GO:0005813,GO:0051087,GO:0005739,GO:0016226,GO:0003674,GO:0005886,GO:0008150,GO:0046872	CG34246-PA				SM00271	TIGR00714	PF07743,PF00226	PS50076			G3DSA:1.20.1280.20,G3DSA:1.10.287.110	SSF47144,SSF46565	145~174								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly28500.1	Niemann-Pick C1 protein	GO:0046718,GO:0005635,GO:0005783,GO:0071383,GO:0007591,GO:0030301,GO:0007291,GO:0004872,GO:0007041,GO:0070062,GO:0006486,GO:0032374,GO:0016021,GO:0016020,GO:0031579,GO:0005576,GO:0046686,GO:0048471,GO:0031902,GO:0005794,GO:0016125,GO:0060548,GO:0006914,GO:0007628,GO:0005887,GO:0045456,GO:0042632,GO:0008206,GO:0008158,GO:0015248,GO:0008203,GO:0006897,GO:0015485,GO:0090150,GO:0071404,GO:0045121,GO:0042493,GO:0016242,GO:0005764,GO:0005765,GO:0004888,GO:0033344,GO:2000189,GO:0007165	CG5722-PA										G3DSA:1.20.1640.10										
aly28509.1	Unknown	GO:0003735,GO:0006412,GO:0005762,GO:0003723	CG7494-PA										G3DSA:3.40.50.790	SSF56808									
aly285131.1	Unknown		n/a																				
aly28519.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly28522.1	Unknown		n/a																				
aly285367.1	Unknown		n/a												112~139								
aly2855.1	Tyrosine-protein kinase-like otk	GO:0031290,GO:0016021,GO:0004672,GO:0004713,GO:0005515,GO:0005886,GO:0007155,GO:0050839,GO:0005524,GO:0004872	CG8964-PA				SM00408,SM00409		PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly2855.10	Unknown		n/a																				
aly2855.11	Unknown		n/a												8~63								
aly2855.12	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2855.2	Tyrosine-protein kinase-like otk	GO:0090090,GO:0006468,GO:0031290,GO:0030215,GO:0016021,GO:0005886,GO:0007155,GO:0004714,GO:0004872,GO:0004672,GO:0017147,GO:0007411,GO:0050839,GO:0005524,GO:0004713	CG8967-PA				SM00219		PF07714	PS50011	PR00109,PR00109,PR00109,PR00109,PR00109	PS00109	G3DSA:1.10.510.10,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112										
aly2855.3	Transcription factor MafK	GO:0043565,GO:0007399,GO:0035071,GO:0048102,GO:0003700,GO:0005634,GO:0006366,GO:0005654,GO:0006355,GO:0060322,GO:0045944,GO:0006351,GO:0003677,GO:0000976,GO:0046982,GO:0042803	CG9954-PB				SM00338		PF03131	PS50217			G3DSA:1.10.880.10,G3DSA:1.20.5.170	SSF47454	94~114									
aly2855.4	Transposable element Tc1 transposase	GO:0004803,GO:0006313,GO:0004519,GO:0005634,GO:0015074,GO:0003677	n/a						PF13358														
aly2855.5	RNA polymerase-associated protein RTF1 homolog	GO:0001711,GO:0005730,GO:0003697,GO:0000122,GO:0005634,GO:0016055,GO:0044822,GO:0080182,GO:0045747,GO:0045944,GO:0035327,GO:0045893,GO:0006352,GO:0003677,GO:0016593,GO:0051571,GO:0019827,GO:0032968,GO:0001832	CG10955-PA																				
aly2855.6	RNA polymerase-associated protein Rtf1	GO:0007219,GO:0005634,GO:0051568,GO:0005654,GO:0045747,GO:0035327,GO:0045893,GO:0006352,GO:0003677,GO:0051571,GO:0042800	CG10955-PA				SM00719		PF03126	PS51360				SSF159042	352~404,476~103,263~290									
aly2855.7	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2855.8	Signal transducing adapter molecule 1	GO:0016197,GO:0007427,GO:0007269,GO:0008269,GO:0046425,GO:0006886,GO:2000274,GO:1903543,GO:0033565,GO:0007259,GO:1903551,GO:0043130,GO:0045743,GO:0005515,GO:0031901,GO:0042059,GO:0048488,GO:0042060	CG6521-PA				SM00326,SM00288		PF00790,PF00018	PS50002,PS50179,PS50330	PR00452,PR00452,PR00452,PR00452		G3DSA:1.25.40.90,G3DSA:2.30.30.40	SSF50044,SSF48464									
aly2855.9	Tyrosine-protein kinase transforming protein Fes	GO:0004715,GO:0006468,GO:0005515,GO:0008595,GO:0007465,GO:0005886,GO:0008288,GO:0018108,GO:0005524,GO:0045467,GO:0045466,GO:0004714,GO:0045464,GO:0046534,GO:0004713,GO:0005887,GO:0042067,GO:0008293,GO:0007169,GO:0045678	CG18085-PA				SM00219		PF01094,PF07714	PS50011	PR00109,PR00109,PR00109,PR00109,PR00109	PS00109,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:3.40.50.2300	SSF56112,SSF53822									
aly285911.1	Unknown		n/a																				
aly28646.1	Unknown		n/a																				
aly28666.1	Armadillo repeat-containing protein 3	GO:0005575,GO:0003674,GO:0008150,GO:0070062,GO:0005737	CG13326-PA						PF14381				G3DSA:1.20.120.20	SSF47857									
aly286781.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly286807.1	Unknown		n/a																				
aly287095.1	39S ribosomal protein L52, mitochondrial	GO:0003735,GO:0006412,GO:0005762	CG1577-PA												28~48								
aly28712.1	Monocarboxylate transporter 9	GO:0015718,GO:0015293,GO:0034220,GO:0008028,GO:0016021,GO:0015355,GO:0005886,GO:0055085,GO:0046415	CG8271-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly28715.1	Unknown		n/a																				
aly2874.1	Phosphatase and actin regulator 1	GO:0031032,GO:0031532,GO:0005829,GO:0008599,GO:0003779,GO:0004864,GO:0045202,GO:0005634,GO:0030054,GO:0043149	CG32264-PD				SM00707,SM00707,SM00707,SM00707		PF02755,PF02755,PF02755,PF02755	PS51073,PS51073,PS51073,PS51073													
aly2874.10	Sorting nexin-29	GO:0035091	CG5439-PA				SM00312,SM00593		PF02759,PF00787	PS50826,PS50195			G3DSA:3.30.1520.10	SSF140741,SSF64268	389~409,451~492,414~441								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2874.11	Cyclin-dependent kinase 11B	GO:0005737,GO:0004693,GO:0006468,GO:0008283,GO:0000278,GO:0051726,GO:0050684,GO:0005634,GO:0006915,GO:0006355,GO:0004674,GO:0008360,GO:0004672,GO:0007155,GO:0007067,GO:0044822,GO:0005524,GO:0001558	CG4268-PA				SM00220		PF00069	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112	536~556,291~321									
aly2874.12	Argininosuccinate lyase	GO:0004056,GO:0042450,GO:0006526,GO:0005212	CG9510-PB	MF_00006				TIGR00838	PF14698,PF00206		PR00145,PR00145,PR00145,PR00145,PR00145,PR00149,PR00149,PR00149,PR00149	PS00163	G3DSA:1.10.275.10,G3DSA:1.10.40.30,G3DSA:1.20.200.10	SSF48557	97~117	00250+4.3.2.1,00330+4.3.2.1		PWY-4984,PWY-5154,PWY-5,PWY-7400,PWY-4983	UPA00068				
aly2874.13	tRNA methyltransferase 10 homolog A	GO:0030488,GO:0000049,GO:0005730,GO:0005634,GO:0005575,GO:0008150,GO:0008168	CG14618-PA			PIRSF016323			PF01746	PS51675					65~85			PWY-7286,PWY-7285,PWY-6829					
aly2874.14	Probable serine hydrolase	GO:0017171,GO:0007586,GO:0009636,GO:0052689,GO:0008152,GO:0007275	CG7632-PA						PF00561				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2874.15	Probable chitinase 3	GO:0005737,GO:0005975,GO:0000272,GO:0005576,GO:0008061,GO:0004568,GO:0006030,GO:0006032,GO:0006036	CG18140-PB				SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00636,SM00636,SM00636,SM00636		PF00704,PF00704,PF00704,PF00704,PF00704,PF01607,PF01607,PF01607,PF01607,PF01607,PF01607	PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940		PS01095,PS01095	G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.10.50.10,G3DSA:3.10.50.10,G3DSA:3.10.50.10,G3DSA:3.10.50.10,G3DSA:3.10.50.10,G3DSA:3.10.50.10	SSF57625,SSF54556,SSF51445,SSF51445,SSF57625,SSF57625,SSF54556,SSF57625,SSF54556,SSF51445,SSF51445,SSF51445,SSF57625,SSF51445,SSF51445,SSF51445,SSF54556,SSF57625,SSF54556		00520+3.2.1.14		PWY-6902					
aly2874.16	Allantoinase	GO:0000256,GO:0004038,GO:0008270,GO:0006144,GO:0050897	CG6106-PA					TIGR03178	PF01979			PS00482	G3DSA:2.30.40.10,G3DSA:3.20.20.140	SSF51556,SSF51338,SSF51338		00230+3.5.2.5,00240+3.5.2.3		PWY-5697,PWY-5686,PWY-5698	UPA00395,UPA00070				
aly2874.17	Nuclear pore complex protein Nup155	GO:0016020,GO:0017056,GO:0005643,GO:0006606,GO:0005634,GO:0005635,GO:0031965,GO:0006913,GO:0006998,GO:0006406,GO:0086014	CG4579-PA					TIGR03178	PF08801,PF01979			PS00482	G3DSA:2.30.40.10,G3DSA:3.20.20.140	SSF51556,SSF51338,SSF51338	1227~1247	00230+3.5.2.5,00240+3.5.2.3	REACT_6185,REACT_474,REACT_15518	PWY-5697,PWY-5686,PWY-5698	UPA00070,UPA00395				
aly2874.18	Synaptogenesis protein syg-2	GO:0046331,GO:0005515,GO:0005886	CG12484-PB				SM00409,SM00409,SM00409,SM00408,SM00408,SM00408		PF08205,PF00047	PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726									
aly2874.19	Unknown	GO:0005515	n/a						PF07647	PS50105			G3DSA:1.10.150.50	SSF47769									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2874.2	Ribosomal protein S6 kinase beta-2	GO:0045087,GO:0051124,GO:0006909,GO:0045927,GO:0030307,GO:0016239,GO:0007165,GO:0007411,GO:0035556,GO:0008543,GO:0005737,GO:0042277,GO:0040007,GO:0048786,GO:0005654,GO:0004674,GO:0010508,GO:0004711,GO:0048477,GO:0046622,GO:0005524,GO:0006468,GO:0033554,GO:0007584,GO:0004672,GO:0006974,GO:0008361,GO:0038095,GO:0007173,GO:0048011,GO:0008340,GO:2001023,GO:0048015,GO:0007015,GO:0045793,GO:0030536,GO:0005840,GO:0040018,GO:0048813,GO:0005515,GO:0043491,GO:0045948,GO:0006412	CG10539-PA						PF00069,PF00433	PS50011		PS00107	G3DSA:3.30.200.20	SSF56112										
aly2874.20	Zinc carboxypeptidase A 1	GO:0007586,GO:0006508,GO:0004181,GO:0008270,GO:0005615	CG8945-PC				SM00631		PF02244,PF00246		PR00765,PR00765,PR00765,PR00765	PS00132	G3DSA:3.30.70.340,G3DSA:3.40.630.10	SSF53187,SSF54897									
aly2874.21	Beta-galactosidase	GO:0005764,GO:0048102,GO:0005975,GO:0035071,GO:0004565	CG3132-PA						PF01301		PR00742,PR00742,PR00742,PR00742,PR00742,PR00742,PR00742	PS01182	G3DSA:3.20.20.80,G3DSA:2.60.120.260	SSF49785,SSF51445		00600+3.2.1.23,00052+3.2.1.23,00531+3.2.1.23,00604+3.2.1.23,00511+3.2.1.23		PWY-6807					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2874.22	CAD protein	GO:0005737,GO:0000050,GO:0006207,GO:0006541,GO:0006526,GO:0006543,GO:0070046,GO:0004087,GO:0044205,GO:0004151,GO:0004088,GO:0046872,GO:0016597,GO:0070409,GO:0005524,GO:0004070	CG18572-PA	MF_01209,MF_00001			SM00851,SM01097,SM01096	TIGR01368,TIGR01369,TIGR00670	PF01979,PF00117,PF02142,PF02787,PF00185,PF02786,PF02786,PF00988,PF02729	PS50975,PS51273,PS50975	PR00101,PR00101,PR00101,PR00101,PR00101,PR00101,PR00100,PR00100,PR00100,PR00099,PR00099,PR00099,PR00099,PR00099,PR00098,PR00098,PR00098,PR00098,PR00098,PR00098,PR00098	PS00867,PS00866,PS00867,PS00482,PS00097,PS00483	G3DSA:3.30.470.20,G3DSA:3.40.50.1370,G3DSA:3.40.50.1380,G3DSA:1.10.1030.10,G3DSA:3.40.50.880,G3DSA:3.30.1490.20,G3DSA:3.40.50.20,G3DSA:3.30.470.20,G3DSA:3.40.50.20,G3DSA:3.50.30.20,G3DSA:3.20.20.140,G3DSA:3.20.20.140,G3DSA:3.40.50.1370	SSF51556,SSF53671,SSF52440,SSF56059,SSF48108,SSF56059,SSF52317,SSF52335,SSF51338,SSF51338,SSF52440,SSF52021	2244~2244	00250+2,1.3.2,00240+3.5.2.3,00250+6.3.5.5,00240+2.1.3.2,00240+6.3.5.5	REACT_1698	PWY-5154,PWY-7400,PWY-5686	UPA00070,UPA00068				
aly2874.23	Unknown		CG15865-PA						PF03281						964~971								
aly2874.24	Beta-galactosidase	GO:0005737,GO:0005794,GO:0016936,GO:0005975,GO:0070062,GO:0035071,GO:0005764,GO:0048102,GO:0004565,GO:0044262,GO:0019388	CG3132-PA										G3DSA:2.60.120.260	SSF49785									
aly2874.3	RPA-interacting protein A	GO:0005634,GO:0046872	n/a						PF14768				G3DSA:3.30.40.10,G3DSA:3.30.40.10										

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2874.4	MLX-interacting protein	GO:0005737,GO:0009744,GO:0070328,GO:1900402,GO:0006355,GO:0003700,GO:0005634,GO:0005741,GO:0006913,GO:0042593,GO:0006357,GO:0006351,GO:0005667,GO:0003677,GO:0046983,GO:0046982,GO:0008134	CG18362-PB				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459	734~775								
aly2874.5	ATP-binding cassette sub-family C member Sur	GO:0007507,GO:0042626,GO:0008281,GO:0008282,GO:0016021,GO:0016887,GO:0006031,GO:0001666,GO:0055085,GO:0005524	CG5772-PB				SM00382,SM00382		PF00005,PF00005,PF00664,PF00664	PS50929,PS50893,PS50929		PS00211	G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF90123,SSF52540,SSF52540,SSF90123									
aly2874.6	cGMP-dependent protein kinase, isozyme 1	GO:0030553,GO:0006468,GO:0030551,GO:0004674,GO:0005524,GO:0004692,GO:0007526	CG3324-PA			PIRSF000559	SM00220,SM00100,SM00100		PF00069,PF00027,PF00027	PS51285,PS50042,PS50011,PS50042	PR00103,PR00103,PR00103,PR00103	PS00888,PS00108	G3DSA:2.60.120.10,G3DSA:2.60.120.10,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF51206,SSF56112,SSF51206									
aly2874.7	RNA binding protein fox-1 homolog 1	GO:0005737,GO:0044212,GO:0008022,GO:0050885,GO:0008380,GO:0007399,GO:0005634,GO:0043484,GO:0007474,GO:0000166,GO:0045893,GO:0003723,GO:0005802,GO:0006397,GO:0048477,GO:0008134,GO:0003729	CG32062-PH				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928	95~115								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2874.8	Integrin beta-PS	GO:0016203,GO:0007494,GO:0030336,GO:0016339,GO:0035160,GO:0007160,GO:0035001,GO:0004872,GO:0005927,GO:0007411,GO:0007298,GO:0005925,GO:0003344,GO:0007417,GO:0007517,GO:0007431,GO:0034446,GO:0051492,GO:0007475,GO:0048803,GO:0009925,GO:0016477,GO:0021551,GO:0033627,GO:0006930,GO:0005178,GO:0031589,GO:0016328,GO:0007608,GO:0016340,GO:0030718,GO:0016324,GO:0007601,GO:0031252,GO:0007629,GO:0008305,GO:0008360,GO:0045214,GO:0005887,GO:0005886,GO:0007155,GO:0008340,GO:0007157,GO:0050839,GO:0035099,GO:0007015,GO:0007427,GO:0007426,GO:0007377,GO:0007391,GO:0007229,GO:0007508,GO:0005515,GO:0046982,GO:0043034	CG1560-PA			PIRSF002512	SM00187		PF08725,PF00362,PF07965,PF07974	PS51257	PR01186,PR01186,PR01186,PR01186,PR01186,PR01186,PR01186,PR01186,PR01186,PR01186	PS00243,PS00243	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:3.40.50.410,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:1.20.5.100,G3DSA:1.20.5.630	SSF103575,SSF57196,SSF69687,SSF69179,SSF53300			REACT_13552							
aly2874.9	Kinesin heavy chain	GO:0019227,GO:0008103,GO:0007269,GO:0035371,GO:0008152,GO:0007303,GO:0008088,GO:0030011,GO:0007411,GO:0005875,GO:0061572,GO:0005737,GO:0040023,GO:0006886,GO:0047497,GO:0005739,GO:0046785,GO:0016482,GO:0005871,GO:0003774,GO:0005524,GO:0048312,GO:0048311,GO:0051299,GO:0048741,GO:0051012,GO:0008017,GO:0007317,GO:0007315,GO:0010970,GO:0007409,GO:0007310,GO:0001754,GO:0008345,GO:0045451,GO:0008574,GO:0007018,GO:0048813,GO:0048812,GO:0003777,GO:0035617,GO:0046843	CG7765-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10	SSF52540	807~827,837~892,615~687,429~547,712~805,338~379								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2875.1	Homeobox protein aristaless	GO:0043234,GO:0043565,GO:0007480,GO:0003700,GO:0005634,GO:0006355,GO:0035015,GO:0035218,GO:0045747,GO:0048800,GO:0022416,GO:0000976,GO:0003677,GO:0045892,GO:0007449	CG3935-PA				SM00389		PF00046,PF03826	PS50071,PS50803	PR00031,PR00031	PS00027	G3DSA:1.10.10.60	SSF46689	260~280								
aly2875.2	Homeobox protein aristaless	GO:0043234,GO:0043565,GO:0007480,GO:0003700,GO:0005634,GO:0006355,GO:0035015,GO:0035218,GO:0045747,GO:0048800,GO:0022416,GO:0000976,GO:0045892,GO:0007449	CG3935-PA				SM00389		PF03826,PF00046	PS50803,PS50071	PR00031,PR00031	PS00027	G3DSA:1.10.10.60	SSF46689	237~257								
aly2877.1	Odorant receptor 59a	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG9820-PA						PF02949														
aly2877.2	Unknown	GO:0005549,GO:0016020,GO:0007608,GO:0004984	n/a						PF02949						132~152								
aly2877.3	Odorant receptor Or1	GO:0005549,GO:0007608,GO:0042048,GO:0016021,GO:0016020,GO:0050911,GO:0004888,GO:0005886,GO:0004984	CG3206-PA						PF02949						380~389								
aly2877.4	Unknown	GO:0005549,GO:0016020,GO:0007608,GO:0004984	n/a						PF02949														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2877.5	Unknown	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0004984	CG10759-PA						PF02949														
aly2877.6	Queuine tRNA-ribosyltransferase subunit QTRTD1 homolog	GO:0006400,GO:0008616,GO:0008270,GO:0008479	CG3434-PA					TIGR00449	PF01702				G3DSA:3.20.20.105	SSF51713				PWY-6700	UPA00392				
aly2877.7	Very low-density lipoprotein receptor	GO:0038026,GO:0038025,GO:0071222,GO:0034447,GO:0048306,GO:0042493,GO:0021517,GO:0005905,GO:0032869,GO:0030229,GO:0021987,GO:0001948,GO:0045177,GO:0005615,GO:1900006,GO:0000122,GO:0016021,GO:0016020,GO:0005509,GO:0034436,GO:0071456,GO:0048471,GO:0007584,GO:0034361,GO:0043235,GO:0009986,GO:0034437,GO:0006869,GO:0034189,GO:0042149,GO:0034185,GO:0008203,GO:0007507,GO:0071347,GO:0006898,GO:0005041,GO:0048813,GO:0042953,GO:0045860,GO:0005634,GO:0004872	CG31094-PK				SM00181,SM00181,SM00181,SM00181,SM00179,SM00179,SM00135,SM00135,SM00135,SM00135,SM00135,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192		PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF14670,PF14670,PF07645,PF00058,PF00058	PS51120,PS51120,PS51120,PS50068,PS50068,PS51120,PS50068,PS50068,PS51120,PS50068,PS50068,PS50068	PR00261,PR00261,PR00261,PR00261,PR00261,PR00261,PR00261	PS01209,PS00010,PS00010,PS01187,PS01209,PS01186,PS01209,PS01209,PS01209,PS01209	G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:2.120.10.30	SSF57424,SSF57184,SSF57184,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF63825,SSF57424								
aly2877.8	Unknown		n/a																				
aly28779.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly28779.10	Hemolin	GO:0016319,GO:0048675,GO:0050808,GO:0045924,GO:0030175,GO:0008049,GO:0005615,GO:0019991,GO:0048812,GO:0060857,GO:0005509,GO:0008366,GO:0035151,GO:0016328,GO:0072499,GO:0045087,GO:0035011,GO:0008050,GO:0007173,GO:0048036,GO:0007409,GO:0005886,GO:0005919,GO:0005918,GO:0007560,G	CG1634-PG				SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408		PF00047,PF07679,PF07679,PF13927	PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726									
aly28779.11	Unknown		n/a																				
aly28779.2	Gastrula zinc finger protein XlCGF26.1 (Fragment)	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG8319-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly28779.3	Zinc finger protein 287	GO:0003700,GO:0005634,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG15269-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly28779.4	Unknown		n/a				SM00868		PF07776					SSF57716									
aly28779.5	Unknown		n/a				SM00355,SM00355,SM00355						G3DSA:3.30.160.60										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly28779.6	Zinc finger protein 596	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF00096,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly28779.7	Zinc finger protein 208	GO:0045931,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178,GO:0008270	CG14938-PA				SM00614,SM00614,SM00614,SM00355		PF00096	PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly28779.8	Zinc finger protein 850	GO:0045931,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00614,SM00614,SM00614,SM00614,SM00355			PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:2.10.110.10,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	636~656								
aly28779.9	Protein TEX261	GO:0006888,GO:0030176,GO:0097020,GO:0030134,GO:0030173	CG3500-PA						PF04148														
aly2879.1	Lachesin	GO:0019897,GO:0048149,GO:0007616,GO:0007615,GO:0007465,GO:0007611,GO:0031225,GO:0045466,GO:0004714,GO:0005886,GO:0007155,GO:0007169,GO:0007156,GO:0008355	CG6669-PA				SM00409,SM00408		PF13895	PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726									
aly2879.2	Unknown	GO:0019897,GO:0048149,GO:0007616,GO:0007615,GO:0007465,GO:0007611,GO:0045466,GO:0005515,GO:0007156,GO:0008355	CG6669-PA							PS50853			G3DSA:2.60.40.10	SSF49265									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2879.3	Zinc finger protein 2 homolog	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG10959-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13465,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly2879.4	Zinc finger protein 345	GO:0005737,GO:0005819,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0005876,GO:0006351	CG8474-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57716,SSF57667,SSF57667	219~239								
aly28816.1	Coronin-6	GO:0003779,GO:0072686,GO:0015629,GO:0030036,GO:0050832,GO:0051015,GO:0005515,GO:0007527	CG9446-PE				SM00320,SM00320,SM00320		PF00400	PS50082,PS50294,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978									
aly28824.1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1	GO:0051384,GO:0016311,GO:0033133,GO:0061621,GO:0044281,GO:0042594,GO:0032868,GO:0003873,GO:0035556,GO:0006096,GO:0006094,GO:0043540,GO:0007476,GO:0005524,GO:0006112,GO:0042802,GO:0031100,GO:0033762,GO:0051591,GO:0070095,GO:0005975,GO:0005829,GO:0004331,GO:0006006,GO:0006000,GO:0006003	CG3400-PG			PIRSF000709			PF01591				G3DSA:3.40.50.300			00051+2.7.1.105+3.1.3.46	REACT_474						
aly28827.1	28S ribosomal protein S18b, mitochondrial	GO:0032543,GO:0005840,GO:0005654,GO:0005739,GO:0005622,GO:0003735,GO:0005763,GO:0006412,GO:0030054	CG10757-PA										G3DSA:4.10.640.10	SSF46911									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly28831.1	Unknown		n/a																				
aly28831.2	Unknown		n/a						PF08163				G3DSA:1.25.10.10										
aly28831.3	Unknown		n/a																				
aly28831.4	Unknown		n/a																				
aly2891.1	Zinc transporter ZIP1	GO:0055069,GO:0016021,GO:0016324,GO:0008344,GO:0016020,GO:0005622,GO:0030001,GO:0071577,GO:0005886,GO:0008340,GO:0046873,GO:0016323,GO:0055085	CG9428-PA						PF02535						118~145								
aly2891.2	Putative transcription factor SOX-14	GO:0043565,GO:0003700,GO:0005634,GO:0007552,GO:0016322,GO:0006355,GO:0048813,GO:0006357,GO:0008301,GO:0006351	CG3090-PA				SM00398		PF00505	PS50118			G3DSA:1.10.30.10	SSF47095									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly29.1	Unknown	GO:0005737,GO:0010629,GO:0005634,GO:0007165	CG7047-PB											SSF81296									
aly29.10	Pre-rRNA-processing protein esf2	GO:0005730,GO:0005634,GO:0000166,GO:0006364,GO:0003723,GO:0003676,GO:0034462,GO:0000447,GO:0000480,GO:0022008,GO:0000472	CG32708-PA						PF00076	PS50102			G3DSA:3.30.70.330	SSF54928	154~174								
aly29.11	Unknown		n/a						PF16037														
aly29.12	Unknown	GO:0005575,GO:0008150,GO:0003674	CG1715-PA												18~38								
aly29.13	Unknown	GO:0004930,GO:0007186,GO:0016021,GO:0008188	CG13995-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly29.2	Tubulin gamma-1 chain	GO:0000242,GO:0005200,GO:0000086,GO:0055037,GO:0008275,GO:0008274,GO:0000226,GO:0051306,GO:0007067,GO:0010457,GO:0005874,GO:0000278,GO:0005737,GO:0007020,GO:0045177,GO:0005819,GO:0005813,GO:0005814,GO:0005815,GO:0051011,GO:0005525,GO:0031513,GO:0051298,GO:0036064,GO:0000212,GO:0051297,GO:0003924,GO:0031252,GO:0031122,GO:0005881,GO:0007052,GO:0000794,GO:0006184,GO:0045298,GO:0051258,GO:0007017,GO:0005827,GO:0006996,GO:0051726,GO:0005829,GO:0000930,GO:0000931,GO:0019001	CG3157-PA				SM00864,SM00865		PF00091,PF03953		PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01164,PR01164,PR01164,PR01164,PR01164,PR01164	PS00227	G3DSA:1.10.287.600,G3DSA:3.40.50.1440,G3DSA:3.30.1330.20	SSF52490,SSF55307			REACT_152							
aly29.3	Alpha-endosulfine	GO:0005737,GO:0051445,GO:0019212,GO:0034047,GO:0000086,GO:0007584,GO:0019901,GO:0005654,GO:0035308,GO:0007052,GO:0004864,GO:0051721,GO:0008601,GO:0030104,GO:0017098,GO:0007067,GO:0007088,GO:0048477,GO:0043086,GO:0051301	CG6513-PA																				
aly29.4	Structural maintenance of chromosomes protein 6	GO:0000781,GO:0016605,GO:0090398,GO:0006281,GO:0000724,GO:0030915,GO:0006974,GO:0031000,GO:0000722,GO:0005524	CG5524-PA						PF13476				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	241~261,316~343,281~308								
aly29.5	Structural maintenance of chromosomes protein 6	GO:0000781,GO:0016605,GO:0090398,GO:0051276,GO:0000724,GO:0006281,GO:0031000,GO:0006974,GO:0030915,GO:0005515,GO:0005694,GO:0000722,GO:0005524	CG5524-PA						PF06470														
aly29.6	Structural maintenance of chromosomes protein 6	GO:0051321,GO:0033676,GO:0006281,GO:0005634,GO:0000724,GO:0030915,GO:0006974,GO:0031000,GO:0005524	CG5524-PA										G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly29.7	G1/S-specific cyclin-E	GO:0000082,GO:0035019,GO:0007307,GO:0045035,GO:0007277,GO:0035736,GO:0005634,GO:0044719,GO:0007259,GO:0043065,GO:0016538,GO:0048477,GO:0060564,GO:0042127,GO:0048665,GO:0000278,GO:0009987,GO:0006974,GO:0045859,GO:0008360,GO:0007155,GO:0019908,GO:0007400,GO:0007423,GO:0007422,GO:0006275,GO:0005515,GO:0007096,GO:0001932,GO:1900087	CG3938-PF				SM00385		PF00134,PF02984			PS00292	G3DSA:1.10.472.10,G3DSA:1.10.472.10	SSF47954,SSF47954										
aly29.8	Protein pigeon	GO:0005575,GO:0008150,GO:0003674	CG10739-PA						PF14959														
aly29.9	Protein RTF2 homolog		CG6443-PA						PF04641														
aly29046.1	Unknown		n/a																				
aly291.1	Unknown	GO:0007476,GO:0004331,GO:0003873,GO:0006000,GO:0005524,GO:0006003	CG3400-PG																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly291.10	Transformer-2 protein homolog beta	GO:0036002,GO:0000381,GO:0000003,GO:0006397,GO:0019101,GO:0030237,GO:0005634,GO:0019102,GO:0000302,GO:0000398,GO:0000166,GO:0071011,GO:0007283,GO:0003723,GO:0005515,GO:0048024,GO:0048026,GO:0003729,GO:0007530,GO:0042802,GO:0000245	CG10128-PG				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928										
aly291.11	Valine--tRNA ligase	GO:0005737,GO:0004818,GO:0005829,GO:0006438,GO:0005739,GO:0000166,GO:0010467,GO:0002161,GO:0006418,GO:0004832,GO:0022008,GO:0005524	CG4062-PC	MF_02004				TIGR00422	PF08264,PF00133		PR00986,PR00986,PR00986,PR00986,PR00986	PS00178	G3DSA:3.90.740.10,G3DSA:1.10.730.10,G3DSA:3.40.50.620,G3DSA:3.40.50.620,G3DSA:3.40.50.620	SSF47323,SSF50677,SSF52374,SSF52374,SSF52374	972~995,252~42	00970+6.1.1.9	REACT_71							
aly291.12	CCR4-NOT transcription complex subunit 3	GO:0005737,GO:0005829,GO:0000288,GO:0000289,GO:0001829,GO:0005634,GO:2000036,GO:0000932,GO:0010467,GO:0006355,GO:0030014,GO:0006351,GO:0005515,GO:0017148,GO:0006417,GO:0022008,GO:0006402,GO:0031047	CG8426-PA						PF04153								REACT_21257						
aly291.13	CCR4-NOT transcription complex subunit 3	GO:0005737,GO:0005829,GO:0000288,GO:0000289,GO:0001829,GO:0005634,GO:2000036,GO:0000932,GO:0010467,GO:0006355,GO:0030014,GO:0006351,GO:0005515,GO:0017148,GO:0006417,GO:0022008,GO:0006402,GO:0031047	CG8426-PA			PIRSF005290			PF04065						41~68,165~202									
aly291.14	Unknown	GO:0003677	CG8359-PA				SM00595		PF02944,PF10545	PS51031,PS51029													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly291.15	Lutropin-choriogonadotropic hormone receptor	GO:0009755,GO:0004930,GO:0007186,GO:0016021,GO:0005886,GO:0005887,GO:0008188,GO:0004964,GO:0016500,GO:0042562	CG7665-PA						PF00001,PF13855	PS50262	PR00373,PR00373,PR00373,PR00373,PR00373,PR00373,PR00373,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:3.80.10.10	SSF81321,SSF52058			REACT_14797						
aly291.16	AN1-type zinc finger protein 1	GO:0008270	CG12795-PB										G3DSA:4.10.1110.10,G3DSA:4.10.1110.10	SSF118310,SSF118310									
aly291.17	Probable ATP-dependent RNA helicase DDX47	GO:0008625,GO:0005730,GO:0044822,GO:0016020,GO:0004004,GO:0006364,GO:0003676,GO:0010501,GO:0008380,GO:0005524,GO:0006397	CG9253-PA				SM00490,SM00487		PF00270,PF00271	PS51194,PS51192		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	373~393								
aly291.18	Kinesin-like protein KIF12	GO:0005737,GO:0016887,GO:0005834,GO:0005874,GO:0008017,GO:0007018,GO:0008152,GO:0005524,GO:0004871,GO:0005871,GO:0007186,GO:0003777,GO:0070062	CG43323-PB				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10	SSF52540	580~600,506~526								
aly291.19	Unknown		CG12911-PD																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly291.2	Unknown		n/a																				
aly291.20	Unknown		n/a																				
aly291.21	Unknown		n/a												263~283								
aly291.3	Unknown		n/a																				
aly291.4	Down syndrome cell adhesion molecule homolog	GO:0007626,GO:0042327,GO:0060060,GO:0048842,GO:0016021,GO:0007476,GO:0030426,GO:0030424,GO:0070593,GO:0048813,GO:0007162,GO:0005886,GO:0007155	CG15312-PD				SM00408,SM00060,SM00409		PF07679	PS50853,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF49265									
aly291.5	Kinase suppressor of Ras 2	GO:0005886,GO:0006468,GO:0007426,GO:0004674,GO:0019992,GO:0005829,GO:0019722,GO:0007476,GO:0005078,GO:0043410,GO:0008595,GO:0004713,GO:0031434,GO:0004672,GO:0008293,GO:0007265,GO:0046872,GO:0005524,GO:0007165	CG2899-PA				SM00220,SM00109		PF13543,PF00130,PF07714	PS50011,PS50081		PS00107,PS00108,PS00479	G3DSA:3.30.200.20,G3DSA:3.30.60.20,G3DSA:1.10.510.10	SSF57889,SSF56112	100~127								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly291.6	Exosome complex component RRP40	GO:0045190,GO:0071049,GO:0005737,GO:0005730,GO:0045830,GO:0006364,GO:0010468,GO:0034475,GO:0071051,GO:0071035,GO:0071034,GO:0071038,GO:0035327,GO:0000467,GO:0043928,GO:0000178,GO:0045006,GO:0000176,GO:0000177,GO:0000175,GO:0034427,GO:0003723	CG31938-PA						PF15985					SSF110324,SSF54791,SSF50249										
aly291.7	Probable RNA 3'-terminal phosphate cyclase-like protein	GO:0005730,GO:0005634,GO:0004521,GO:0042254,GO:0000479,GO:0003723,GO:0009267,GO:0006396,GO:0003963	CG11130-PA			PIRSF005378		TIGR03400	PF05189,PF01137			PS01287	G3DSA:3.65.10.20,G3DSA:3.65.10.20	SSF55205										
aly291.8	Chitotriosidase 1	GO:0005975,GO:0005615,GO:0008843,GO:0009617,GO:0000272,GO:0005764,GO:0005576,GO:0008061,GO:0006955,GO:0004568,GO:0006032	CG43374-PC				SM00636,SM00494,SM00494		PF00704,PF01607,PF01607	PS50940,PS50940		PS01095	G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.10.50.10	SSF54556,SSF57625,SSF57625,SSF51445,SSF51445	174~194	00520+3.2.1.14		PWY-6902					
aly291.9	Hermansky-Pudlak syndrome 4 protein	GO:0007599,GO:0007596,GO:0050821,GO:0003674,GO:0007040,GO:0035280,GO:0005737,GO:0016020,GO:0031902,GO:0042803,GO:0030318,GO:0048075,GO:0006605,GO:0060967,GO:1903955,GO:0070923,GO:0042470,GO:0031085,GO:0042827,GO:0005764,GO:0005765,GO:0046983	CG4966-PA																				
aly2919.1	Unknown	GO:0004383,GO:0004872	CG14877-PA										G3DSA:3.40.50.2300	SSF53822									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2919.2	Unknown		n/a																				
aly2919.3	Unknown	GO:0004383,GO:0004872	CG14877-PA																				
aly292.1	mRNA-capping enzyme	GO:0004484,GO:0008138,GO:0006470,GO:0004725,GO:0004651,GO:0006370,GO:0050355,GO:0008192,GO:0005634,GO:0006396,GO:0005525	CG1810-PA			PIRSF036958			PF03919,PF01331				G3DSA:3.30.470.30,G3DSA:2.40.50.140	SSF56091,SSF50249				PWY-7375					
aly292.2	Beta-lactamase-like protein 2 homolog	GO:0005575,GO:0003674,GO:0046872,GO:0008150,GO:0016787	CG12375-PA				SM00849		PF00753				G3DSA:3.60.15.10	SSF56281									
aly292.3	NADH dehydrogenase [ubiqui] flavoprotein 1, mitochondrial	GO:0051287,GO:0051539,GO:0008137,GO:0005739,GO:0006120,GO:0005743,GO:0005747,GO:0010181,GO:0046872,GO:0003954,GO:0055114	CG9140-PA				SM00928	TIGR01959	PF10589,PF01512,PF10531			PS00644,PS00645		SSF140490,SSF142019,SSF142984									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly292.4	Tribbles homolog 2	GO:0032436,GO:0043405,GO:0055106,GO:0005737,GO:0031434,GO:0005634,GO:0007369,GO:0004674,GO:0004672,GO:0045839,GO:0005524,GO:0042803,GO:0005856,GO:0006468,GO:0008134,GO:0045081,GO:0004860,GO:0043433,GO:0045599,GO:0007370,GO:0031625,GO:0051726,GO:0016772,GO:0051443,GO:2000060,GO:0046982	CG5408-PA				SM00220		PF00069	PS50011			G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10	SSF56112										
aly292.5	Transcription initiation factor IIB	GO:0005667,GO:0001174,GO:0005634,GO:0051101,GO:0006357,GO:0008270,GO:0006367,GO:0017025,GO:0008134	CG5193-PB				SM00385,SM00385		PF00382,PF00382,PF08271	PS51134	PR00685,PR00685,PR00685,PR00685,PR00685,PR00685,PR00685,PR00685	PS00782,PS00782	G3DSA:2.20.25.10,G3DSA:1.10.472.10,G3DSA:1.10.472.10	SSF57783,SSF47954,SSF47954			REACT_1788						
aly292.6	Signal peptide, CUB and EGF like domain-containing protein 2	GO:0019897,GO:0005509,GO:0042802,GO:0005615	n/a				SM00042,SM00032		PF00431	PS01180,PS50923			G3DSA:2.60.120.290,G3DSA:2.10.70.10	SSF57535,SSF49854									
aly2928.1	Unknown		n/a																				
aly2928.10	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2928.11	Unknown		n/a							PS50172					117~137								
aly2928.12	Eukaryotic translation initiation factor 3 subunit F	GO:0005852,GO:0035071,GO:0048102,GO:0016282,GO:0006446,GO:0045747,GO:0005515,GO:0033290,GO:0001731,GO:0006413,GO:0003743	CG9769-PA				SM00232		PF01398,PF13012														
aly2928.13	BolA-like protein 3	GO:0005576	n/a						PF01722				G3DSA:3.30.70.1500	SSF82657									
aly2928.14	Ribosome biogenesis protein BOP1 homolog	GO:0035206,GO:0005730,GO:0030687,GO:0042254,GO:0005654,GO:0000463,GO:0006364,GO:0000466,GO:0043021,GO:0022008	CG5033-PA	MF_03027			SM01035,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF08145,PF08145	PS50294,PS50082,PS50294		PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978									
aly2928.15	Rho GTPase-activating protein 4	GO:0005070,GO:0005737,GO:0007264,GO:0007010,GO:0043547,GO:0030336,GO:0097190,GO:0005829,GO:0005096,GO:0005654,GO:0048365,GO:0043065,GO:0051056,GO:0009967,GO:0048011,GO:0007266,GO:0005925	n/a						PF00611					SSF103657	69~96								
aly2928.16	Protein charlatan	GO:0043565,GO:0001700,GO:0007458,GO:0007423,GO:0007399,GO:0000122,GO:0003700,GO:0005634,GO:0007422,GO:0003705,GO:0009612,GO:0001654,GO:0048813,GO:0045944,GO:0006351,GO:0005515,GO:0042683,GO:0046872,GO:0001078,GO:0007526	CG11798-PF				SM00355,SM00355,SM00355,SM00355							SSF57667	474~485								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2928.17	Regulator of G protein signaling 20	GO:0005737,GO:0038032,GO:0005802,GO:0005634,GO:0016020,GO:0005096,GO:0008277,GO:0005886	CG5036-PB				SM00315		PF00615	PS50132	PR01301,PR01301,PR01301,PR01301		G3DSA:1.10.167.10,G3DSA:1.10.196.10	SSF48097									
aly2928.2	Unknown		n/a																				
aly2928.3	Unknown		n/a																				
aly2928.4	Unknown		n/a																				
aly2928.5	Unknown		n/a																				
aly2928.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2928.7	Unknown		n/a																				
aly2928.8	Unknown		n/a																				
aly2928.9	Unknown		n/a																				
aly29286.1	Unknown		CG9170-PB												152~172								
aly2931.1	Unknown		n/a																				
aly2931.10	Unknown		n/a												33~53								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2931.11	Unknown		n/a																				
aly2931.2	Unknown		n/a																				
aly2931.3	Unknown		n/a																				
aly2931.4	Unknown		n/a																				
aly2931.5	Unknown		n/a																				
aly2931.6	Unknown	GO:0003676	n/a						PF03184														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2931.7	Unknown		n/a												897~917								
aly2931.8	Unknown		n/a																				
aly2931.9	Unknown		n/a																				
aly2932.1	Unknown		n/a																				
aly2932.2	Unknown		n/a																				
aly29383.1	Unknown		n/a												117~137,34~57								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly294.1	Zinc finger BED domain-containing protein 4	GO:0005737,GO:0005634,GO:0005654,GO:0003676,GO:0003677,GO:0046983,GO:0046872	CG13775-PA				SM00614		PF02892	PS50808				SSF53098,SSF140996,SSF57667									
aly294.10	Lysine-specific demethylase 6A	GO:0003016,GO:0032525,GO:0048568,GO:0072358,GO:0035264,GO:0051568,GO:0001701,GO:0005634,GO:0032452,GO:0045746,GO:0016577,GO:0071557,GO:0001843,GO:0046872,GO:0071558,GO:0010468,GO:0042802,GO:0008285,GO:0048570,GO:0021915,GO:0048333,GO:0042060,GO:0003007,GO:0060070,GO:0035327,GO:0007507,GO:0051213,GO:0005705,GO:0035097,GO:0061086,GO:0045498,GO:0005515,GO:0000978,GO:0044666	CG5640-PA				SM00558,SM00028,SM00028,SM00028,SM00028,SM00028		PF13414,PF02373,PF00515	PS50005,PS50293,PS50005,PS50005,PS51184,PS50005			G3DSA:1.25.40.10	SSF48452,SSF51197,SSF51197									
aly294.11	39S ribosomal protein L42, mitochondrial	GO:0070126,GO:0006996,GO:0070124,GO:0070125,GO:0044822,GO:0005886,GO:0005739,GO:0032543,GO:0003735,GO:0005743,GO:0005761,GO:0005762,GO:0005763,GO:0006412	CG12921-PA						PF10210														
aly294.12	Microspherule protein 1	GO:0005705,GO:0015629,GO:0031011,GO:0046972,GO:0030054,GO:0005737,GO:0000123,GO:0005730,GO:0005634,GO:0043995,GO:0043996,GO:0005654,GO:0071339,GO:0006351,GO:0006281,GO:0022008,GO:0006310,GO:0043982,GO:0044545,GO:0043981,GO:0043984,GO:0006355,GO:0045944,GO:0007099,GO:0005515,GO:0007095	CG1135-PA				SM00240		PF00498,PF13325	PS50006			G3DSA:2.60.200.20	SSF49879									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly294.13	Unknown		n/a																				
aly294.14	Cleft lip and palate transmembrane protein 1-like protein	GO:0016021,GO:0006915	CG4332-PA						PF05602														
aly294.15	Putative phosphoenolpyruvate synthase	GO:0016301,GO:0005524	n/a						PF01326,PF00391				G3DSA:3.30.470.20,G3DSA:3.50.30.10,G3DSA:3.30.1490.20	SSF52009,SSF56059									
aly294.16	Unknown	GO:0005737,GO:0019010	CG10527-PA				SM00696		PF11901														
aly294.17	Unknown		n/a												204~224								
aly294.18	Unknown		n/a												119~139								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly294.19	Unknown		n/a																				
aly294.2	Protein flightless-1	GO:0030239,GO:0060438,GO:0016021,GO:0008039,GO:0051014,GO:0003779,GO:0007629,GO:0010004,GO:0005509,GO:0005515,GO:0005886,GO:0007527	CG3413-PD							PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52075	478~505								
aly294.20	Unknown	GO:0005737,GO:0019010	CG10527-PA				SM00696		PF11901,PF12248														
aly294.21	C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8	GO:0005737,GO:0004867,GO:0005886,GO:0005615,GO:0019010	CG10527-PA				SM00696,SM00696		PF11901,PF11901,PF12248,PF12248														
aly294.22	RNA-binding protein 38	GO:0035062,GO:0033119,GO:0030154,GO:0007293,GO:0000184,GO:0000785,GO:0007297,GO:0003676,GO:0000166,GO:0008069,GO:0005737,GO:0000381,GO:0005730,GO:0005634,GO:0030720,GO:0030529,GO:0003730,GO:0048477,GO:0006405,GO:0006406,GO:0071011,GO:0016325,GO:0071013,GO:0019094,GO:0007314,GO:0045451,GO:0009953,GO:0005829,GO:0005703,GO:0000398,GO:0008380,GO:0008298,GO:0003723,GO:0017148,GO:0007275,GO:0006397,GO:0003729	CG16901-PB				SM00360		PF14259	PS50102			G3DSA:3.30.70.330	SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly294.23	Mediator of RNA polymerase II transcription subunit 30	GO:0005634,GO:0001104,GO:0006355,GO:0006357,GO:0006351,GO:0016592	CG17183-PA						PF11315														
aly294.24	Unknown		CG14984-PB																				
aly294.25	Unknown		n/a																				
aly294.26	Unknown		n/a																				
aly294.27	Unknown		n/a																				
aly294.28	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly294.29	Unknown		n/a																				
aly294.3	Insulin-like growth factor-binding protein complex acid labile subunit	GO:0044267,GO:0070062,GO:0005654,GO:0042567,GO:0005576,GO:0007165,GO:0005515,GO:0007155,GO:0005520,GO:0005615	CG5819-PA				SM00364,SM00364,SM00364,SM00364,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365		PF00560,PF00560,PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058	529~564								
aly294.30	Unknown		n/a																				
aly294.31	Unknown		n/a																				
aly294.32	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly294.33	Unknown		n/a																				
aly294.34	Unknown		n/a																				
aly294.4	Unknown		n/a																				
aly294.5	Leucine-rich repeat-containing G-protein coupled receptor 4	GO:0032922,GO:0048565,GO:0005887,GO:0090263,GO:0072282,GO:0035239,GO:0030282,GO:0001649,GO:2001013,GO:0072224,GO:0001942,GO:0072202,GO:0007186,GO:0007623,GO:0045087,GO:0034122,GO:0090190,GO:0007283,GO:0045892,GO:0045893,GO:0061290,GO:0036335,GO:0050710,GO:0030539,GO:0050673,GO:0004888,GO:0046849,GO:0005515	CG5819-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly294.6	DNA-binding protein SATB2	GO:0021902,GO:0007494,GO:0060021,GO:0001764,GO:0003677,GO:0005737,GO:0043565,GO:0000122,GO:0005634,GO:0007476,GO:0005654,GO:0071310,GO:0015677,GO:0016363,GO:0010468,GO:0048704,GO:0048608,GO:0009880,GO:0016348,GO:0000118,GO:0000790,GO:0051216,GO:0006338,GO:0003700,GO:0006355,GO:0045944,GO:0006351,GO:0005667,GO:0003680,GO:0003682,GO:0002076	CG5799-PA				SM00389,SM00389		PF00046,PF00046,PF16534	PS50071,PS50071			G3DSA:1.10.10.60,G3DSA:1.10.10.60	SSF46689,SSF46689									
aly294.7	Mid1-interacting protein 1-like	GO:0005737,GO:0005634,GO:0005874,GO:0017022	CG2765-PC						PF07084														
aly294.8	Unknown		n/a												295~315								
aly294.9	SHC-transforming protein 1	GO:0005737,GO:0007426,GO:0040008,GO:0035011,GO:0007173,GO:0008293,GO:0035556,GO:0001525,GO:0038202	CG3715-PA				SM00462,SM00252		PF00640,PF00017	PS50001,PS01179	PR00629,PR00629,PR00629,PR00629,PR00629,PR00629,PR00401,PR00401,PR00401		G3DSA:2.30.29.30,G3DSA:3.30.505.10	SSF50729,SSF55550									
aly2946.1	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	GO:0006909,GO:0004149,GO:0045252,GO:0033512,GO:0046949,GO:0006099,GO:0005739,GO:0009353,GO:0048037,GO:0008152,GO:0004147,GO:0016746,GO:0043754	CG5599-PA					TIGR01347	PF00198,PF00364			PS00189	G3DSA:2.40.50.100,G3DSA:3.30.559.10	SSF51230,SSF52777		00310+2.3.1.61,00020+2.3.1.61		PWY-5084	UPA00868				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2946.2	WD repeat-containing protein 60	GO:0006996,GO:0072372,GO:0070062,GO:0030030,GO:0097542,GO:0005515,GO:0005615	CG15701-PA										G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978										
aly2954.1	Regulator of nonsense transcripts 1 homolog	GO:0005737,GO:2000624,GO:0035145,GO:0000184,GO:0035195,GO:0003677,GO:0004386,GO:0008270,GO:0071456,GO:0016246,GO:0005524	CG1559-PA						PF13087,PF09416,PF13086,PF13245				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540										
aly2954.10	Unknown	GO:0005575,GO:0008150,GO:0052689	CG3841-PA						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly2954.11	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689	CG4382-PB						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly2954.12	Putative uncharacterized transposon-derived protein F52C9.6		n/a																				
aly2954.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2954.2	Arrestin domain-containing protein 2	GO:0031410,GO:0007165,GO:0005886	CG1105-PA				SM01017,SM01017		PF00339,PF02752					SSF81296,SSF81296									
aly2954.3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like protein 1	GO:0016757	n/a						PF00535				G3DSA:3.90.550.10	SSF53448									
aly2954.4	Hsp70-Hsp90 organizing protein 3	GO:0005737,GO:0051131,GO:0006457,GO:0042542,GO:0005634,GO:0010286,GO:0051082,GO:0009408,GO:0070678,GO:0009644,GO:0051879	CG2720-PA				SM00028,SM00028,SM00028		PF13414,PF07719	PS50005,PS50005,PS50293			G3DSA:1.25.40.10	SSF48452									
aly2954.5	Integrator complex subunit 3 homolog	GO:0016180,GO:0005794,GO:0003674,GO:0032039	CG17665-PA						PF10189					SSF48371,SSF48371									
aly2954.6	Myelin expression factor 2	GO:0005737,GO:0006351,GO:0003729,GO:0009952,GO:0030529,GO:0000122,GO:0005634,GO:0000166,GO:0008595,GO:0008298,GO:0003730,GO:0003723,GO:0000978,GO:0007067,GO:0007277,GO:0001078,GO:0035282,GO:0045451	CG9373-PA				SM00360,SM00360,SM00360		PF00076,PF00076,PF00076	PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928									
aly2954.7	Sodium channel protein Nach	GO:0035002,GO:0016021,GO:0005272,GO:0035725,GO:0006814	CG13490-PA						PF00858				G3DSA:1.10.287.770,G3DSA:1.10.287.820										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2954.8	Unknown		n/a						PF02949						95~115								
aly2954.9	Odorant receptor 2a	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0004888,GO:0005886,GO:0004984,GO:0032590	CG3206-PA						PF02949														
aly29652.1	Putative 115 kDa protein in type-1 retrotransposable element R1DM		n/a						PF14529				G3DSA:3.60.10.10	SSF56219	309~329								
aly2966.1	Dopamine receptor 1	GO:0007612,GO:0007613,GO:0004952,GO:0035240,GO:0042594,GO:0090328,GO:0008542,GO:0060158,GO:0008355,GO:0001588,GO:0004930,GO:0007212,GO:0016021,GO:0040040,GO:0001963,GO:0007606,GO:0071329,GO:0008306,GO:0005887,GO:0008227,GO:0009744,GO:0010579,GO:0043052,GO:0007191	CG9652-PE						PF00001	PS50262	PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly2971.1	Poly(rC)-binding protein 3	GO:0016071,GO:0000381,GO:0005829,GO:0017130,GO:0044822,GO:0030529,GO:0003723,GO:0003677,GO:0005634,GO:0040040,GO:0070062	CG7437-PK				SM00322,SM00322,SM00322		PF00013,PF00013,PF00013	PS50084,PS50084,PS50084			G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10	SSF54791,SSF54791,SSF54791									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2971.2	Unknown		n/a																				
aly2971.3	Unknown		n/a																				
aly2971.4	Unknown		n/a																				
aly2971.5	Unknown		n/a																				
aly2976.1	Zinc finger protein 782	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG10959-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF13912,PF13912,PF00096,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57716,SSF57667	149~183								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2976.10	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase, mitochondrial	GO:0006655,GO:0008444,GO:0005783,GO:0008654,GO:0032049,GO:0006644,GO:0005739,GO:0005743,GO:0005509,GO:0046474,GO:0046339,GO:0005524,GO:0044281	CG7718-PA			PIRSF000850			PF13091	PS50035			G3DSA:3.30.870.10	SSF56024		00564+2.7.8.5		PWY-5269,PWY-5668	UPA00084				
aly2976.11	Rhomboid-related protein 3	GO:0004252,GO:0016021,GO:0007173,GO:0005509,GO:0005886,GO:0016485,GO:0006508,GO:0008236	CG33166-PB			PIRSF037470			PF01694				G3DSA:1.20.1540.10	SSF144091									
aly2976.12	Unknown	GO:0004252,GO:0016021,GO:0007173,GO:0005509,GO:0005886,GO:0006508,GO:0008236	CG33166-PB										G3DSA:1.10.238.10	SSF47473									
aly2976.13	Spermatogenesis-associated protein 20	GO:0003824,GO:0007283,GO:0030154,GO:0007275,GO:0005576	CG8613-PA			PIRSF006402			PF03190				G3DSA:3.40.30.10,G3DSA:1.50.10.10,G3DSA:1.50.10.10	SSF48208,SSF48208,SSF52833									
aly2976.14	Ubiquitin carboxyl-terminal hydrolase nonstop	GO:0000124,GO:0006351,GO:0021782,GO:0016568,GO:0006325,GO:0043161,GO:0005634,GO:0004197,GO:0016578,GO:0006355,GO:0004843,GO:0006511,GO:0008270,GO:0005515,GO:0061136,GO:0007411,GO:0007412,GO:0016579,GO:0036459,GO:0008347,GO:0045893	CG4166-PB						PF00443,PF02148	PS50235,PS50271		PS00973,PS00972	G3DSA:3.30.40.10	SSF57850,SSF54001									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2976.15	Cytohesin-1	GO:0000187,GO:0005737,GO:0001700,GO:0016192,GO:0031234,GO:0040018,GO:0030155,GO:0005802,GO:0008586,GO:0090162,GO:0005086,GO:0005829,GO:0008289,GO:0005886,GO:0032012,GO:0070507,GO:0030100,GO:0005923,GO:0043547	CG11628-PC				SM00222,SM00233		PF01369,PF00169	PS50190,PS50003			G3DSA:2.30.29.30,G3DSA:1.10.1000.11,G3DSA:1.10.220.20	SSF50729,SSF48425									
aly2976.16	Protein yellow	GO:0060179,GO:0016853,GO:0048067,GO:0005576,GO:0042438,GO:0007275	CG1629-PA						PF03022		PR01366,PR01366		G3DSA:2.120.10.30	SSF63829									
aly2976.2	Zinc finger protein 664	GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG15436-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776,PF00096	PS50157,PS50157,PS50157,PS50157			G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57716,SSF57667									
aly2976.3	Unknown		n/a										G3DSA:2.120.10.30	SSF63829,SSF63829									
aly2976.4	Zinc finger CCCH domain containing protein 10	GO:0044822,GO:0046872	n/a				SM00356,SM00356			PS50103,PS50103,PS50103					200~220								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2976.5	Unknown		n/a																				
aly2976.6	Unknown		n/a																				
aly2976.7	E3 ubiquitin-protein ligase SMURF2	GO:0005737,GO:0001700,GO:0008101,GO:0016874,GO:0048619,GO:0045121,GO:0040008,GO:0007293,GO:0010629,GO:0042787,GO:0005515,GO:0005886,GO:0030514,GO:0004842,GO:0005634,GO:0007179	CG4943-PA				SM00456,SM00456,SM00456,SM00119,SM00239		PF00168,PF00397,PF00397,PF00397,PF00632	PS50020,PS50004,PS50020,PS50237,PS50020		PS01159,PS01159	G3DSA:2.60.40.150,G3DSA:3.30.2160.10,G3DSA:2.20.70.10,G3DSA:2.20.70.10,G3DSA:2.20.70.10	SSF51045,SSF51045,SSF56204,SSF49562,SSF51045						UPA00143				
aly2976.8	Probable isoaspartyl peptidase/L-asparaginase GA20639	GO:0005737,GO:0016787,GO:0008798,GO:0035071,GO:0048102,GO:0033345,GO:0004067	CG7860-PA						PF01112					SSF56235									
aly2976.9	Probable isoaspartyl peptidase/L-asparaginase CG7860	GO:0005737,GO:0016787,GO:0008798,GO:0035071,GO:0048102,GO:0033345,GO:0004067	CG7860-PA						PF01112					SSF56235									
aly29837.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2984.1	Unknown	GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG2663-PA										G3DSA:3.40.525.10	SSF52087									
aly2984.10	Phosphatidylinositol 4-kinase alpha	GO:0005737,GO:0048599,GO:0006644,GO:0016020,GO:0030660,GO:0004430,GO:0016310,GO:0005829,GO:0046854,GO:0007165,GO:0044281,GO:0005575,GO:0005488,GO:0005886,GO:0008582,GO:0006661,GO:0035329,GO:0005925,GO:0048015,GO:0005524,GO:0070062	CG10260-PD											SSF48371,SSF48371,SSF48371,SSF48371,SSF48371									
aly2984.11	Luciferin 4-monooxygenase	GO:0008218,GO:0016207,GO:0005777,GO:0008152,GO:0046872,GO:0047077,GO:0005524	CG9993-PA						PF00501,PF13193				G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:3.30.300.30,G3DSA:3.40.50.980	SSF56801									
aly2984.12	Unknown		n/a												7~34								
aly2984.13	Luciferin 4-monooxygenase	GO:0046872,GO:0005324,GO:0005777,GO:0003824,GO:0008152,GO:0008218,GO:0047077,GO:0005524	CG4830-PA						PF00501,PF13193				G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:3.30.300.30,G3DSA:3.40.50.980	SSF56801									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2984.14	SHC SH2 domain-binding protein 1 homolog B	GO:0007112,GO:0045171,GO:0030496,GO:0008335,GO:0030246,GO:0035323,GO:2000177,GO:0035324,GO:0045169,GO:0008543	CG10722-PB						PF13229				G3DSA:2.160.20.10,G3DSA:2.160.20.10	SSF51126									
aly2984.2	Alpha-tocopherol transfer protein-like	GO:0016020,GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG2663-PA				SM00516		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087,SSF46938									
aly2984.3	Alpha-tocopherol transfer protein-like	GO:0016020,GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG2663-PA						PF00650	PS50191	PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF46938,SSF52087									
aly2984.4	Alpha-tocopherol transfer protein-like	GO:0016020,GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG2663-PA				SM00516		PF00650	PS50191			G3DSA:3.40.525.10	SSF52087,SSF46938									
aly2984.5	Aldo-keto reductase AKR2E4	GO:0004032,GO:0008202,GO:0055114,GO:0016491	CG9436-PA			PIRSF000097			PF00248		PR00069,PR00069,PR00069,PR00069,PR00069	PS00063,PS00062,PS00798	G3DSA:3.20.20.100	SSF51430									
aly2984.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2984.7	Structure-specific endonuclease subunit SLX1 homolog	GO:0006310,GO:0006281,GO:0017108,GO:0004520,GO:0033557,GO:0005515,GO:0007095,GO:0046872	CG18271-PB	MF_03100			SM00465		PF01541	PS50164			G3DSA:3.30.40.10	SSF82771									
aly2984.8	Zinc finger HIT domain-containing protein 2	GO:0022008,GO:0046872	CG31223-PA						PF04438	PS51083				SSF144232									
aly2984.9	Phosphatidylinositol 4-kinase alpha	GO:0005737,GO:0048599,GO:0008582,GO:0030660,GO:0004430,GO:0016310,GO:0005886,GO:0005575,GO:0046854,GO:0035329,GO:0048015,GO:0005524	CG10260-PD				SM00145,SM00146		PF00613,PF00454,PF00454	PS50290,PS51545		PS00915,PS00916	G3DSA:3.30.1010.10,G3DSA:1.10.1070.11,G3DSA:1.25.40.70	SSF56112,SSF56112,SSF48371									
aly29892.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473	367~368								
aly29892.2	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0022857,GO:0005886,GO:0055085	CG4797-PB						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly2994.1	Galactose-1-phosphate uridylyltransferase	GO:0005794,GO:0005975,GO:0006012,GO:0005829,GO:0033501,GO:0008108,GO:0005575,GO:0003824,GO:0008270,GO:0006258,GO:0019388,GO:0008344,GO:0044281	CG9232-PA					TIGR00209	PF01087				G3DSA:3.30.428.10	SSF54197		00520+2.7.7.12,00052+2.7.7.12		PWY-6317,PWY-6527	UPA00214				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly2994.2	Unknown		n/a																				
aly29954.1	Unknown		n/a																				
aly2996.1	Semaphorin-2A	GO:0030534,GO:0007632,GO:0070983,GO:0042756,GO:0007431,GO:0005829,GO:0016020,GO:0016201,GO:0007629,GO:0005576,GO:0004872,GO:0005515,GO:0007411,GO:0071678,GO:0012505	CG4700-PB				SM00630		PF01403	PS51004,PS50835			G3DSA:2.130.10.10,G3DSA:3.30.1680.10	SSF101912,SSF103575									
aly2997.1	Methionine--tRNA ligase, cytoplasmic	GO:0005737,GO:0004825,GO:0000049,GO:0006431,GO:0000166,GO:0022008,GO:0005875,GO:0005524	CG15100-PA						PF09334		PR01041,PR01041,PR01041	PS00178	G3DSA:3.40.50.620,G3DSA:1.20.1050.10,G3DSA:2.170.220.10	SSF57770,SSF47616,SSF52374,SSF52374		00450+6.1.1.10,00970+6.1.1.10	REACT_71						
aly2997.2	[Pyruvate dehydrogenase (acetyl-transferring)] kinase, mitochondrial	GO:0006468,GO:0004672,GO:0005759,GO:0004740,GO:0006006,GO:0006090,GO:0005524	CG8808-PC				SM00387		PF02518,PF10436	PS50109			G3DSA:1.20.140.20,G3DSA:3.30.565.10	SSF69012,SSF55874			REACT_1046						
aly300.1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase	GO:0007476,GO:0004331,GO:0003873,GO:0006000,GO:0005524,GO:0006003	CG3400-PG				SM00855		PF00300,PF01591		PR00991,PR00991,PR00991	PS00175	G3DSA:3.40.50.1240,G3DSA:3.40.50.300	SSF52540,SSF53254		00051+2.7.1.105+3.1.3.46	REACT_474		UPA00109				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly300.10	Zinc finger CCHC domain containing protein 4	GO:0008168,GO:0008270,GO:0003676	CG12863-PA				SM00343		PF00098,PF10237	PS50158,PS50216,PS51270		PS00092		SSF161245									
aly300.11	Protein lin-37 homolog	GO:0017053,GO:0000122,GO:0031523,GO:0007283,GO:0003674,GO:0007307,GO:0048477,GO:0007049	CG15119-PA						PF15306						218~238								
aly300.12	Partner of Y14 and mago	GO:0005737,GO:0035145,GO:0000184,GO:0008150,GO:0003723,GO:0005515	CG30176-PA						PF09282					SSF101931									
aly300.13	Unknown		n/a						PF15873														
aly300.14	ATP-dependent RNA helicase DDX42	GO:0005737,GO:0005634,GO:0004004,GO:0004386,GO:0003723,GO:0003676,GO:0005524	CG6418-PB				SM00487,SM00490		PF00271,PF00270	PS51192,PS51194,PS51195		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									
aly300.15	ATP-dependent RNA helicase DDX42	GO:0005737,GO:0005634,GO:0004004,GO:0004386,GO:0003723,GO:0003676,GO:0005524	CG6418-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly300.16	Unknown		n/a												926~946								
aly300.17	Unknown		CG43737-PB												66~86								
aly300.18	Broad-complex core protein isoform 6	GO:0010629,GO:0003677,GO:0008219,GO:0007458,GO:0005634,GO:0007552,GO:0048808,GO:0046872,GO:0048477,GO:0071390,GO:0035075,GO:0035072,GO:0035071,GO:0035070,GO:0006914,GO:0048747,GO:0042332,GO:0040034,GO:0001752,GO:0003700,GO:0009608,GO:0007562,GO:0035193,GO:0006355,GO:0048813,GO:0045944,GO:0000977	CG11491-PP				SM00355,SM00355,SM00225		PF13912,PF00651,PF13894	PS50157,PS50097,PS50157		PS00028,PS00028	G3DSA:3.30.710.10	SSF57667,SSF54695										
aly300.19	Broad-complex core protein isoform 6	GO:0010629,GO:0003677,GO:0008219,GO:0007458,GO:0005634,GO:0007552,GO:0048808,GO:0046872,GO:0048477,GO:0071390,GO:0035075,GO:0035072,GO:0035071,GO:0035070,GO:0006914,GO:0048747,GO:0042332,GO:0040034,GO:0001752,GO:0003700,GO:0009608,GO:0007562,GO:0035193,GO:0006355,GO:0048813,GO:0045944,GO:0000977	CG11491-PP				SM00355,SM00355		PF13912	PS50157,PS50157		PS00028,PS00028		SSF57667										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly300.2	Unknown	GO:0008270,GO:0003676	n/a				SM00586		PF07535	PS51265													
aly300.20	Ras-responsive element-binding protein 1	GO:1903691,GO:0003676,GO:0007275,GO:0005737,GO:0016604,GO:2000394,GO:0070062,GO:0000122,GO:1900026,GO:0005634,GO:0005654,GO:0006366,GO:0046872,GO:0016607,GO:0033601,GO:0045893,GO:0007265,GO:0010634,GO:0003700,GO:0005730,GO:0006355,GO:0000979	CG17829-PA				SM00355,SM00355,SM00355,SM00355		PF12874,PF05605	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.60.60	SSF57667,SSF57667										
aly300.21	Probable ATP-dependent RNA helicase DDX52	GO:0005730,GO:0044822,GO:0016020,GO:0004004,GO:0006364,GO:0010501,GO:0005524,GO:0003729	CG5589-PA				SM00487		PF00270,PF00271	PS51192,PS51194,PS51195		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540										
aly300.22	Protein halfway	GO:0035075,GO:0035073,GO:0005622,GO:0005575,GO:0003674,GO:0035556	CG3095-PA										G3DSA:3.80.10.10	SSF52058									
aly300.23	Protein halfway	GO:0035075,GO:0035073,GO:0005622,GO:0005575,GO:0003674,GO:0035556	CG3095-PA										G3DSA:3.80.10.10	SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly300.3	Acyl carrier protein, mitochondrial	GO:0006633,GO:0005739,GO:0006120,GO:0031177,GO:0000036,GO:0070469	CG9160-PC	MF_01217					PF00550	PS50075			G3DSA:1.10.1200.10	SSF47336					UPA00094				
aly300.4	Protein HID1	GO:0005737,GO:0005794,GO:0005797,GO:0070062,GO:0006886,GO:0000138,GO:0031001,GO:0005881,GO:0090498	CG8841-PC						PF09742														
aly300.5	Unknown		n/a																				
aly300.6	SPRY domain-containing SOCS box protein 3	GO:0005622,GO:0005575,GO:0016567,GO:0003674,GO:0005515,GO:0008150,GO:0035556	CG10516-PA				SM00449		PF00622	PS50188				SSF49899									
aly300.7	Annexin B10	GO:0016020,GO:0005543,GO:0005544,GO:0003779,GO:0008150,GO:0005509	CG9579-PB				SM00335,SM00335,SM00335,SM00335,SM00335,SM00335		PF00191,PF00191,PF00191,PF00191,PF00191		PR00196,PR00196,PR00196,PR00196,PR00196,PR00196	PS00223,PS00223	G3DSA:1.10.220.10,G3DSA:1.10.220.10,G3DSA:1.10.220.10,G3DSA:1.10.220.10,G3DSA:1.10.220.10	SSF47874,SSF47874	274~294								
aly300.8	Amyloid protein-binding protein 2	GO:0005737,GO:0006909,GO:0008152,GO:0046907,GO:0006886,GO:0007018,GO:0060632,GO:0030659,GO:0005515,GO:0005871,GO:0005634,GO:0005874,GO:0005875,GO:0003777,GO:0045451	CG10695-PA				SM00028,SM00028		PF13374,PF13374				G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly300.9	Complement component 1 Q subcomponent binding protein, mitochondrial	GO:0070131,GO:0031690,GO:0030984,GO:0050687,GO:2000510,GO:0050848,GO:0030449,GO:0048025,GO:0007274,GO:0005737,GO:0043065,GO:0090023,GO:0000122,GO:0005540,GO:0045785,GO:0005634,GO:0003714,GO:0005739,GO:0042256,GO:0001849,GO:0032695,GO:0005759,GO:1901165,GO:0045087,GO:0051897,GO:0009986,GO:0006915,GO:0005886,GO:0014065,GO:0006958,GO:0039536,GO:0039534,GO:0097177,GO:0005829,GO:0005730,GO:0008380,GO:1900026,GO:0005576,GO:0006351,GO:0032689,GO:0003729,GO:0006397	CG6459-PA						PF02330				G3DSA:3.10.280.10	SSF54529										
aly3001.1	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0005737,GO:0007567,GO:0045786,GO:0070403,GO:0003824,GO:0051287,GO:0097070,GO:0004022,GO:0006066,GO:0016404,GO:0006693,GO:0007179,GO:0008152,GO:0007565,GO:0004957,GO:0030728,GO:0070493,GO:0055114	CG18814-PB						PF00106		PR01167,PR01167,PR01167,PR01167,PR01167,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735		00010+1.1.1.1,00260+1.1.1.1,00071+1.1.1.1,00626+1.1.1.1,00982+1.1.1.1,00625+1.1.1.1,00980+1.1.1.1,00		PWY-6342,PWY-7118,PWY-6871,PWY-7013,PWY-7396,PWY-7557,PWY-5057,PWY-6802,PWY-6587,PWY-5486,PWY-					
aly3001.10	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0016491,GO:0005737,GO:0030728,GO:0070062,GO:0007179,GO:0004022,GO:0016323,GO:0003824,GO:0045786,GO:0055114,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106		PR00080,PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3001.2	Alcohol dehydrogenase 1	GO:0048812,GO:0004022,GO:0055114,GO:0008152,GO:0016491	CG4842-PA						PF00106		PR00080,PR00080,PR00080,PR01167,PR01167,PR01167,PR01167	PS00061	G3DSA:3.40.50.720	SSF51735		00010+1.1.1.1,00260+1.1.1.1,00071+1.1.1.1,00626+1.1.1.1,00982+1.1.1.1,00625+1.1.1.1,00980+1.1.1.1,00592+1.1.1.1,00350+1.1.1.1,00830+1.1.1.1		PWY-6342,PWY-7118,PWY-6871,PWY-7013,PWY-7396,PWY-7557,PWY-5057,PWY-6802,PWY-6587,PWY-5486,PWY-7111,PWY-5076,PWY-6333,PWY-5082,PWY-5079,PWY-5078,PWY-6313,PWY-3162,PWY-5480,PWY-5751					
aly3001.3	Unknown		CG32432-PA				SM00192,SM00192,SM00042		PF00057	PS01180,PS50068,PS01180	PR00261,PR00261	PS01209,PS01209	G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.60.120.290	SSF57424,SSF49854	1059~1079								
aly3001.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3001.5	Fringe glycosyltransferase	GO:0048749,GO:0005783,GO:0007450,GO:0008587,GO:0007293,GO:0030173,GO:0008375,GO:0001745,GO:0007219,GO:0016021,GO:0016020,GO:0007476,GO:0007451,GO:0045746,GO:0045747,GO:0046872,GO:0048477,GO:0005795,GO:0005794,GO:0005797,GO:0048190,GO:0035017,GO:0008593,GO:0008194,GO:0036099,GO:0006493,GO:0036011,GO:0033829,GO:0016757,GO:0006004,GO:0001708	CG10580-PA						PF02434														
aly3001.6	Cysteine proteinase 3	GO:0005773,GO:0005811,GO:0005875,GO:0004197,GO:0006508,GO:0008234	CG8947-PA				SM00848,SM00645		PF00112,PF08246		PR00705,PR00705,PR00705	PS00639,PS00640,PS00139	G3DSA:3.90.70.10	SSF54001									
aly3001.7	Unknown	GO:0009593,GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0004970	CG15324-PA										G3DSA:3.40.190.10,G3DSA:3.40.190.10	SSF53850,SSF53850,SSF53850									
aly3001.8	Unknown	GO:0016021,GO:0009593,GO:0015276	CG13576-PA										G3DSA:3.40.190.10	SSF53850,SSF53850									
aly3001.9	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0005737,GO:0007567,GO:0045786,GO:0003824,GO:0051287,GO:0097070,GO:0004022,GO:0016404,GO:0006693,GO:0048812,GO:0007179,GO:0070403,GO:0007565,GO:0004957,GO:0030728,GO:0070493,GO:0055114	CG4842-PA						PF00106		PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly30029.1	Unknown		n/a										G3DSA:2.60.40.1180		105~105								
aly30029.2	Lysosomal alpha-mannosidase	GO:0005764,GO:0070062,GO:0030246,GO:0006464,GO:0007611,GO:0006013,GO:0005576,GO:0008270,GO:0004559,GO:0005537	CG6206-PA						PF01074				G3DSA:3.20.110.10	SSF88713									
aly3011.1	Unknown	GO:0003674,GO:0016020,GO:0008150	CG32225-PA						PF01299														
aly3011.10	Neutral alpha-glucosidase AB	GO:0017177,GO:0006457,GO:0042470,GO:0005975,GO:0070062,GO:0005794,GO:0043687,GO:0044822,GO:0016020,GO:0030246,GO:0005788,GO:0018279,GO:0005576,GO:0004553,GO:0044267,GO:0033919,GO:0004558,GO:0005875	CG14476-PB						PF01055,PF13802					SSF51011,SSF51445,SSF74650									
aly3011.11	Neutral alpha-glucosidase AB	GO:0017177,GO:0042470,GO:0005975,GO:0005783,GO:0005794,GO:0030246,GO:0005576,GO:0004553,GO:0033919,GO:0004558,GO:0005875	CG14476-PB						PF01055,PF13802					SSF74650,SSF74650,SSF51445									
aly3011.12	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3011.13	Unknown		n/a																				
aly3011.2	Unknown		n/a																				
aly3011.3	Cofilin/actin-depolymerizing factor homolog	GO:0016319,GO:0042052,GO:0008585,GO:0007298,GO:0001745,GO:0005875,GO:0015629,GO:0005654,GO:0000902,GO:0000281,GO:0003779,GO:0016363,GO:0048749,GO:0042067,GO:0007409,GO:0030041,GO:0030042,GO:0001737,GO:0001736,GO:0010591,GO:0007015,GO:0000915,GO:0005829,GO:0036011	CG4254-PA				SM00102		PF00241	PS51263			G3DSA:3.40.20.10	SSF55753	157~170								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3011.4	Cadherin EGF LAG seven-pass G-type receptor 1	GO:0016319,GO:0016318,GO:0007409,GO:0016339,GO:0032956,GO:0016358,GO:0030177,GO:0060490,GO:0007164,GO:0007165,GO:0007166,GO:0046928,GO:0070593,GO:0007411,GO:0030178,GO:0007417,GO:0001702,GO:0005654,GO:0004930,GO:0050839,GO:0007367,GO:0005057,GO:0016021,GO:0016020,GO:0004888,GO:0045746,GO:0005509,GO:0042067,GO:0001843,GO:0007186,GO:0007626,GO:0035159,GO:0045176,GO:0007218,GO:0042060,GO:0048057,GO:0001738,GO:0060488,GO:0060489,GO:0005887,GO:0005886,GO:0007267,GO:0007266,GO:0048105,GO:0007156,GO:0001736,GO:0009952,GO:0042249,GO:0005911,GO:0050770,GO:0090175,GO:0042472,GO:0090179,GO:0016055,GO:0007464,GO:0051963,GO:0048813,GO:0090251,GO:0001764,GO:0046983,GO:0001942,GO:0004872	CG11895-PF						PF00002	PS50261													
aly3011.5	Leucine-rich repeat protein SHOC-2	GO:0005737,GO:0005634,GO:0046579,GO:0000164,GO:0019903,GO:0005515	CG10307-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364		PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									
aly3011.6	Seipin	GO:0005783,GO:0006635,GO:0090207,GO:0005789,GO:0032469,GO:0010884,GO:0003674,GO:0042594,GO:0046890,GO:0010883,GO:0046339,GO:0016021,GO:0046473,GO:0008610	CG9904-PA						PF06775														
aly3011.7	Valine--tRNA ligase, mitochondrial 1	GO:0004812,GO:0005829,GO:0006438,GO:0005739,GO:0000166,GO:0009793,GO:0002161,GO:0006418,GO:0004832,GO:0005524,GO:0009507	CG5660-PA					TIGR00422	PF00133,PF08264		PR00986,PR00986,PR00986,PR00986,PR00986	PS00178	G3DSA:1.10.730.10,G3DSA:1.10.730.10,G3DSA:3.90.740.10,G3DSA:3.40.50.620,G3DSA:3.40.50.620	SSF50677,SSF47323,SSF52374,SSF52374,SSF52374	930~957	00970+6.1.1.9	REACT_71						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3011.8	Unknown	GO:0046872	n/a							PS50157		PS00028											
aly3011.9	O-acetyl-ADP-ribose deacetylase MACROD2	GO:0006974,GO:0019213,GO:0051725,GO:0007420,GO:0005634,GO:0042278,GO:0016798,GO:0005575,GO:0008150,GO:0003674	CG18812-PC				SM00506		PF01661	PS51154			G3DSA:3.40.220.10	SSF52949									
aly30135.1	Unknown		n/a																				
aly3014.1	Unknown	GO:0046331	CG5953-PA				SM00595		PF10545	PS51029					155~175								
aly3014.2	Unknown	GO:0046872	n/a				SM00355,SM00355,SM00355,SM00355		PF12874	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028		SSF57667	273~309								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3014.3	Peptidyl-prolyl cis-trans isomerase FKBP1A	GO:0060347,GO:0032513,GO:0016020,GO:0006457,GO:0019221,GO:0055010,GO:0003007,GO:0051280,GO:0008144,GO:1902991,GO:0004871,GO:0044325,GO:0030018,GO:0032925,GO:0005737,GO:0032092,GO:0070062,GO:0019855,GO:0043206,GO:0042098,GO:0051209,GO:0033017,GO:0005528,GO:0003755,GO:0007183,GO:0032880,GO:0043123,GO:0031398,GO:0006936,GO:0000413,GO:0031000,GO:0046332,GO:0010039,GO:0060314,GO:1990000,GO:0031012,GO:0061077,GO:0043679,GO:0006974,GO:0050776,GO:0018208,GO:0005829,GO:0001933,GO:0042803,GO:0048185	CG11001-PA						PF00254	PS50059			G3DSA:3.10.50.40	SSF54534										
aly3014.4	Calbindin-32	GO:0006874,GO:0005509	CG6702-PA				SM00054,SM00054,SM00054,SM00054		PF13202,PF13499,PF00036	PS50222,PS50222,PS50222,PS50222,PS50222		PS00018,PS00018,PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly3014.5	Unknown	GO:0005575,GO:0008150,GO:0003674	CG34026-PA						PF15868														
aly3014.6	E3 ubiquitin-protein ligase RNF123	GO:0005737,GO:0016567,GO:0016874,GO:0008270,GO:0005515	CG6752-PA				SM00449		PF00622	PS50188				SSF49899									
aly3014.7	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3014.8	Collagen-like protein 6	GO:0005201,GO:0005587,GO:0005581,GO:0007391,GO:0005604,GO:0019012,GO:0035848	CG4145-PC						PF01391,PF01391,PF01391														
aly3015.1	Atrial natriuretic peptide receptor 1	GO:0017046,GO:0019901,GO:0006468,GO:0050880,GO:0048662,GO:0016941,GO:0030828,GO:0043235,GO:0016021,GO:0005886,GO:0006182,GO:0005622,GO:0042417,GO:0007166,GO:0004672,GO:0007168,GO:0035556,GO:0009190,GO:0004383,GO:0005524,GO:0005525	CG31183-PA				SM00044		PF00211,PF07714,PF01094	PS50125,PS50011	PR00255,PR00255,PR00255,PR00255	PS00452	G3DSA:3.30.200.20,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:1.10.510.10,G3DSA:3.30.70.1230	SSF56112,SSF53822,SSF55073	1015~1035									
aly3016.1	Unknown		n/a										G3DSA:3.60.10.10	SSF56219									
aly3016.10	Torso-like protein	GO:0007362,GO:0005122,GO:0009880,GO:0040018,GO:0008595,GO:0005576,GO:0008293	CG6705-PB				SM00457																
aly3016.11	Torso-like protein	GO:0007362,GO:0005122,GO:0009880,GO:0040018,GO:0008595,GO:0005576,GO:0008293	CG6705-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3016.12	Tetratricopeptide repeat protein 5	GO:0005737,GO:0006281,GO:0005654,GO:0045944,GO:0005515,GO:0003677,GO:0003682	n/a				SM00028,SM00028,SM00028		PF16669,PF13181,PF13181,PF07719	PS50293,PS50005,PS50005,PS50293			G3DSA:1.25.40.10	SSF48452,SSF48452	42~62								
aly3016.13	Unknown	GO:0008270,GO:0003676	n/a				SM00451,SM00451																
aly3016.14	Unknown		n/a						PF03148														
aly3016.15	Unknown	GO:0016021,GO:0005272,GO:0015280,GO:0006814	CG8546-PC						PF00858				G3DSA:1.10.287.820										
aly3016.16	Acid-sensing ion channel 4	GO:0045177,GO:0005261,GO:0015280,GO:0016021,GO:0006814,GO:0035725,GO:0005887,GO:0005248,GO:0005272,GO:0098655	CG34059-PA						PF00858				G3DSA:2.60.470.10,G3DSA:2.60.470.10										
aly3016.17	Unknown		CG6329-PA										G3DSA:2.10.60.10										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3016.2	Unknown		n/a							PS50081		PS01359	G3DSA:3.30.40.10	SSF57903	159~179,101~149								
aly3016.3	Ankyrin repeat and sterile alpha motif domain-containing protein 1B	GO:0005737,GO:0043197,GO:0045211,GO:0014069,GO:0015030,GO:0046875,GO:0030054	CG4393-PB				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796,PF12796	PS50088,PS50088,PS50088,PS50088,PS50088,PS50297,PS50088	PR01415,PR01415		G3DSA:1.25.40.20	SSF48403	279~299								
aly3016.4	Transmembrane 7 superfamily member 3	GO:0016021,GO:0070062,GO:0005886	n/a						PF13886														
aly3016.5	Paired box protein Pax-6	GO:0048749,GO:0043565,GO:0035214,GO:0003700,GO:0044854,GO:0005634,GO:0003705,GO:0006355,GO:0010628,GO:0045944,GO:0006351,GO:0008056,GO:0007275,GO:0016319	CG11186-PA				SM00389,SM00351		PF00292,PF00046	PS51057,PS50071	PR00027,PR00027,PR00027,PR00027	PS00027,PS00034	G3DSA:1.10.10.10,G3DSA:1.10.10.60,G3DSA:1.10.10.10	SSF46689,SSF46689	187~207								
aly3016.6	Unknown		n/a																				
aly3016.7	Unknown		n/a										G3DSA:1.20.5.500										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3016.8	Unknown	GO:0004857,GO:0045980,GO:0050830,GO:0005739	CG13551-PA						PF04568				G3DSA:1.20.5.500	SSF64602									
aly3016.9	Unknown		n/a																				
aly3017.1	Protein MEMO1	GO:0032886	CG8031-PA					TIGR04336	PF01875														
aly3017.2	Unknown		n/a												43~67								
aly3017.3	Ferrochelatase, mitochondrial	GO:0006783,GO:0006782,GO:0051537,GO:0004325,GO:0005743,GO:0046872,GO:0005875	CG2098-PA						PF00762				G3DSA:3.40.50.1400	SSF53800		00860+4.99.1.1			UPA00252				
aly3017.4	SEC23-interacting protein	GO:0005737,GO:0070971,GO:0007030,GO:0001675,GO:0043231,GO:0005793,GO:0005801,GO:0008970,GO:0044822,GO:0097038,GO:0007338,GO:0012507,GO:0046872,GO:0006886	CG8552-PA						PF02862	PS51043													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3017.5	Unknown		n/a																				
aly302.1	Unknown	GO:0005634,GO:0016020	CG17816-PG						PF15501						424~424								
aly302.2	Unknown	GO:0016020	CG17816-PG																				
aly302.3	Unknown	GO:0005634,GO:0008270	n/a						PF07776														
aly302.4	Microtubule-associated serine/threonine-protein kinase 1	GO:0005737,GO:0005856,GO:0006468,GO:0007010,GO:0000287,GO:0045793,GO:0004674,GO:0005886,GO:0007298,GO:0035556,GO:0005524	CG6498-PA				SM00228,SM00220		PF08926,PF08926,PF00069	PS50011,PS51285,PS50106,PS51151		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:2.30.42.10	SSF56112,SSF50156	1420~1462,271~291								
aly302.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly30212.1	Unknown	GO:0006468,GO:0016021,GO:0004872,GO:0004672,GO:0035556,GO:0004383,GO:0005524,GO:0006182	CG3216-PC																				
aly3026.1	Unknown		n/a																				
aly3026.2	Protein angel	GO:0005575,GO:0003674,GO:0008150,GO:0007275	CG12273-PA						PF03372				G3DSA:3.60.10.10	SSF56219									
aly3026.3	Unknown		n/a																				
aly3030.1	Unknown	GO:0003676	n/a							PS50879			G3DSA:3.30.420.10	SSF53098									
aly3030.2	Protein IWS1 homolog	GO:0005737,GO:0050684,GO:0090239,GO:0005634,GO:2001253,GO:0005654,GO:0006355,GO:0010793,GO:0006351,GO:0003677,GO:0051028,GO:0008380,GO:0006397	CG9915-PB						PF08711	PS51319			G3DSA:1.20.930.10	SSF47676									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3030.3	Unknown		n/a																				
aly3030.4	Unknown	GO:0006888,GO:0016192,GO:0016081,GO:0000149,GO:0000046,GO:0070050,GO:0097352,GO:0097111,GO:0007269,GO:0005886,GO:0005484,GO:0031201,GO:0000421	CG7452-PB																				
aly3030.5	RNA-binding protein 25	GO:0005737,GO:0016607,GO:0000381,GO:0071011,GO:0005634,GO:0044822,GO:0000398,GO:0000166,GO:0005654,GO:0003676,GO:0006397,GO:0042981,GO:0008380,GO:0005681,GO:0003729	CG4119-PA				SM00360		PF00076				G3DSA:3.30.70.330	SSF54928									
aly3030.6	Unknown	GO:0000381,GO:0071011,GO:0005634,GO:0000398,GO:0000166,GO:0003676,GO:0003729	CG4119-PA																				
aly3030.7	RNA-binding protein 25	GO:0005737,GO:0016607,GO:0000381,GO:0071011,GO:0005634,GO:0044822,GO:0000398,GO:0000166,GO:0005654,GO:0003676,GO:0003729,GO:0042981,GO:0008380,GO:0005681,GO:0006397	CG4119-PA				SM00311		PF01480	PS51025			G3DSA:1.20.1390.10										
aly3030.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3030.9	Unknown		n/a																				
aly30305.1	Unknown		n/a																				
aly30309.1	Unknown		n/a												10~30								
aly3037.1	Trypsin-3	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG9564-PC				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly3037.2	Dual serine/threonine and tyrosine protein kinase	GO:0005737,GO:0006468,GO:0016324,GO:0048568,GO:0030054,GO:0005886,GO:0007165,GO:0004714,GO:0016323,GO:0004674,GO:0005003,GO:0004712,GO:0005509,GO:0005887,GO:0004672,GO:0007169,GO:0005524,GO:0004713	CG14396-PC				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly3037.3	Dual serine/threonine and tyrosine protein kinase	GO:0005737,GO:0016324,GO:0016323,GO:0004674,GO:0004712,GO:0004713,GO:0005524	n/a												498~518								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3037.4	Protein boule-like	GO:0005737,GO:0007126,GO:0043204,GO:0008494,GO:0005634,GO:0030154,GO:0007476,GO:0007275,GO:0000166,GO:0045948,GO:0007283,GO:0046331,GO:0008315,GO:0003723,GO:0045836,GO:0006417,GO:0048137,GO:0007140,GO:0003729	CG4760-PF				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928										
aly30378.1	Endoribonuclease Dcr-1	GO:0033227,GO:0042078,GO:0030422,GO:0007279,GO:0070883,GO:0031054,GO:0007294,GO:0005737,GO:0007367,GO:0004525,GO:0005634,GO:0030727,GO:0035087,GO:0006309,GO:0016246,GO:0046872,GO:0005524,GO:0004386,GO:0090502,GO:0090501,GO:0042594,GO:0035195,GO:0035196,GO:0004530,GO:0003727,GO:0048813,GO:0003725,GO:0003723,GO:0005515,GO:0016443,GO:0016442,GO:0006396,GO:0045448	CG4792-PA				SM00535		PF00636	PS50142		PS00517	G3DSA:1.10.1520.10,G3DSA:1.10.1520.10	SSF69065,SSF69065										
aly30378.2	Endoribonuclease Dcr-1	GO:0033227,GO:0042078,GO:0030422,GO:0007279,GO:0070883,GO:0031054,GO:0007294,GO:0005737,GO:0007367,GO:0004525,GO:0005634,GO:0030727,GO:0035087,GO:0006309,GO:0016246,GO:0046872,GO:0005524,GO:0004386,GO:0090502,GO:0090501,GO:0042594,GO:0035195,GO:0035196,GO:0004530,GO:0003727,GO:0048813,GO:0003725,GO:0003723,GO:0005515,GO:0016443,GO:0016442,GO:0006396,GO:0045448	CG4792-PA				SM00535		PF00636	PS50142			G3DSA:1.10.1520.10,G3DSA:1.10.1520.10	SSF69065,SSF69065	198~218									
aly304.1	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG5065-PA						PF07993				G3DSA:3.40.50.720	SSF51735,SSF51735			REACT_22258						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly304.10	Unknown		n/a																				
aly304.11	Unknown		n/a																				
aly304.12	Unknown		n/a												252~281								
aly304.13	Extracellular serine/threonine protein kinase four-jointed	GO:0044719,GO:0006468,GO:0045198,GO:0007446,GO:0007444,GO:0042067,GO:0016021,GO:0005886,GO:0016348,GO:0001736,GO:0060071,GO:0007267,GO:0007219,GO:0007474,GO:0004672,GO:0017147,GO:0035159,GO:0000139,GO:0001737,GO:0007449,GO:0005576	CG10917-PA								PR02072,PR02072,PR02072,PR02072,PR02072,PR02072,PR02072												
aly304.14	Unknown		n/a												110~137								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly304.2	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG12268-PA						PF03015,PF07993				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly304.3	Fatty acyl-CoA reductase 1	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0046474,GO:0035336,GO:0008611	CG1441-PA						PF07993,PF03015				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly304.4	Loss of heterozygosity 12 chromosomal region 1 protein homolog		CG11802-PA						PF10158														
aly304.5	Ubiquitin-fold modifier-conjugating enzyme 1	GO:0046331	CG8386-PA			PIRSF008716			PF08694					SSF54495									
aly304.6	Fatty acyl-CoA reductase 1	GO:0005737,GO:0045177,GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0035149,GO:0035002,GO:0050062,GO:0010025,GO:0046474,GO:0035336,GO:0008611	CG1443-PA						PF07993				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly304.7	Probable pseudouridine-5'-phosphatase	GO:0016787,GO:1990738,GO:0042060,GO:0009117,GO:0008152,GO:0046872	CG15441-PA					TIGR01509	PF13419				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF56784									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly304.8	Unknown		n/a																				
aly304.9	Unknown		n/a																				
aly30607.1	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG5065-PA						PF07993				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly307.1	63 kDa sperm flagellar membrane protein	GO:0031514,GO:0008407,GO:0007602,GO:0046331,GO:0005509,GO:0005886,GO:0031225	CG11101-PB				SM00179,SM00181,SM00181,SM00181		PF01390,PF07645	PS50026,PS50026,PS50024	PR01217,PR01217,PR01217,PR01217	PS01186,PS00022,PS01187,PS01186,PS00010	G3DSA:2.10.25.10	SSF57184,SSF57184,SSF82671									
aly307.2	Unknown		CG4734-PA							PS01180,PS01180			G3DSA:2.60.120.290,G3DSA:2.60.120.290										
aly307.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3071.1	Unknown		n/a																				
aly3072.1	Disks large-associated protein 4	GO:0007480,GO:0016020,GO:0023052,GO:0045202,GO:0007267,GO:0005918	CG8390-PA						PF03359						474~501								
aly3072.2	Enhancer of polycomb homolog 1	GO:0032777,GO:0000785,GO:0035267,GO:0000123,GO:0000122,GO:0006325,GO:0005634,GO:0005654,GO:0045814,GO:0043967,GO:0043968,GO:0031965,GO:0045892,GO:0045893,GO:0035886,GO:0005725,GO:0070983,GO:0005700,GO:0005701,GO:0045944,GO:0006351,GO:0040008	CG7776-PE																				
aly3074.1	Probable G-protein coupled receptor 101	GO:0043235,GO:0004930,GO:0016021,GO:0004939,GO:0005887,GO:0007267,GO:0071880,GO:0007186	CG12290-PA						PF00001	PS50262	PR00237,PR00237,PR00237		G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly3074.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3077.1	Unknown		n/a																				
aly3077.2	Unknown		n/a																				
aly3077.3	E3 ubiquitin-protein ligase IAP-3	GO:0007423,GO:0050829,GO:0006915,GO:0039648,GO:0006964,GO:0043154,GO:0043066,GO:0008270,GO:0005515,GO:0043281,GO:0061057,GO:0016874,GO:0070534,GO:0033160	CG8293-PA				SM00238,SM00238		PF00653,PF00653	PS50089,PS50143,PS50143		PS01282	G3DSA:1.10.1170.10,G3DSA:1.10.1170.10	SSF57924,SSF57924									
aly3077.4	Unknown		n/a																				
aly3077.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3079.1	Fatty acid synthase	GO:0006633,GO:0047451,GO:0006631,GO:0004320,GO:0042587,GO:0015939,GO:0031325,GO:0008144,GO:0035338,GO:0008270,GO:0001649,GO:0016491,GO:0005737,GO:0070062,GO:0016295,GO:0005835,GO:0016020,GO:0071353,GO:0005739,GO:0006112,GO:0030879,GO:0005794,GO:0006767,GO:0006766,GO:0044822,GO:0004315,GO:0016788,GO:0003824,GO:0047117,GO:0008152,GO:0005886,GO:0044255,GO:0055114,GO:0006084,GO:0042470,GO:0005829,GO:0004312,GO:0004313,GO:0016296,GO:0019432,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319,GO:0044281	CG17374-PC				SM00825,SM00827		PF00109,PF00698,PF02801,PF16197				G3DSA:3.40.366.10,G3DSA:3.40.366.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10	SSF53901,SSF55048,SSF53901,SSF52151,SSF52151	383~403								
aly3079.2	Fatty acid synthase	GO:0047117,GO:0047451,GO:0006633,GO:0005811,GO:0016295,GO:0004320,GO:0016296,GO:0004312,GO:0004313,GO:0009058,GO:0004316,GO:0004317,GO:0004314,GO:0004315,GO:0004319,GO:0055114,GO:0008270	CG3523-PC				SM00829			PS51257			G3DSA:3.40.50.720	SSF51735										
aly3079.3	Apolipoprotein D	GO:0022626,GO:0005783,GO:0006869,GO:0042246,GO:0048678,GO:0030425,GO:0000302,GO:0001525,GO:0051895,GO:0010642,GO:0005615,GO:0014012,GO:2000405,GO:0048471,GO:0043025,GO:0005319,GO:0007420,GO:0048662,GO:0006629,GO:2000098,GO:0009267,GO:0042308,GO:0008340,GO:0034599,GO:0060588,GO:0070062,GO:1900016,GO:0007568,GO:0015485,GO:0042493,GO:0071638,GO:0005576,GO:0006006	CG4604-PA			PIRSF036893			PF00061		PR01273,PR01273,PR01273	PS00213	G3DSA:2.40.128.20	SSF50814									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly308.1	Larval cuticle protein LCP-30	GO:0040003,GO:0042381,GO:0005214,GO:0008010,GO:0031012,GO:0005576,GO:0042302	CG8502-PC						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly308.2	Unknown		n/a																				
aly3087.1	Unknown		n/a												18~45,72~99,47~67								
aly3087.2	Heat shock 70 kDa protein 14	GO:0009408,GO:0005829,GO:0016020,GO:0005840,GO:0005524	CG7182-PA						PF00012		PR00301,PR00301,PR00301,PR00301,PR00301		G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.90.640.10	SSF53067,SSF53067									
aly3087.3	Multiple inositol polyphosphate phosphatase 1	GO:0031931,GO:0031929,GO:0052826,GO:0005788,GO:0034417,GO:0003993	CG4317-PA			PIRSF000894			PF00328				G3DSA:3.40.50.1240	SSF53254									
aly3087.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3087.5	Unknown		n/a																				
aly3087.6	GTP-binding protein Rhes	GO:0031681,GO:0043949,GO:0007626,GO:0016020,GO:0003924,GO:0005622,GO:0005575,GO:0008150,GO:0001963,GO:0008152,GO:0031397,GO:0006184,GO:0005886,GO:0007264,GO:0051897,GO:0033235,GO:0005525	CG13375-PA				SM00173,SM00174,SM00175	TIGR00231	PF00071	PS51421	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly30897.1	Unknown		n/a																				
aly3090.1	Unknown	GO:0005515	CG34113-PO				SM00409		PF07686	PS50835			G3DSA:2.60.40.10	SSF48726									
aly30917.1	Protein prune homolog	GO:0005737,GO:0046872,GO:0004427,GO:0019889,GO:0005634,GO:0030145,GO:0048072,GO:0016462,GO:0004309,GO:0005925,GO:0006798	CG3461-PA						PF02833							00190+3.6.1.1							
aly30924.1	Head-specific guanylate cyclase	GO:0005737,GO:0020037,GO:0016056,GO:0007601,GO:0004383,GO:0016849,GO:0005525,GO:0008074,GO:0046956,GO:0035556,GO:0009190,GO:0006182	CG1912-PA				SM00044		PF00211	PS50125		PS00452	G3DSA:3.30.70.1230	SSF55073									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly30973.1	Unknown	GO:0004842	CG10254-PB																				
aly30988.1	Unknown		n/a																				
aly31.1	Large proline-rich protein bag6-A	GO:0030324,GO:0032435,GO:0050821,GO:0009790,GO:0031593,GO:0070628,GO:0005634,GO:0001822,GO:0043022,GO:0018393,GO:0006810,GO:0007283,GO:0007130,GO:0042771,GO:0007420,GO:0071816,GO:0071818,GO:0005829,GO:0070059,GO:0006511,GO:0045861,GO:0016568	CG7546-PD				SM00213		PF12057,PF00240	PS50053		PS00299	G3DSA:3.10.20.90	SSF54236	1243~1274								
aly31.2	Unknown		n/a																				
aly31.3	Putative peptidyl-prolyl cis-trans isomerase dodo	GO:0005634,GO:0007173,GO:0000413,GO:0003755	CG17051-PA				SM00456		PF00397,PF00639	PS50198,PS50020		PS01159	G3DSA:3.10.50.40,G3DSA:2.20.70.10	SSF54534,SSF51045	99~119								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly31.4	Unknown		n/a																				
aly31.5	Glutamine synthetase 2 cytoplasmic	GO:0005737,GO:0004356,GO:0006542,GO:0045213,GO:0005524,GO:0006538,GO:0007416	CG1743-PD						PF03951,PF00120			PS00181,PS00180	G3DSA:3.10.20.70,G3DSA:3.30.590.10	SSF54368,SSF55931		00330+6.3.1.2,00630+6.3.1.2,00250+6.3.1.2,00910+6.3.1.2	REACT_13	PWY-6964,PWY-6963,PWY-5675,PWY-381,PWY-6549					
aly31.6	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	GO:0005737,GO:0016791,GO:0005634,GO:0008420,GO:0004721,GO:0070940,GO:0006378,GO:0006397	CG14216-PA						PF04722														
aly31.7	Protein zer-1 homolog	GO:0016567,GO:0031462,GO:0004842,GO:0051438	CG12084-PA										G3DSA:1.25.10.10,G3DSA:3.80.10.10	SSF52047,SSF48371	82~102								
aly31.8	Leucine-rich repeats and immunoglobulin-like domains protein 3	GO:0005615,GO:0016021,GO:0007476,GO:0007474,GO:0030659,GO:0005515,GO:0005886,GO:0032474	CG32372-PA				SM00365,SM00365,SM00365,SM00365,SM00365,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058									
aly31.9	Unknown		n/a												476~504,374~420								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly310.1	Teneurin-m	GO:0034116,GO:0051124,GO:0042051,GO:0034110,GO:0097090,GO:0045467,GO:0050808,GO:0008045,GO:0001745,GO:0007274,GO:0030054,GO:0005737,GO:0001941,GO:0043005,GO:0043025,GO:0042802,GO:0042803,GO:0016200,GO:2000331,GO:0031005,GO:0008039,GO:0031122,GO:0045211,GO:0008360,GO:0005887,GO:0005886,GO:0007155,GO:0048499,GO:0048058,GO:0031594,GO:0040017,GO:0048790,GO:0022416,GO:0046982,GO:0005578	CG5723-PE				SM00181,SM00181,SM00181,SM00181,SM00181,SM00181	TIGR01643	PF05593,PF15636	PS50026,PS50026,PS50026,PS50026		PS00022,PS01186,PS00022,PS01186,PS01186,PS01186,PS00022,PS01186,PS00022,PS00022,PS01186,PS00022,PS01186,PS00022	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.170.300.10,G3DSA:2.120.10.30	SSF101898	408~428								
aly310.10	Patatin-like phospholipase domain-containing protein 3	GO:0016020,GO:0006642,GO:0006629,GO:0036153,GO:0051264,GO:0051265,GO:0016021,GO:0005811,GO:0016042,GO:0055088,GO:0019432,GO:0019433,GO:0010884,GO:0008152,GO:0004623,GO:0008340,GO:0004806	CG5295-PB						PF01734					SSF52151									
aly310.11	Protein Cep78 homolog	GO:0003674,GO:0008150,GO:0005813	CG7886-PA				SM00368,SM00368,SM00368,SM00368				PR02062,PR02062,PR02062,PR02062,PR02062		G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047	376~413								
aly310.12	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly310.13	Growth arrest and DNA damage-inducible proteins-interacting protein 1	GO:0005634,GO:0005739,GO:0007049,GO:0071850	CG7172-PA						PF10147						130~150,155~191,210~231								
aly310.14	Clathrin light chain	GO:0008021,GO:0005938,GO:0016183,GO:0016192,GO:0006886,GO:0032050,GO:0072583,GO:0071439,GO:0005198,GO:0030125,GO:0005905,GO:0007269,GO:0030130,GO:0030132,GO:0030135,GO:0030136	CG6948-PA						PF01086								REACT_11123						
aly310.15	N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein	GO:0017176,GO:0016021,GO:0016020,GO:0005789,GO:0030176,GO:0016757,GO:0006506,GO:0000506	CG6401-PA						PF08288,PF00534				G3DSA:3.40.50.2000	SSF53756		00563+2.4.1.198			UPA00196				
aly310.16	Unknown		n/a																				
aly310.17	Unknown		n/a																				
aly310.2	Polypeptide N-acetylgalactosaminyltransferase-like 6	GO:0005795,GO:0046872,GO:0005783,GO:0006486,GO:0016021,GO:0004653,GO:0030246,GO:0000139,GO:0009312	CG2103-PA						PF00535				G3DSA:3.90.550.10	SSF53448									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly310.3	Calnexin	GO:0006457,GO:0005783,GO:0030246,GO:0005789,GO:0048488,GO:0005737,GO:0001895,GO:0016063,GO:0070062,GO:0043209,GO:0016021,GO:0051082,GO:0034185,GO:0005509,GO:0043025,GO:0010522,GO:0001948,GO:0005790,GO:0032839,GO:0044822,GO:0035255,GO:0072583,GO:0005886,GO:0030424,GO:0061077,GO:0043234,GO:0042470,GO:0097038,GO:0007568,GO:0005840,GO:0043197,GO:0044233	CG11958-PD						PF00262		PR00626,PR00626,PR00626,PR00626,PR00626,PR00626	PS00805,PS00805,PS00804	G3DSA:2.10.250.10,G3DSA:2.60.120.200	SSF63887,SSF49899										
aly310.4	Arylsulfatase J	GO:0044267,GO:0043687,GO:0005788,GO:0006665,GO:0005576,GO:0006687,GO:0008152,GO:0003943,GO:0046872,GO:0004065,GO:0044281	CG8646-PB						PF00884			PS00149,PS00523	G3DSA:3.30.1120.10,G3DSA:3.30.1120.10,G3DSA:3.40.720.10	SSF53649,SSF53649										
aly310.5	Unknown		n/a																				
aly310.6	Tyrosine-protein phosphatase corkscrew (Fragment)	GO:0007498,GO:0006470,GO:0007418,GO:0008543,GO:0008069,GO:0007362,GO:0045500,GO:0043066,GO:0005737,GO:0000278,GO:0008595,GO:0007173,GO:0045314,GO:0007424,GO:0007427,GO:0004728,GO:0004726,GO:0004725,GO:0007444,GO:0007465,GO:0007428,GO:0005515,GO:0008293	CG3954-PB				SM00252,SM00252,SM00194,SM00404		PF00102,PF00102,PF00017,PF00017	PS50056,PS50055,PS50001,PS50001	PR00401,PR00401,PR00401,PR00401,PR00401,PR00700,PR00700,PR00700,PR00700,PR00700,PR00700	PS00383	G3DSA:3.30.505.10,G3DSA:3.30.505.10,G3DSA:3.90.190.10,G3DSA:3.90.190.10	SSF52799,SSF52799,SSF55550,SSF55550										
aly310.7	Protein yippee like 5	GO:0005575,GO:0046872,GO:0008150,GO:0008270	CG1989-PA						PF03226														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly310.8	TBC1 domain family member 19	GO:0032313,GO:0005096,GO:0005097	CG7742-PA				SM00164		PF00566	PS50086				SSF47923									
aly310.9	Alkylated DNA repair protein alkB homolog 8	GO:0030488,GO:0000049,GO:0016706,GO:0005829,GO:0000166,GO:0008270,GO:0016630,GO:0008168,GO:0005506,GO:0005634,GO:0055114,GO:0002098	CG17807-PA						PF13532,PF08241	PS51471			G3DSA:2.60.120.590,G3DSA:3.30.70.330,G3DSA:3.40.50.150	SSF53335,SSF51197									
aly3100.1	Gamma-tubulin complex component 2 homolog	GO:0008275,GO:0000226,GO:0007067,GO:0005815,GO:0005874,GO:0051225,GO:0007020,GO:0007126,GO:0072686,GO:0030953,GO:0005813,GO:0000922,GO:0005875,GO:0051011,GO:0051297,GO:0015631,GO:0008017,GO:0007052,GO:0007017,GO:0051726,GO:0007283,GO:0043015	CG3917-PA						PF04130								REACT_152						
aly3109.1	Inactive hydroxysteroid dehydrogenase-like protein 1	GO:0016229,GO:0008285,GO:0007030,GO:0006909,GO:0005783,GO:0005739,GO:0008152,GO:0016491	CG13284-PB			PIRSF000126			PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735									
aly3109.10	Probable H/ACA ribonucleoprotein complex subunit 1	GO:0005732,GO:0030532,GO:0031118,GO:0030559,GO:0005730,GO:0005654,GO:0006364,GO:0009267,GO:0030515,GO:0022008,GO:0031429	CG4038-PA						PF04410				G3DSA:2.40.10.230	SSF50447									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3109.11	Sodium/potassium-transporting ATPase subunit beta-2	GO:0007424,GO:0008324,GO:0098655,GO:0035151,GO:0035158,GO:0006812,GO:0019991,GO:0035725,GO:0006814,GO:0005391,GO:0006813,GO:0005890,GO:0061343,GO:0060857,GO:0005886,GO:0007605,GO:0035159,GO:0030424,GO:0005918	CG9261-PC						PF00287			PS00390	G3DSA:2.60.40.1660,G3DSA:1.20.5.170											
aly3109.2	Unknown		n/a																				
aly3109.3	Cyclic nucleotide-gated cation channel beta-3	GO:0030553,GO:0042391,GO:0006810,GO:1902495,GO:0005887,GO:0071805,GO:0006813,GO:0006812,GO:0005223,GO:0005222,GO:0007601,GO:0008076,GO:0001750,GO:0007605,GO:0022843,GO:0005249,GO:0055085,GO:0007165	CG3182-PA							PS50042			G3DSA:1.10.287.70,G3DSA:2.60.120.10	SSF51206,SSF81324										
aly3109.4	Potassium voltage-gated channel subfamily H member 6	GO:0042391,GO:0005887,GO:0071805,GO:0006813,GO:0007268,GO:0008076,GO:0004871,GO:0007605,GO:0086091,GO:0022843,GO:0005249,GO:0005886,GO:0055085	CG3182-PA				SM00100		PF00027	PS50042			G3DSA:1.10.287.630,G3DSA:2.60.120.10	SSF81324,SSF51206										
aly3109.5	Cyclic nucleotide-gated cation channel alpha-3	GO:0030553,GO:0042391,GO:0050896,GO:1902495,GO:0005249,GO:0071805,GO:0005221,GO:0006812,GO:0005223,GO:0005222,GO:0046549,GO:0001750,GO:0007601,GO:0019935,GO:0005887,GO:0055085,GO:0017071	CG43395-PJ						PF00027	PS50042			G3DSA:2.60.120.10	SSF51206										
aly3109.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3109.7	Succinate--hydroxymethylglutarate CoA-transferase	GO:0003824,GO:0005739,GO:0008152,GO:0047369	CG10877-PA						PF07491,PF02515				G3DSA:3.40.50.10540,G3DSA:3.40.50.10540,G3DSA:3.30.1540.10	SSF89796									
aly3109.8	Unknown		n/a												26~53								
aly3109.9	Membrane magnesium transporter 1	GO:0005794,GO:0016021,GO:0072546,GO:0000139,GO:0015693,GO:0015095,GO:0005769,GO:0031901	CG15168-PA						PF10270						113~117								
aly311.1	Unknown		n/a																				
aly311.10	Alpha-(1,3)-fucosyltransferase C	GO:0036065,GO:0006486,GO:0016021,GO:0016020,GO:0008417,GO:0005886,GO:0032580,GO:0046920	CG40305-PB						PF00852,PF17039					SSF53756					UPA00378				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly311.11	Forkhead box protein B1	GO:0006351,GO:0007595,GO:0021510,GO:0009790,GO:0043524,GO:0007412,GO:0009653,GO:0061381,GO:0043565,GO:0000122,GO:0033504,GO:0005634,GO:0022029,GO:0061379,GO:0021855,GO:0061374,GO:0003690,GO:0008542,GO:0000981,GO:0021794,GO:0007389,GO:0008134,GO:0009888,GO:0008301,GO:0001655,GO:0061030,GO:0001756,GO:0061377,GO:0051090,GO:0021767,GO:0003700,GO:0003705,GO:0006355,GO:0006357,GO:0030901,GO:0005667	CG11152-PA				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00657,PS00658	G3DSA:1.10.10.10	SSF46785										
aly311.12	Ubiquitin carboxyl-terminal hydrolase 3	GO:0005737,GO:0042393,GO:0031647,GO:0000278,GO:0006281,GO:0090263,GO:0043161,GO:0005634,GO:0004197,GO:0008587,GO:0016578,GO:0006355,GO:0000790,GO:0006511,GO:0008270,GO:0061136,GO:0016579,GO:0004843,GO:0045880	CG5798-PA				SM00290		PF02148,PF00443	PS50235,PS50271		PS00972,PS00973	G3DSA:3.30.40.10	SSF57850,SSF54001										
aly311.13	40S ribosomal protein S17	GO:0000028,GO:0005840,GO:0005622,GO:0003735,GO:0006414,GO:0006412,GO:0022627	CG3922-PB	MF_00511					PF00833			PS00712	G3DSA:1.10.60.20	SSF116820										
aly311.14	46 kDa FK506 binding nuclear protein	GO:0000412,GO:0006457,GO:0018208,GO:0035626,GO:0005730,GO:0016242,GO:0005634,GO:0016020,GO:0005875,GO:0005528,GO:0005515,GO:0003677,GO:0003755,GO:0010507,GO:0070594	CG6226-PA			PIRSF001473			PF00254	PS50059			G3DSA:3.10.50.40	SSF54534	99~119									
aly311.15	Protein AF-9	GO:0090090,GO:0008023,GO:0005674,GO:0007379,GO:0070062,GO:0032783,GO:2000096,GO:0006355,GO:0006351,GO:0006367,GO:0005669,GO:0009952	CG4913-PB						PF03366	PS51037													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly311.16	Unknown		n/a																				
aly311.2	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	GO:0004487,GO:0004329,GO:0009396,GO:0005975,GO:0005615,GO:0005829,GO:0000287,GO:0004477,GO:0004488,GO:0042301,GO:0003824,GO:0009256,GO:0005739,GO:0046653,GO:0006730,GO:0055114	CG18466-PB	MF_01576					PF00763,PF02882		PR00085,PR00085,PR00085,PR00085,PR00085,PR00085,PR00085	PS00767,PS00766	G3DSA:3.40.192.10,G3DSA:3.40.50.720	SSF53223,SSF51735		00670+1.5.1.5+3.5.4.9,00720+1.5.1.5+3.5.4.9		PWY-1722,PWY-3841,PWY-5030,PWY-5497,PWY-2201,PWY-6613	UPA00193				
aly311.3	Furin-like protease 2	GO:0004252,GO:0051048,GO:0016021,GO:0005886,GO:0016485,GO:0006508	CG18734-PB				SM00261,SM00261,SM00261,SM00261,SM00261,SM00261,SM00261,SM00261,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181		PF16470,PF14843,PF00082,PF01483	PS51257	PR00723,PR00723,PR00723	PS00138,PS00136,PS00137	G3DSA:2.10.220.10,G3DSA:2.60.120.260,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:3.40.50.200,G3DSA:3.30.70.850,G3DSA:2.10.220.10,G3DSA:2.10.220.10,G3DSA:2.10.220.10	SSF49785,SSF52743,SSF57184,SSF54897,SSF57184,SSF57184										
aly311.4	Secretory carrier-associated membrane protein 1	GO:0008021,GO:0005802,GO:0043195,GO:0055038,GO:0007616,GO:0016079,GO:0016021,GO:0006887,GO:0030424,GO:0042589,GO:0045202,GO:0015031,GO:0030672,GO:0007274	CG9195-PA						PF04144						94~121								
aly311.5	Pre-mRNA-splicing factor RBM22	GO:0005737,GO:0036002,GO:0033120,GO:0000381,GO:0071011,GO:0005634,GO:0045292,GO:0000398,GO:0000166,GO:0017069,GO:0003676,GO:0043009,GO:0046872,GO:0071013,GO:0005681,GO:0003729	CG14641-PA				SM00360,SM00356		PF00076	PS50103,PS50102			G3DSA:3.30.70.330	SSF54928,SSF90229									
aly311.6	WD repeat-containing protein 61	GO:0005737,GO:0003700,GO:0005634,GO:0045944,GO:0005515,GO:0016593,GO:0035327,GO:0032968,GO:0055087	CG3909-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400	PS50294,PS50082,PS50082,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly311.7	WD repeat-containing protein 61	GO:0005737,GO:0003700,GO:0005634,GO:0045944,GO:0005515,GO:0016593,GO:0035327,GO:0032968,GO:0055087	CG3909-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50082,PS50294,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978										
aly311.8	Cuticle protein	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG15006-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly311.9	Cuticle protein	GO:0040003,GO:0005214,GO:0008011,GO:0008010,GO:0031012,GO:0022008,GO:0042302	CG31876-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233			125~145								
aly3110.1	Unknown		n/a																				
aly3113.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG1213-PA						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171		G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3113.2	Octopamine receptor	GO:0004930,GO:0007186,GO:0071418,GO:0071928,GO:0016021,GO:0007211,GO:0005887,GO:0005886,GO:0004989,GO:0008226,GO:0008227,GO:1900738	CG7431-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR01102,PR01102,PR01102,PR01102	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly3113.3	Lysyl oxidase homolog 2	GO:0003714,GO:0002040,GO:0035064,GO:0001837,GO:0070492,GO:0018277,GO:0043542,GO:0001666,GO:0005615,GO:0005634,GO:0016020,GO:0032332,GO:0016570,GO:0046688,GO:0005507,GO:0005694,GO:0006464,GO:0045892,GO:0007155,GO:0055114,GO:0005604,GO:0005044,GO:0004720,GO:0030199,GO:0006351,GO:0003682,GO:0001935	CG4402-PA				SM00202		PF01186,PF00530,PF00530	PS50287,PS50287	PR00258,PR00258,PR00258,PR00258,PR00074,PR00074	PS00926	G3DSA:3.10.250.10,G3DSA:3.10.250.10	SSF56487,SSF56487									
aly3113.4	ABC transporter G family member 20	GO:0043190,GO:0042626,GO:0006810,GO:0005215,GO:0016020,GO:0055085,GO:0005524	CG33970-PA				SM00382		PF00005,PF01061	PS51012,PS50893		PS00211	G3DSA:3.40.50.300	SSF52540									
aly31173.1	Dynein beta chain, ciliary	GO:0005737,GO:0042623,GO:0007605,GO:0007018,GO:0005858,GO:0005875,GO:0030030,GO:0005524,GO:0016887,GO:0031514,GO:0030286,GO:0005874,GO:0003774,GO:0003777	CG3723-PC						PF03028														
aly31177.1	Choline/ethanolamine kinase	GO:0004103,GO:0006646,GO:0006657,GO:0006656,GO:0016310,GO:0005829,GO:0006664,GO:0004305,GO:0044281,GO:0046474,GO:0005524	CG2201-PB										G3DSA:3.10.450.110	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3123.1	Unknown		n/a																				
aly3125.1	Unknown		n/a																				
aly3125.10	Unknown	GO:0003677	n/a						PF05225														
aly3125.11	Unknown		n/a																				
aly3125.12	Peptidyl-prolyl cis-trans isomerase	GO:0005737,GO:0006457,GO:0005515,GO:0005622,GO:0008270,GO:0003755,GO:0042277	CG5071-PB						PF00160	PS50089,PS50072		PS00518	G3DSA:2.40.100.10,G3DSA:3.30.40.10	SSF57850,SSF50891									
aly3125.2	Sodium-independent sulfate anion transporter	GO:0045434,GO:0005794,GO:0005783,GO:0015301,GO:0016021,GO:0005886,GO:0005765,GO:0008271,GO:0008272,GO:0008509,GO:0070062	CG7005-PA						PF01740,PF00916	PS50801		PS01130	G3DSA:3.30.750.24	SSF52091									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3125.3	Prominin-like protein	GO:0016021,GO:0048812,GO:0005886	CG7740-PB						PF05478,PF05478	PS51257													
aly3125.4	Sodium-independent sulfate anion transporter	GO:0005794,GO:0005783,GO:0015301,GO:0005215,GO:0016021,GO:0005886,GO:0015116,GO:0005765,GO:0008271,GO:0008272,GO:0098656,GO:0008509,GO:0015381,GO:0070062	CG6125-PA						PF00916														
aly3125.5	Desumoylating isopeptidase 1	GO:0005737,GO:0003012,GO:0005634,GO:0008233	CG6972-PA						PF05903						255~275,181~215								
aly3125.6	Nuclear protein localization protein 4 homolog	GO:0017056,GO:0098586,GO:0005643,GO:0043161,GO:0005829,GO:0005654,GO:0006511,GO:0008270,GO:0022008,GO:0031625,GO:0005634,GO:0043130	CG4673-PA			PIRSF010052			PF05020,PF11543,PF05021				G3DSA:3.10.20.90	SSF54236									
aly3125.7	Unknown	GO:0008270	n/a				SM00547			PS50199		PS01358	G3DSA:4.10.1060.10	SSF90209									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3125.8	WD repeat domain phosphoinositide-interacting protein 2	GO:0050688,GO:0035069,GO:0016236,GO:0019898,GO:0034045,GO:0005737,GO:0080025,GO:0005776,GO:0000045,GO:0005654,GO:0010506,GO:0043234,GO:0006914,GO:0034497,GO:0044804,GO:0006497,GO:0006995,GO:0000421,GO:0000422,GO:0005829,GO:0032266,GO:0005515	CG7986-PE				SM00320,SM00320						G3DSA:2.130.10.10	SSF50978										
aly3125.9	Unknown		n/a																				
aly3128.1	Uncharacterized protein CG3556	GO:0005575,GO:0031419,GO:0005576,GO:0015889	CG3556-PA						PF01122,PF00432				G3DSA:1.50.10.20,G3DSA:1.50.10.20	SSF48239,SSF48239										
aly3128.2	Ectonucleoside triphosphate diphosphohydrolase 5	GO:0005737,GO:0016787,GO:0016049,GO:0005783,GO:0006487,GO:0008283,GO:0051084,GO:0046034,GO:0004382,GO:0017110,GO:0017111,GO:0045134,GO:0045821,GO:0014066,GO:0070062	CG3059-PF						PF01150														
aly3128.3	Zinc finger protein 511	GO:0005634,GO:0006355,GO:0006351,GO:0003677,GO:0046872,GO:0007275	CG13951-PA				SM00355,SM00355,SM00355					PS00028,PS00028											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3128.4	Phosphoglycerate mutase 1	GO:0031430,GO:0005975,GO:0043209,GO:0005829,GO:0004082,GO:0004083,GO:0044281,GO:0016868,GO:0004619,GO:0006096,GO:0030018,GO:0006094	CG1721-PA	MF_01039			SM00855	TIGR01258	PF00300			PS00175	G3DSA:3.40.50.1240	SSF53254		00010+5.4.2.11,00260+5.4.2.11,00680+5.4.2.11		PWY-5484,PWY-1622	UPA00109				
aly3128.5	Unknown		n/a												376~396								
aly3128.6	Unknown		n/a																				
aly3128.7	Mitochondrial import inner membrane translocase subunit Tim22	GO:0042721,GO:0015450,GO:0006626,GO:0045039,GO:0015266,GO:0005744,GO:0016021	CG31229-PA						PF02466														
aly3128.8	Unknown		n/a																				
aly3128.9	Protein spinster homolog 1	GO:0040011,GO:0003376,GO:0031982,GO:0005743,GO:0006914,GO:0090398,GO:0046624,GO:0055085,GO:0005765,GO:0097352,GO:0016021	CG14439-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly313.1	Chorion peroxidase	GO:0042744,GO:0005615,GO:0020037,GO:0030707,GO:0006979,GO:0004666,GO:0001516,GO:0004601,GO:0007304,GO:0007306,GO:0042743,GO:0046872,GO:0005875,GO:0055114	CG7660-PB						PF03098	PS50292	PR00457,PR00457,PR00457,PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									
aly313.2	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0030672,GO:0016021,GO:0016020,GO:0008513,GO:0022857,GO:0001669,GO:0005886,GO:0006836,GO:0055085,GO:0030054	CG15221-PB						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473									
aly313.3	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0030672,GO:0016021,GO:0016020,GO:0022857,GO:0046331,GO:0001669,GO:0005886,GO:0006836,GO:0055085,GO:0030054	CG3690-PA						PF07690	PS50850			G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473,SSF103473									
aly313.4	Unknown	GO:0005215,GO:0016021,GO:0055085	CG31103-PB										G3DSA:1.20.1250.20	SSF103473									
aly313.5	Putative carbonic anhydrase 5	GO:0006730,GO:0004089,GO:0008270,GO:0005576	CG3940-PA				SM01057		PF00194	PS51144			G3DSA:3.10.200.10	SSF51069									
aly313.6	Putative carbonic anhydrase 5	GO:0006730,GO:0004089,GO:0008270,GO:0005576	CG3940-PA				SM01057		PF00194	PS51144		PS00162	G3DSA:3.10.200.10	SSF51069		00910+4.2.1.1		PWY-6142,PWY-241,PWY-7117,PWY-7115					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly313.7	Protein TBRG4	GO:0044822,GO:0045333,GO:0005739,GO:0004672	CG13850-PA				SM00952		PF08368,PF08373	PS51286,PS50006													
aly31349.1	Unknown		n/a																				
aly31353.1	Phosphoinositide 3-kinase regulatory subunit 4	GO:0006468,GO:0005770,GO:0006963,GO:0031410,GO:0002784,GO:0016236,GO:0005776,GO:0035032,GO:0004674,GO:0034198,GO:0042149,GO:0005930,GO:0005524	CG9746-PA																				
aly31387.1	Septin-interacting protein 1	GO:0071008,GO:0000390,GO:0071011,GO:0071013,GO:0000398,GO:0006355,GO:0003677,GO:0005578,GO:0005681	CG7238-PA						PF12457														
aly314.1	Protein amalgam	GO:0050767,GO:0042332,GO:0005515,GO:0009986,GO:0019991,GO:0043005,GO:0005886,GO:0016337,GO:0005918,GO:0043025,GO:0031225	CG34353-PC				SM00408,SM00408,SM00408,SM00409,SM00409,SM00406		PF07686,PF07679,PF07679	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726										
aly314.10	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly314.11	Unknown		n/a										G3DSA:2.120.10.30	SSF101898									
aly314.12	Unknown		n/a										G3DSA:2.120.10.30	SSF69322									
aly314.13	Unknown		n/a										G3DSA:2.120.10.30	SSF63829									
aly314.14	Unknown	GO:0005515	n/a										G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50969,SSF50969,SSF50969									
aly314.15	Pro-resilin	GO:0040003,GO:0032992,GO:0005214,GO:0030023,GO:0008010,GO:0031012,GO:0005576,GO:0008061,GO:0042302	CG13338-PA						PF00379	PS51155		PS00233											
aly314.16	F-box only protein 28	GO:0043652	CG3428-PA						PF00646	PS50181			G3DSA:1.20.1280.50	SSF81383	229~263								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly314.17	Zinc finger protein 26	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12874,PF12756,PF13909,PF13909,PF13909	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly314.18	Adrenodoxin-like protein, mitochondrial	GO:0051537,GO:0005739,GO:0008150,GO:0005759,GO:0046872,GO:0055114,GO:0009055	CG4205-PA						PF00111	PS51085	PR00355,PR00355,PR00355	PS00814	G3DSA:3.10.20.30	SSF54292									
aly314.19	RE1-silencing transcription factor	GO:0043922,GO:0071385,GO:0010629,GO:0035690,GO:2000798,GO:0046676,GO:0003676,GO:0003677,GO:0003700,GO:0001078,GO:0070933,GO:0043065,GO:0000122,GO:0005634,GO:0002244,GO:0050768,GO:0045665,GO:0045955,GO:2000740,GO:0043280,GO:0046872,GO:2000706,GO:0008285,GO:0071257,GO:0017053,G	CG1233-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly314.2	Proton-coupled amino acid transporter 1	GO:0005280,GO:0015992,GO:0005783,GO:0055085,GO:0035524,GO:1902600,GO:0016021,GO:0006865,GO:0015816,GO:0015193,GO:0005765,GO:0015078,GO:0005886,GO:0006811,GO:0015187,GO:0015808,GO:0015180	CG43693-PG						PF01490														
aly314.20	Unknown		n/a																				
aly314.3	Probable beta-hexosaminidase fdl	GO:0005794,GO:0005770,GO:0005975,GO:0007420,GO:0006491,GO:0032428,GO:0016231,GO:0004563,GO:0006517,GO:0005886,GO:0004553,GO:0016063,GO:0006032,GO:0005783	CG8824-PB						PF00728,PF14845		PR00738,PR00738,PR00738,PR00738		G3DSA:3.30.379.10,G3DSA:3.20.20.80	SSF55545,SSF51445		00604+3.2.1.52,00520+3.2.1.52,00511+3.2.1.52,00603+3.2.1.52,00513+3.2.1.52,00531+3.2.1.52		PWY-6902					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly314.4	Unknown		n/a																				
aly314.5	Unknown		n/a																				
aly314.6	GTP cyclohydrolase 1	GO:0005737,GO:0006728,GO:0060308,GO:0009880,GO:0035185,GO:0043095,GO:0003934,GO:0035998,GO:0048072,GO:0048067,GO:0008363,GO:0008270,GO:0006729,GO:0046654,GO:2000274,GO:0005525	CG9441-PA	MF_00223				TIGR00063	PF01227			PS00860,PS00859	G3DSA:1.10.286.10,G3DSA:3.30.1130.10	SSF55620		00790+3.5.4.16		PWY-5663,PWY-6147,PWY-7442,PWY-5664,PWY-6703,PWY-6983	UPA00848				
aly314.7	Unknown		n/a											SSF50969	178~198								
aly314.8	Unknown		n/a																				
aly314.9	Unknown		n/a										G3DSA:2.140.10.10	SSF63829									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3146.1	Unknown		n/a																				
aly315.1	Collagen alpha 1(XV) chain	GO:0005201,GO:0030154,GO:0030246,GO:0005788,GO:0031012,GO:0007165,GO:0008045,GO:0001525,GO:0007005,GO:0005581,GO:0005582,GO:0016021,GO:0005198,GO:0005576,GO:0022617,GO:2001046,GO:0014732,GO:0007155,GO:0005615,GO:0070062,GO:0030574,GO:0030198,GO:0071711,GO:0014899	CG42543-PR				SM00210		PF06482,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391				G3DSA:3.10.100.10	SSF56436,SSF49899									
aly315.10	Glucose-fructose oxidoreductase domain-containing protein 1	GO:0005576,GO:0016491	CG17712-PA						PF01408				G3DSA:3.30.360.10,G3DSA:3.30.360.10,G3DSA:3.40.50.720	SSF51735,SSF55347									
aly315.11	10 kDa heat shock protein, mitochondrial	GO:0005737,GO:0005811,GO:0006457,GO:0006458,GO:0005739,GO:0051082,GO:0005759,GO:0005524	CG11267-PA	MF_00580			SM00883		PF00166		PR00297,PR00297,PR00297,PR00297	PS00681	G3DSA:2.30.33.40	SSF50129									
aly315.12	Esterase FE4	GO:0005575,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135			PS00122,PS00941	G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly315.13	Esterase E4	GO:0060179,GO:0007476,GO:0052689	CG9858-PA						PF00135			PS00122,PS00941	G3DSA:3.40.50.1820	SSF53474									
aly315.14	THAP domain containing protein 2	GO:0005730,GO:0046872,GO:0003677	n/a				SM00980,SM00692		PF05485	PS50950				SSF57716									
aly315.15	Cysteine synthase	GO:0005737,GO:0030554,GO:0004122,GO:0004124,GO:0006535,GO:0016740,GO:0019343,GO:0008340	CG1753-PA						PF00291			PS00901	G3DSA:3.40.50.1100,G3DSA:3.40.50.1100,G3DSA:3.40.50.1100	SSF53686									
aly315.16	Unknown		n/a																				
aly315.17	Unknown		n/a																				
aly315.18	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly315.19	Cytochrome P450 6B7	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0042742,GO:0005506,GO:0055114,GO:0009055	CG2397-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly315.2	Unknown		n/a												15~35								
aly315.3	Multiple C2 and transmembrane domain-containing protein 1	GO:0016021,GO:0005622,GO:0008150,GO:0005509,GO:0019722	CG33146-PA				SM00239		PF08372,PF00168,PF00168				G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562	334~354								
aly315.4	Cysteine sulfinic acid decarboxylase	GO:0007632,GO:0000098,GO:0042412,GO:0004782,GO:0000096,GO:0019752,GO:0019483,GO:0004068,GO:0003824,GO:0034641,GO:0048066,GO:0006212,GO:0004351,GO:0044281,GO:0030170	CG7811-PA						PF00282				G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383									
aly315.5	Serine/threonine-protein kinase RIO1	GO:0004674,GO:0022008,GO:0004672,GO:0005524,GO:0060252	CG11660-PB			PIRSF038147	SM00090		PF01163			PS01245	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly315.6	ATP-binding cassette sub-family G member 1	GO:0043231,GO:0009897,GO:0034375,GO:0034374,GO:0005887,GO:0055037,GO:0017127,GO:0005789,GO:0034041,GO:0042157,GO:0016887,GO:0042987,GO:1901998,GO:0055091,GO:0005548,GO:0042626,GO:0055099,GO:0033993,GO:0005543,GO:0005739,GO:0055085,GO:0005654,GO:0034436,GO:0034437,GO:0010745,GO:0010875,GO:0005524,GO:0033700,GO:0005794,GO:0005215,GO:0006810,GO:0042803,GO:0043531,GO:0005886,GO:0010872,GO:0042632,GO:0043691,GO:0010033,GO:0008203,GO:0043190,GO:0019534,GO:0015485,GO:0032367,GO:0009720,GO:0000139,GO:0010887,GO:0006355,GO:0033344,GO:0045542,GO:0046983,GO:0046982,GO:0005768,GO:0044281	CG32091-PB				SM00382		PF01061,PF00005	PS50893		PS00211	G3DSA:3.40.50.300	SSF52540										
aly315.7	WW domain-binding protein 11	GO:0005737,GO:0016607,GO:0050699,GO:0071011,GO:0071013,GO:0050790,GO:0044822,GO:1903146,GO:0000398,GO:0008599,GO:0005654,GO:1903955,GO:0006364,GO:0005634,GO:0008380,GO:0006396,GO:0006397	CG2685-PA						PF09429						308~328								
aly315.8	Arf-GAP with dual PH domain-containing protein 1	GO:0005737,GO:0043547,GO:0032312,GO:0005634,GO:0005096,GO:0005575,GO:0008060,GO:0008270,GO:0007166,GO:0005886,GO:0043533,GO:0046872,GO:0043087	CG8243-PA				SM00105,SM00233,SM00233		PF00169,PF00169,PF01412	PS50003,PS50115,PS50003	PR00405,PR00405,PR00405		G3DSA:2.30.29.30,G3DSA:2.30.29.30	SSF57863,SSF50729,SSF50729									
aly315.9	Musculin	GO:0000122,GO:0003700,GO:0005634,GO:0060021,GO:0014707,GO:0045944,GO:0006351,GO:0060539,GO:0001206,GO:0046983,GO:0046982,GO:0007522,GO:0000981,GO:0000980	CG5005-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3157.1	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246	n/a				SM00034,SM00034		PF00059,PF00059	PS50041,PS51257			G3DSA:3.10.100.10,G3DSA:3.10.100.10	SSF56436,SSF56436									
aly3157.2	Unknown		n/a																				
aly3157.3	Unknown		n/a																				
aly3157.4	ATP-dependent DNA helicase PIF1	GO:0000723,GO:0006310,GO:0000002,GO:0006281,GO:0005634,GO:0003677,GO:0005739,GO:0043141,GO:0003678,GO:0005524	CG3238-PA						PF05970				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540									
aly3157.5	Unknown		n/a																				
aly3157.6	Zinc carboxypeptidase A 1	GO:0007586,GO:0006508,GO:0004181,GO:0008270,GO:0005615	CG4017-PA				SM00631		PF00246,PF02244		PR00765,PR00765,PR00765,PR00765	PS00132,PS00133	G3DSA:3.40.630.10,G3DSA:3.30.70.340	SSF54897,SSF53187									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3157.7	Lachesin	GO:0007424,GO:0016331,GO:0019991,GO:0035151,GO:0043005,GO:0050767,GO:0009986,GO:0007606,GO:0035160,GO:0005575,GO:0042803,GO:0005918,GO:0061343,GO:0003674,GO:0005515,GO:0005886,GO:0016337,GO:0007156,GO:0043025,GO:0031225	CG12191-PA				SM00409,SM00409,SM00408,SM00408,SM00406,SM00406		PF07686,PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly3157.8	Unknown		n/a																				
aly3158.1	Transcription factor E2F2	GO:0008284,GO:0001047,GO:0035206,GO:0003677,GO:0000082,GO:0000083,GO:0001077,GO:0007307,GO:0072332,GO:0043565,GO:0019730,GO:0000122,GO:0005634,GO:0007476,GO:0005654,GO:0006367,GO:0000981,GO:0048666,GO:0045850,GO:0000278,GO:1990086,GO:0001012,GO:0008134,GO:0009987,GO:0005667,GO:0042023,GO:0045893,GO:0045476,GO:0040007,GO:0051726,GO:0003700,GO:0007444,GO:0048813,GO:0010628,GO:0045944,GO:0005515,GO:0060537,GO:0035189	CG6376-PD						PF02319,PF16421				G3DSA:1.10.10.10	SSF144074,SSF46785									
aly3158.2	Protein archease-like	GO:0005575,GO:0008033,GO:0022008,GO:0046872,GO:0003674	CG6353-PA						PF01951				G3DSA:3.55.10.10	SSF69819									
aly3158.3	Unknown	GO:0007018,GO:0005869,GO:0035206	CG9893-PA						PF07426						157~177								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3158.4	Pre-mRNA 3'-end-processing factor FIP1	GO:0006398,GO:0005634,GO:0003723,GO:0017022,GO:0006397	CG1078-PA						PF05182														
aly3158.5	Pumilio homolog 2	GO:0042078,GO:0048149,GO:0008258,GO:0007616,GO:0008582,GO:0034063,GO:0042059,GO:0050804,GO:0031594,GO:0007067,GO:0005737,GO:0045786,GO:0000900,GO:1900246,GO:0001709,GO:0003730,GO:0048471,GO:0016477,GO:0048477,GO:0044822,GO:0031965,GO:0007281,GO:0008595,GO:0060964,GO:0045892,GO:0061176,GO:0007268,GO:0000288,GO:0097482,GO:0010494,GO:0045727,GO:0007280,GO:0048813,GO:0003723,GO:0017148,GO:0006417,GO:0061177,GO:2000637	CG9755-PA				SM00025,SM00025,SM00025,SM00025,SM00025,SM00025,SM00025		PF00806,PF00806,PF00806,PF00806,PF00806,PF00806,PF00806,PF00806	PS50302,PS50302,PS50302,PS50302,PS50302,PS50303,PS50302,PS50302,PS50302			G3DSA:1.25.10.10	SSF48371									
aly31635.1	Unknown		n/a																				
aly3165.1	Chorion class A protein Ld2/Ld41	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														
aly3165.2	Chorion class A protein Ld2/Ld41	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3165.3	Chorion class A protein Ld5	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723,PF01723														
aly3165.4	Chorion class A protein Ld2/Ld41	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723,PF01723														
aly3165.5	Chorion class A protein Ld2/Ld41	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														
aly3165.6	Unknown		n/a																				
aly3167.1	Tachykinin-like peptides receptor 86C	GO:0007218,GO:0006935,GO:0016021,GO:0007217,GO:0004950,GO:0005887,GO:0008188,GO:0004995,GO:0002121,GO:0007186	CG6515-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly3167.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3167.3	Unknown		n/a																				
aly3169.1	Death-associated inhibitor of apoptosis 2	GO:0006964,GO:0090307,GO:0008270,GO:0050829,GO:0070936,GO:0005876,GO:0005737,GO:0043154,GO:0009966,GO:0061630,GO:0005634,GO:0043066,GO:0042787,GO:0043281,GO:0048471,GO:0070534,GO:0043027,GO:0033160,GO:0089720,GO:0045087,GO:1990001,GO:0061057,GO:0016874,GO:0031625,GO:0007423,GO:0016567,GO:0005515	CG8293-PA				SM00184		PF13920	PS50089			G3DSA:3.30.40.10	SSF57850									
aly3169.2	Apoptosis inhibitor IAP	GO:0090263,GO:0019899,GO:0046673,GO:0007289,GO:0008270,GO:0007298,GO:0007275,GO:0008354,GO:0005737,GO:0005634,GO:0008407,GO:0019788,GO:0048800,GO:0043066,GO:0042787,GO:0031398,GO:0045035,GO:0006915,GO:0009987,GO:0007283,GO:1990001,GO:0004869,GO:0007423,GO:0043154,GO:0051865,GO:0097340,GO:0005515	CG12284-PB				SM00238,SM00238		PF00653,PF00653,PF13920	PS50143,PS50143,PS51257,PS50089		PS01282	G3DSA:1.10.1170.10,G3DSA:1.10.1170.10,G3DSA:3.30.40.10	SSF57924,SSF57924,SSF57924									
aly3169.3	DNA mismatch repair protein Msh2	GO:0006298,GO:0030983,GO:0000228,GO:0007049,GO:0010165,GO:0043570,GO:0006302,GO:0006301,GO:0032138,GO:0032137,GO:0005524,GO:0031573,GO:0000403,GO:0008094,GO:0000400,GO:0010224,GO:0042771,GO:0006311,GO:0045128,GO:0000406,GO:0000404,GO:0000710,GO:0032301,GO:0032302,GO:0003684	CG4215-PA			PIRSF005813	SM00533,SM00534		PF05188,PF00488,PF05190,PF05192			PS00486	G3DSA:1.10.1420.10,G3DSA:3.40.50.300	SSF52540,SSF48334	417~448,159~179,386~406									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3169.4	Unknown		n/a																				
aly3169.5	Unknown		n/a																				
aly3169.6	Monocarboxylate transporter 10	GO:0015349,GO:0008028,GO:0005215,GO:0016021,GO:0034220,GO:0005887,GO:0055085,GO:0015173	CG10019-PB						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly3169.7	Unknown		n/a																				
aly31707.1	Unknown		n/a																				
aly3176.1	Unknown	GO:0003899,GO:0003677,GO:0006383,GO:0005666	CG5147-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3176.2	Unknown		n/a																				
aly3176.3	Trafficking protein particle complex subunit 2	GO:0005794,GO:0033227,GO:0006888,GO:0016192,GO:0007224,GO:0005634,GO:0007283,GO:0003674,GO:0006351,GO:0048471,GO:0030008,GO:0005783	CG5161-PA						PF04628				G3DSA:3.30.450.70	SSF64356									
aly3176.4	Unknown		n/a																				
aly3176.5	Kinetochore protein NDC80 homolog	GO:0005634,GO:0007052,GO:0031262,GO:0051301,GO:0007059,GO:0007067,GO:0000776,GO:0000777	n/a						PF03801						380~400,606~648,529~549,298~339,578~598								
aly3176.6	Unknown		n/a																				
aly3176.7	Nucleolar complex protein 3 homolog	GO:0005730,GO:0005634,GO:0005575,GO:0003674,GO:0008150,GO:0003682	CG1234-PA						PF07540,PF03914						294~314,392~445								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3176.8	Regulator of G protein signaling loco	GO:0055059,GO:0010001,GO:0007310,GO:0008105,GO:0007419,GO:0008277,GO:0007303,GO:0003015,GO:0042594,GO:0008069,GO:0007049,GO:0005737,GO:0043547,GO:0005057,GO:0019991,GO:0045179,GO:0016324,GO:0001965,GO:0060857,GO:0007186,GO:0038032,GO:0032291,GO:0005092,GO:0050790,GO:0005096,GO:0050832,GO:0014045,GO:0009786,GO:0005886,GO:0009408,GO:0006979,GO:0000578,GO:0030866	CG5248-PD				SM00228,SM00462		PF00595	PS50106,PS01179			G3DSA:2.30.29.30,G3DSA:2.30.42.10	SSF50729,SSF50156										
aly3177.1	Protein Wnt-7b	GO:0048675,GO:0016332,GO:0050808,GO:0030324,GO:0060710,GO:0048568,GO:0048144,GO:0005788,GO:0042592,GO:0010628,GO:0072054,GO:0009798,GO:0007275,GO:0071300,GO:0072053,GO:0007517,GO:0001701,GO:0005615,GO:0000122,GO:0003338,GO:0072205,GO:0072207,GO:0060560,GO:0045669,GO:0021871,GO:0008284,GO:0005796,GO:1902262,GO:0030182,GO:0060425,GO:0060428,GO:0070307,GO:0060033,GO:0045879,GO:0060070,GO:0046330,GO:0060669,GO:0005886,GO:0060484,GO:0022009,GO:0072061,GO:0072060,GO:0060482,GO:0007424,GO:0045165,GO:0042475,GO:0009952,GO:0072236,GO:0016055,GO:0072089,GO:0044237,GO:0005578,GO:0005109,GO:0005576,GO:0060535,GO:0051145,GO:0005102,GO:0032364,GO:0061180	CG1916-PA				SM00097		PF00110		PR01349,PR01349,PR01349,PR01349	PS00246					REACT_14797						
aly3177.10	Putative ferric-chelate reductase 1 homolog	GO:0000293,GO:0016021,GO:0055114	CG8399-PB				SM00664,SM00665		PF03351,PF02014	PS50939,PS51019,PS50836													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3177.11	Basement membrane-specific heparan sulfate proteoglycan core protein	GO:0008022,GO:0008104,GO:0042052,GO:0048704,GO:0046716,GO:0031012,GO:0003674,GO:0050829,GO:0005925,GO:0001525,GO:0005615,GO:0030198,GO:0002020,GO:0002062,GO:0046872,GO:0005576,GO:0060351,GO:0005796,GO:0070062,GO:0005605,GO:0005604,GO:0007420,GO:0001958,GO:0048738,GO:0045824,GO:0005578	CG8403-PA				SM00181,SM00181,SM00282,SM00282,SM00282		PF02210,PF02210,PF00054	PS50025,PS50025,PS50025		PS00022,PS01186,PS01186	G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.200	SSF57184,SSF57184,SSF57184,SSF49899,SSF49899										
aly3177.12	Alpha-N-acetylgalactosaminidase	GO:0005737,GO:0008456,GO:0005975,GO:0009311,GO:0016139,GO:0005764,GO:0004557,GO:0004553,GO:0046477	CG5731-PA						PF16499,PF16499		PR00740,PR00740,PR00740,PR00740,PR00740	PS00512	G3DSA:3.20.20.70,G3DSA:3.20.20.70	SSF51445		00052+3.2.1.22,00600+3.2.1.22,00603+3.2.1.22,00561+3.2.1.22		PWY-6527					
aly3177.13	Unknown		n/a																				
aly3177.2	GATA zinc finger domain-containing protein 1	GO:0003700,GO:0006355,GO:0005634,GO:0008270,GO:0043565	CG13367-PA				SM00401		PF00320	PS50114			G3DSA:3.30.50.10										
aly3177.3	U6 snRNA-associated Sm-like protein LSm6	GO:0005737,GO:0046540,GO:0008033,GO:0070062,GO:0030532,GO:0030490,GO:0005730,GO:0000932,GO:0000398,GO:0003723,GO:0005688,GO:0006402,GO:0046982,GO:0044822,GO:0005681,GO:0005732	CG9344-PA			PIRSF006609	SM00651		PF01423				G3DSA:2.30.30.100	SSF50182									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3177.4	Unknown		CG15650-PA																				
aly3177.5	Unknown		CG34115-PA																				
aly3177.6	Calcium-independent phospholipase A2-gamma	GO:0047499,GO:0016042,GO:0005829,GO:0005789,GO:0008152,GO:0004622,GO:0048471,GO:0000139,GO:0016021,GO:0006629	CG6718-PB						PF01734				G3DSA:3.40.1090.10	SSF52151	77~104								
aly3177.7	Unknown		CG3568-PA						PF16062														
aly3177.8	Unknown		CG2909-PA						PF16062														
aly3177.9	DNA polymerase epsilon subunit 2	GO:0000723,GO:0006974,GO:0006297,GO:0008622,GO:0042276,GO:0006281,GO:0000278,GO:0005634,GO:0006270,GO:0000082,GO:0032201,GO:0006289,GO:0003887,GO:0006260,GO:0006261,GO:0003677,GO:0005654,GO:0000722,GO:0006283,GO:0043231	CG10489-PA			PIRSF000799			PF04042,PF12213							00240+2.7.7.7,00230+2.7.7.7	REACT_152,REACT_383,REACT_22172						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly318.1	Trypsin, alkaline A	GO:0004252,GO:0004175,GO:0005615,GO:0006508	CG31954-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly318.10	Lysine-specific demethylase lid	GO:0070822,GO:0032922,GO:0006351,GO:0045893,GO:0043970,GO:0006325,GO:0034721,GO:0005634,GO:0043992,GO:0007526,GO:0034720,GO:0016706,GO:0016577,GO:0032453,GO:0034647,GO:0008270,GO:0005515,GO:0003677,GO:0055114,GO:0045475	CG9088-PA				SM00558,SM00545,SM01014,SM00501,SM00249		PF01388,PF02373,PF02928,PF00628,PF02375	PS51183,PS50016,PS50089,PS51184,PS51011		PS01359	G3DSA:3.30.40.10,G3DSA:1.10.150.60	SSF57903,SSF46774,SSF51197									
aly318.11	Synaptic vesicle 2-related protein	GO:0008021,GO:0030672,GO:0016021,GO:0015075,GO:0015101,GO:0055085,GO:0030054	CG4324-PA										G3DSA:1.20.1250.20	SSF103473									
aly318.12	Synaptic vesicle 2-related protein	GO:0030672,GO:0016021,GO:0015075,GO:0022857,GO:0015101,GO:0055085,GO:0030054	CG4324-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly318.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly318.14	Cadherin-related tumor suppressor	GO:0016318,GO:0018149,GO:0045926,GO:0016339,GO:0007157,GO:0045198,GO:0007164,GO:0004872,GO:0048105,GO:0016337,GO:0030178,GO:0030054,GO:0032880,GO:0000904,GO:0040008,GO:0016020,GO:0007476,GO:0050839,GO:0005509,GO:0042067,GO:0008285,GO:0008283,GO:0046620,GO:0035159,GO:0045317,GO:0005887,GO:0005886,GO:0044331,GO:0035329,GO:0007156,GO:0001737,GO:0001736,GO:0007446,GO:0090176,GO:0045296,GO:0005622,GO:0045571,GO:0016021	CG3352-PA				SM00112,SM00179,SM00179,SM00179,SM00181,SM00181,SM00181,SM00181,SM00181,SM00282,SM00282		PF02210,PF00054,PF00008,PF00008,PF00028	PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50025,PS50268,PS50268,PS50268,PS50026,PS50026,PS50268,PS50268,PS50025,PS50268,PS50268,PS50268,PS50026,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50026,PS50268,PS50268,PS50268,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00232,PS00022,PS00232,PS00232,PS00232,PS00022,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00022,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS01186,PS00232,PS00022,PS00232	G3DSA:2.10.25.10,G3DSA:2.60.40.60,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.10.25.10,G3DSA:2.60.40.60	SSF49899,SSF49899,SSF49899,SSF49313,SSF57196,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF57196	4949~4949								
aly318.15	Inactive pancreatic lipase-related protein 1	GO:0004806,GO:0006629,GO:0052689,GO:0016042,GO:0005575,GO:0005576,GO:0005509,GO:0016298	CG34447-PB						PF00151		PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly318.16	Phospholipase A1 member A	GO:0005576,GO:0016298,GO:0006629,GO:0052689,GO:0016042	CG18641-PC						PF00151		PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly318.17	Vesicular glutamate transporter 2	GO:0035249,GO:0008021,GO:0043005,GO:0030672,GO:0031982,GO:0015293,GO:0015813,GO:0005313,GO:0006814,GO:0055085,GO:0089711,GO:0005326,GO:0006836,GO:0006811,GO:0030285,GO:0005316,GO:0016021,GO:0030054	CG9887-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473										
aly318.18	Protein aubergine	GO:0030423,GO:0007279,GO:0046594,GO:0030717,GO:0034584,GO:0035282,GO:0005875,GO:0005737,GO:0043186,GO:0006342,GO:0010529,GO:0016246,GO:0048477,GO:0006446,GO:0045089,GO:0046012,GO:0046011,GO:0071011,GO:0071013,GO:0007317,GO:0060213,GO:0007282,GO:0007076,GO:0001556,GO:0007318,GO:0050829,GO:0000398,GO:0003723,GO:0005515,GO:0017145,GO:0046843	CG6137-PA				SM00949,SM00950		PF02171,PF02170,PF16486	PS50822,PS50821			G3DSA:3.30.420.10,G3DSA:3.40.50.2300,G3DSA:2.170.260.10	SSF101690,SSF53098										
aly318.19	Coiled-coil domain-containing protein 170	GO:0005575,GO:0003674,GO:0008150	CG43338-PB											SSF57997	505~532,460~480,357~398,94~142,174~257,272~292,52~89,543~577,17~37,596~616								
aly318.2	Signal-induced proliferation-associated 1-like protein 1	GO:0005737,GO:0005856,GO:0005099,GO:0050770,GO:0043197,GO:0031532,GO:0090630,GO:0060293,GO:0005096,GO:0061001,GO:0032861,GO:0045211,GO:0048167,GO:0014069,GO:0046582,GO:0048013,GO:0007265,GO:0043087,GO:0002121,GO:0030054	CG44086-PH				SM00228		PF02145	PS50085			G3DSA:2.30.42.10	SSF111347,SSF50156	924~944								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly318.20	Unknown		n/a																				
aly318.21	Unknown		CG15544-PA																				
aly318.22	Uridine phosphorylase 1	GO:0005737,GO:0006139,GO:0043097,GO:0042332,GO:0005829,GO:0006206,GO:0044206,GO:0006218,GO:0009166,GO:0009116,GO:0042149,GO:0046135,GO:0004850,GO:0055086,GO:0044281	CG6330-PA					TIGR01719	PF01048				G3DSA:3.40.50.1580	SSF53167		00983+2.4.2.3,00240+2.4.2.3			UPA00574				
aly318.23	Tetraspanin-31	GO:0008284,GO:0016021,GO:0016020,GO:0008150,GO:0005887,GO:0003674	CG6323-PA						PF00335		PR00259,PR00259,PR00259												
aly318.24	Transmembrane protein 177	GO:0005575,GO:0008150,GO:0016021,GO:0003674	CG33506-PA												120~140								
aly318.25	Condensin-2 complex subunit D3	GO:0035064,GO:0000278,GO:0016020,GO:0005654,GO:0042585,GO:0031618,GO:0007076,GO:0000799,GO:0051301	n/a											SSF48371,SSF48371,SSF48371,SSF48371,SSF48371	1022~1042,1130~1164								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly318.26	ATP-dependent DNA helicase Q5	GO:0008026,GO:0003676,GO:0003678,GO:0016591,GO:0051304,GO:0007067,GO:0051301,GO:0005737,GO:0010165,GO:0031965,GO:0005634,GO:0005654,GO:0006260,GO:0032508,GO:0005524,GO:0005525,GO:0045930,GO:0034244,GO:0006281,GO:0004003,GO:0017116,GO:0003924,GO:0004386,GO:0006974,GO:0006310,GO:0045002,GO:0005730,GO:0006259,GO:0000993	CG4879-PB				SM00490,SM00487	TIGR00614	PF00270,PF16124,PF00271	PS51194,PS51192		PS00690	G3DSA:3.40.50.300,G3DSA:1.10.10.10,G3DSA:3.40.50.300	SSF52540									
aly318.27	DNA polymerase beta	GO:0006290,GO:0003677,GO:0055093,GO:0005876,GO:0005737,GO:0007435,GO:0005634,GO:0010332,GO:0003887,GO:0071707,GO:0006260,GO:0048536,GO:0046872,GO:0006287,GO:0006284,GO:0006974,GO:0045471,GO:0051402,GO:0006954,GO:0008630,GO:0048535,GO:0007568,GO:0048872,GO:0003684,GO:0016829,GO:0071897,GO:0016446	n/a				SM00483,SM00278,SM00278		PF14791,PF14792,PF14716,PF10391		PR00870,PR00870,PR00870,PR00870,PR00870,PR00869,PR00869,PR00869,PR00869,PR00869		G3DSA:1.10.150.20,G3DSA:3.30.460.10,G3DSA:3.30.210.10,G3DSA:1.10.8.310	SSF47802,SSF81585,SSF81301		00240+2.7.7.7,00230+2.7.7.7								
aly318.28	Multidrug resistance-associated protein 7	GO:0042626,GO:0005765,GO:0016021,GO:0006810,GO:0008559,GO:0005886,GO:0055085,GO:0005524	CG7806-PA				SM00382		PF00664,PF00664,PF00005	PS50893,PS50929,PS50929		PS00211	G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF90123,SSF90123,SSF52540	1365~1367								
aly318.29	Coiled-coil domain-containing protein 97	GO:0005686	CG7810-PA						PF09747						198~218								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly318.3	Cilia- and flagella-associated protein 44	GO:0005575,GO:0008150,GO:0042995,GO:0003674,GO:0005515	CG31652-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320						G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978,SSF50978,SSF50978,SSF50978	1664~1684,651~680,900~927,1577~1597,1605~1632,1731~1758,1366~1407,1012~1032,1821~1841,1300~1334								
aly318.30	Unknown	GO:0005575,GO:0008150,GO:0003674	CG13272-PA																				
aly318.31	Unknown		n/a										G3DSA:2.10.60.10										
aly318.32	Mitochondrial import receptor subunit TOM70	GO:0044267,GO:0015450,GO:0071806,GO:0070062,GO:0006626,GO:0016020,GO:0005739,GO:0008320,GO:0005742,GO:0005515,GO:0016021	CG6756-PA				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF13414,PF13414,PF13181,PF07719,PF13432	PS50005,PS50005,PS50293,PS50005,PS50005,PS50005,PS50005,PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452	56~76								
aly318.33	39S ribosomal protein L48, mitochondrial	GO:0003735,GO:0032543,GO:0005762,GO:0005761	CG17642-PA						PF00338					SSF54999									
aly318.34	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly318.35	Unknown		n/a						PF13358														
aly318.36	Unknown		n/a																				
aly318.37	Unknown		n/a									PS00518	G3DSA:3.30.40.10										
aly318.38	Menin	GO:0018024,GO:0032925,GO:0050680,GO:0008340,GO:0009411,GO:0000785,GO:0051568,GO:0046329,GO:0009651,GO:0001666,GO:0032092,GO:0010212,GO:0071375,GO:0031571,GO:0005634,GO:0010332,GO:0000165,GO:0043433,GO:0034968,GO:0048728,GO:0051974,GO:0003690,GO:0016363,GO:0045668,GO:0046529,GO:0002076,GO:0061469,GO:0000278,GO:0044212,GO:0010812,GO:0071333,GO:0032154,GO:0006289,GO:0006974,GO:0046330,GO:0009408,GO:0006979,GO:0030511,GO:0003309,GO:0000403,GO:0000400,GO:0006351,GO:0007420,GO:0005829,GO:0000122,GO:0036297,GO:0035097,GO:0071559,GO:1902807,GO:0045944,GO:0045736,GO:0046697,GO:0003682,GO:0044665	CG13778-PC						PF05053,PF05053,PF05053														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly318.39	Uncharacterized protein KIAA1143 homolog		CG42245-PA						PF15377						58~85								
aly318.4	LYR motif-containing protein 5		CG6115-PA						PF05347														
aly318.40	Transforming growth factor beta regulator 1	GO:0005634,GO:0022008,GO:0007049	CG31111-PA																				
aly318.41	Exportin-1	GO:0034504,GO:0051168,GO:0006611,GO:0042493,GO:0010824,GO:0042176,GO:0005487,GO:0007275,GO:0008565,GO:0000122,GO:0006886,GO:0030529,GO:0000055,GO:0003723,GO:0005737,GO:0031965,GO:0019904,GO:0000776,GO:0005049,GO:0051028,GO:0005643,GO:0005642,GO:1900037,GO:0005730,GO:0008536,GO:0000056,GO:0046825,GO:0007099,GO:0005515,GO:0015031,GO:0015030,GO:0005634	CG13387-PA				SM01102,SM00913		PF03810,PF08767,PF08389	PS50166			G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371	1058~1060								
aly318.42	Cleft lip and palate transmembrane protein 1 homolog	GO:0016021,GO:0030154,GO:0007275	CG3702-PA						PF05602														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly318.43	E3 ubiquitin-protein ligase RNF8	GO:0042393,GO:0007286,GO:0045190,GO:0000781,GO:0008270,GO:0007067,GO:0070936,GO:0061630,GO:0051301,GO:0006303,GO:0006302,GO:0005730,GO:0043486,GO:0005634,GO:0006511,GO:0070535,GO:0070534,GO:0042803,GO:0034244,GO:0006974,GO:0004842,GO:0010212,GO:0033523,GO:0016874,GO:0033522,GO:0031625,GO:0035861,GO:0030496,GO:0000151,GO:0051865,GO:0045739,GO:0003682	CG13605-PB				SM00184,SM00240		PF00498,PF13920	PS50006,PS50089		PS00518	G3DSA:3.30.40.10,G3DSA:2.60.200.20	SSF57850,SSF49879	432~459,187~250,259~355,360~394,399~419									
aly318.44	Leucine-rich repeat-containing protein 4	GO:0005887,GO:0043197,GO:0005154,GO:0016021,GO:0058076,GO:0000281,GO:0042059,GO:0048019,GO:0045211,GO:0007175,GO:0005515,GO:0060076,GO:0022008,GO:0048477,GO:0097119,GO:0030054	CG12283-PB				SM00408,SM00369,SM00369,SM00369,SM00369,SM00369,SM00409,SM00082		PF13855,PF13855,PF07679	PS51450,PS50835,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:2.60.40.10,G3DSA:3.80.10.10	SSF48726,SSF52058										
aly318.5	Synaptotagmin 1	GO:0008021,GO:0016020,GO:0050803,GO:0060024,GO:0005886,GO:0031594,GO:0031340,GO:0030285,GO:0048488,GO:0048489,GO:0016021,GO:0006887,GO:0005544,GO:0017158,GO:0005509,GO:0001786,GO:0042803,GO:0005215,GO:0007317,GO:0030276,GO:0007269,GO:0007268,GO:0030672,GO:0008345,GO:0043195,GO:0016192,GO:0016079,GO:0030054,GO:0048791,GO:1900073,GO:0005515,GO:0019905,GO:0000149	CG3139-PA				SM00239,SM00239		PF00168,PF00168	PS50004,PS50004		PR00399,PR00399,PR00399,PR00399,PR00360,PR00360,PR00360	G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562										
aly318.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly318.7	Leucine-rich repeat and fibronectin type III domain-containing protein 1-like protein	GO:0005515,GO:0016021,GO:0045202,GO:0005887,GO:0005886,GO:0030054	CG4192-PA				SM00082,SM00408,SM00369,SM00369,SM00369,SM00369,SM00369,SM00409		PF13855,PF13855,PF07679	PS51450,PS51450,PS51450,PS51450,PS51450,PS50835,PS51450,PS51450,PS51450			G3DSA:2.60.40.10,G3DSA:3.80.10.10	SSF52058,SSF48726	698~732								
aly318.8	Hsc70-interacting protein 2	GO:0043234,GO:0030544,GO:0031072,GO:0005829,GO:0051087,GO:0005515,GO:0070389	CG32789-PA				SM00028,SM00028,SM00028,SM00727		PF13414,PF13181	PS50005,PS50005,PS50293,PS50005			G3DSA:1.25.40.10	SSF48452	246~273								
aly318.9	39S ribosomal protein L38, mitochondrial	GO:0005840,GO:0005739,GO:0003735,GO:0005762,GO:0006412,GO:0008429	CG15871-PA						PF01161				G3DSA:3.90.280.10	SSF49777									
aly31816.1	Unknown	GO:0003700,GO:0005634,GO:0008270,GO:0006351	CG1647-PA				SM00868		PF07776					SSF57716									
aly3182.1	Unknown		n/a																				
aly3194.1	Putative deoxyribonuclease TATDN1	GO:0004536,GO:0005634,GO:0006308,GO:0043229,GO:0016888,GO:0046872	CG3358-PE			PIRSF005902			PF01026			PS01091,PS01090	G3DSA:3.20.20.140	SSF51556									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3194.2	Transmembrane protein 214	GO:0005794,GO:0006915,GO:0016021,GO:0005811,GO:0005789,GO:0005881,GO:0003674,GO:0008150	CG33129-PE						PF10151														
aly3194.3	Protein fem-1 homolog B	GO:0005737,GO:0005634,GO:0006915,GO:0005575,GO:0016567,GO:0008150,GO:2000001,GO:0005515,GO:0003674	CG9025-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796	PS50088,PS50088,PS50297,PS50088,PS50088			G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403									
aly3194.4	Unknown		n/a																				
aly3199.1	Hemicentin-1	GO:0005604,GO:0070062,GO:0050896,GO:0007601,GO:0005509,GO:0005515,GO:0030054,GO:0005938	CG34114-PB				SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408		PF13895,PF07686,PF13927,PF13927,PF08205	PS50835,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF48726									
aly32.1	Unknown		n/a																				
aly32.2	tRNA pseudouridine(38/39) synthase	GO:0004730,GO:0031119,GO:0005634,GO:0009982,GO:0009451,GO:0003723,GO:0001522	CG3045-PA					TIGR00071	PF01416,PF01416				G3DSA:3.30.70.660,G3DSA:3.30.70.580	SSF55120									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly32.3	Unknown		n/a																				
aly320.1	Mothers against decapentaplegic homolog 4	GO:0048589,GO:0030509,GO:0001076,GO:0001077,GO:0014033,GO:0007369,GO:0001822,GO:0032444,GO:0030511,GO:0046872,GO:0042127,GO:0060548,GO:0000790,GO:0030513,GO:0007179,GO:0044212,GO:0060395,GO:0030616,GO:0060391,GO:0005667,GO:0003251,GO:0003677,GO:0072133,GO:0035556,GO:0010862,GO:0072134,GO:0005654,GO:0006366,GO:0000987,GO:0007183,GO:0001702,GO:0017015,GO:0001085,GO:0042733,GO:0005518,GO:0009952,GO:0010718,GO:0006355,GO:0006357,GO:0000977,GO:0000978,GO:0046982,GO:0007492,GO:0030308,GO:0007498,GO:0090575,GO:0042177,GO:0060956,GO:0007411,GO:0001666,GO:0005737,GO:0001701,GO:0005634,GO:0003190,GO:0003198,GO:0042802,GO:0042803,GO:0008285,GO:0008283,GO:0045892,GO:0045893,GO:0001658,GO:0051797,GO:0051098,GO:0001228,GO:0005622,GO:0045944,GO:0005515,GO:0048733,GO:0042118,GO:0032909,GO:0060021,GO:0036302,GO:0003360,GO:0005813,GO:0003682,GO:0070412,GO:0048729,GO:0070411,GO:0071559,GO:0032525,GO:0048663,GO:0048859,GO:0003279,GO:0003700,GO:0071141	CG13188-PA				SM00524		PF03166	PS51076			G3DSA:2.60.200.10	SSF49879									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly320.10	Tumor necrosis factor ligand superfamily member 13	GO:0009897,GO:0005886,GO:0097191,GO:0005164,GO:0035006,GO:0050829,GO:0005737,GO:0007254,GO:0045176,GO:0070062,GO:0043652,GO:0016020,GO:0048298,GO:0008284,GO:0032813,GO:0045087,GO:0006915,GO:0002636,GO:0016064,GO:0006955,GO:0005615,GO:0045167,GO:0050776,GO:0044214,GO:0002426,GO:0070050,GO:1900074,GO:0005515	CG12919-PA						PF00229	PS50049		PS00251	G3DSA:2.60.120.40	SSF49842	80~100,126~146									
aly320.11	Unknown	GO:0016020,GO:0005164,GO:0006955	n/a						PF00229	PS50049		PS00251	G3DSA:2.60.120.40	SSF49842									
aly320.12	28S ribosomal protein S31, mitochondrial	GO:0005730,GO:0044822,GO:0003735,GO:0005743,GO:0005763,GO:0006412	CG5904-PA						PF15433														
aly320.13	Glucose-6-phosphate 1-epimerase	GO:0007030,GO:0034389,GO:0044262,GO:0016853,GO:0030246,GO:0005975,GO:0047938	CG9008-PD			PIRSF016020			PF01263				G3DSA:2.70.98.10	SSF74650		00010+5.1.3.15		PWY-7238,PWY-5384,PWY-7343,PWY-621,PWY-622,PWY-6731,PWY-6737,PWY-2723,PWY-6981,PWY-5940						
aly320.14	Protein disulfide-isomerase A3	GO:0006662,GO:0006457,GO:0005783,GO:0043209,GO:0001238,GO:0009986,GO:0005811,GO:0044822,GO:0005634,GO:0005788,GO:0034976,GO:0003756,GO:0045454,GO:0005925,GO:0015035,GO:0005875,GO:0070062	CG8983-PA					TIGR01130,TIGR01126,TIGR01126	PF00085,PF00085,PF13848	PS51352,PS51352	PR00421,PR00421,PR00421	PS00194,PS00194	G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10	SSF52833,SSF52833,SSF52833,SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly320.15	Adenylate kinase isoenzyme 6 homolog	GO:0016887,GO:0005634,GO:0046939,GO:0004017,GO:0009267,GO:0005524	CG8816-PA	MF_00039					PF13238				G3DSA:3.40.50.300	SSF52540		00230+2.7.4.3		PWY-7219					
aly320.16	Elongation factor 1-alpha	GO:0005737,GO:0005853,GO:0005829,GO:0005811,GO:0003924,GO:0006412,GO:0008340,GO:0003746,GO:0006414,GO:0005875,GO:0005525	CG8280-PA	MF_00118_A				TIGR00483	PF03143,PF00009,PF03144	PS51722	PR00315,PR00315,PR00315,PR00315,PR00315	PS00301	G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:3.40.50.300	SSF50447,SSF52540,SSF50465									
aly320.17	FERM domain containing protein 5	GO:0005856,GO:0005737,GO:0008092,GO:0019898	CG5022-PA				SM00295		PF09379,PF09380,PF00373	PS50057	PR00935,PR00935,PR00935,PR00935,PR00661,PR00661,PR00661,PR00661	PS00660	G3DSA:3.10.20.90,G3DSA:1.20.80.10,G3DSA:2.30.29.30	SSF50729,SSF54236,SSF47031									
aly320.18	STE20/SPS1-related proline alanine-rich protein kinase	GO:0018107,GO:0018105,GO:0090188,GO:0032147,GO:0035220,GO:0050727,GO:0008065,GO:0008217,GO:0035556,GO:0007413,GO:0042981,GO:0023014,GO:0043268,GO:0005737,GO:0007346,GO:0005634,GO:0016020,GO:0071476,GO:0004674,GO:0004672,GO:1901380,GO:0005524,GO:0005856,GO:0006468,GO:0016324,GO:0016323,GO:0008362,GO:0008366,GO:2000681,GO:2000687,GO:0031098,GO:1901017,GO:2000021,GO:0004702,GO:0001933	CG7693-PA				SM00220		PF12202,PF00069	PS50011		PS00107	G3DSA:3.30.200.20,G3DSA:3.10.20.90,G3DSA:1.10.510.10	SSF56112										
aly320.19	Nucleoside diphosphate-linked moiety X motif 19, mitochondrial	GO:0016787,GO:0046872,GO:0006909,GO:0005739,GO:0005777	CG10194-PA						PF00293	PS51462			G3DSA:3.90.79.10,G3DSA:3.90.79.10,G3DSA:3.90.79.10	SSF55811,SSF55811,SSF55811									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly320.2	Dynein beta chain, ciliary	GO:0005737,GO:0042623,GO:0007605,GO:0007018,GO:0005858,GO:0005875,GO:0030030,GO:0005524,GO:0016887,GO:0031514,GO:0030286,GO:0005874,GO:0003774,GO:0003777	CG3723-PC						PF12777,PF12775,PF08393,PF08385,PF03028,PF12781,PF12780,PF07728,PF12774				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540,SSF52540	1245~1265,1563~1583,3574~3608,3038~3096,817~837,738~758,3111~3131,4477~4477,3275~3316,3630~3650,131								
aly320.20	Mitochondrial intermediate peptidase	GO:0004222,GO:0005739,GO:0005759,GO:0016485,GO:0006508,GO:0046872	CG7791-PA						PF01432				G3DSA:1.10.1370.10,G3DSA:1.10.1370.10,G3DSA:3.40.390.10	SSF55486									
aly320.21	Cullin-4B	GO:0035518,GO:0031175,GO:0070914,GO:0007307,GO:0007049,GO:0005737,GO:0070062,GO:0005654,GO:0042787,GO:1900087,GO:0005886,GO:0031461,GO:0004842,GO:0031465,GO:0031625,GO:0005829,GO:0000152,GO:0051533,GO:0045732,GO:0006511,GO:0007095,GO:0003684	CG8711-PA				SM00182,SM00884		PF10557,PF00888	PS50069		PS01256	G3DSA:1.10.10.10,G3DSA:1.20.1310.10,G3DSA:1.20.1310.10,G3DSA:1.20.1310.10,G3DSA:4.10.1030.10,G3DSA:1.10.10.10,G3DSA:1.20.1310.10	SSF74788,SSF46785,SSF75632				UPA00143					
aly320.22	Neurogenic protein big brain	GO:0009992,GO:0005261,GO:0007498,GO:0016337,GO:0007219,GO:0031410,GO:0016021,GO:0044719,GO:0030707,GO:0015250,GO:0015254,GO:0015793,GO:0005372,GO:0006812,GO:0005216,GO:0034220,GO:0006833,GO:0046331,GO:0005912,GO:0005887,GO:0005886,GO:0055085,GO:0007399,GO:0007398,GO:0015267,GO:0098655	CG4722-PB						PF00230		PR00783,PR00783,PR00783,PR00783		G3DSA:1.20.1080.10	SSF81338									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly320.23	Ras-related protein Rab6	GO:0008103,GO:0042147,GO:0045467,GO:0007293,GO:0045202,GO:0007411,GO:0001745,GO:0030054,GO:0031982,GO:0016023,GO:0006886,GO:0006887,GO:0043025,GO:0005525,GO:0005794,GO:0003924,GO:0050832,GO:0032482,GO:0008152,GO:0060078,GO:0007264,GO:0043204,GO:0045451,GO:0006891,GO:0006890,G	CG6601-PA				SM00174,SM00175,SM00173,SM00176	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly320.24	Unknown		n/a																				
aly320.25	Beta-arrestin-1	GO:0005737,GO:0006351,GO:0042335,GO:0009968,GO:0031647,GO:0016023,GO:0006355,GO:0005634,GO:0007369,GO:0031143,GO:0045746,GO:0035641,GO:0005905,GO:0007165,GO:0005886,GO:0015031,GO:0061099,GO:0002092,GO:0001934,GO:0002168	CG1487-PA				SM01017		PF00339,PF02752		PR00309,PR00309,PR00309,PR00309,PR00309	PS00295	G3DSA:2.60.40.840,G3DSA:2.60.40.640	SSF81296,SSF81296									
aly320.26	U2 snRNP-associated SURP motif-containing protein	GO:0005634,GO:0003729,GO:0003723,GO:0006396,GO:0000166	CG9346-PA				SM00360,SM00648,SM00582		PF04818,PF00076,PF01805	PS51391,PS50102,PS50128			G3DSA:3.30.70.330,G3DSA:1.25.40.90	SSF54928,SSF48464,SSF109905	104~124,1~28								
aly320.27	Kinesin-like protein KIF21A	GO:0005737,GO:0008152,GO:0008017,GO:0007018,GO:0030425,GO:0030424,GO:0005524,GO:0016887,GO:0005871,GO:0005874,GO:0003774,GO:0003777	CG5300-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10	SSF52540	702~739,413~433,786~820,452~486,959~986,747~767,903~923,517~537,638~668								
aly320.28	LIX1-like protein	GO:0005737,GO:0035003,GO:0006914,GO:0097352,GO:0007476	CG13139-PA						PF14954														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly320.29	Unknown		CG11279-PA						PF09495														
aly320.3	Kinesin-like protein KIF13A	GO:0050803,GO:0035371,GO:0032438,GO:0008333,GO:0035459,GO:0016887,GO:0005871,GO:0005874,GO:0010008,GO:0005813,GO:0006886,GO:0043001,GO:0005524,GO:0042803,GO:0051294,GO:0008017,GO:0032588,GO:0000235,GO:0008152,GO:0030496,GO:0000910,GO:0072383,GO:0007018,GO:0003777,GO:0005515,GO:0005769	CG8183-PE				SM01052,SM00240,SM00129		PF00225,PF16183,PF00498,PF12473,PF01302	PS50067,PS50245	PR00380,PR00380,PR00380,PR00380	PS00845,PS00411	G3DSA:2.60.200.20,G3DSA:3.40.850.10,G3DSA:2.30.30.190	SSF49879,SSF74924,SSF52540	368~388,1498~1539,740~767,592~624								
aly320.30	Unknown		n/a												392~412								
aly320.31	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly320.32	Histone deacetylase 6	GO:0032041,GO:0000209,GO:0010469,GO:0032418,GO:0030425,GO:0016235,GO:0098779,GO:0048487,GO:0006099,GO:0034983,GO:0048156,GO:0008270,GO:0043241,GO:0031593,GO:0030286,GO:0043162,GO:0005874,GO:0071218,GO:0043242,GO:0005737,GO:0005654,GO:0070846,GO:1901300,GO:0070840,GO:0070842,GO:0006476,GO:0004407,GO:0006886,GO:0009636,GO:0040029,GO:0005875,GO:0016575,GO:0006511,GO:0009967,GO:0042903,GO:0022904,GO:0048471,GO:0045598,GO:0051879,GO:0070845,GO:0070201,GO:0090042,GO:0016236,GO:0008017,GO:0070301,GO:0031252,GO:0008013,GO:0000118,GO:0031625,GO:0016234,GO:0001047,GO:0051646,GO:0043234,GO:0010870,GO:0030424,GO:0010033,GO:0043204,GO:0010634,GO:0090035,GO:0005901,GO:0042826,GO:0005829,GO:0007026,GO:0070848,GO:0006355,GO:0035967,GO:0043130,GO:0051787,GO:0006351,GO:0006515,GO:0043014,GO:0045861,GO:0051788,GO:0005634	CG6170-PG				SM00290		PF00850,PF00850,PF02148	PS50271	PR01270,PR01270,PR01270		G3DSA:3.40.800.20,G3DSA:3.40.800.20,G3DSA:3.30.40.10	SSF52768,SSF52768,SSF57850									
aly320.33	Arginine/serine-rich coiled-coil protein 2		n/a						PF15477														
aly320.34	TRAF-type zinc finger domain-containing protein 1	GO:0045824,GO:0034097,GO:0008270	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly320.35	Unknown		n/a																				
aly320.36	TBC1 domain family member 22B	GO:0032313,GO:0005096,GO:0006909,GO:0005097	CG5745-PA				SM00164		PF00566	PS50086			G3DSA:1.10.8.270	SSF47923,SSF47923									
aly320.37	Uncharacterized protein KIAA1841		CG6761-PA						PF11822					SSF54695									
aly320.38	60S ribosomal protein L6	GO:0005840,GO:0022625,GO:0051297,GO:0016020,GO:0044822,GO:0005634,GO:0003735,GO:0007052,GO:0036464,GO:0000022,GO:0005925,GO:0006412,GO:0051298	CG11522-PB						PF01159,PF03868				G3DSA:2.30.30.30	SSF50104									
aly320.39	Two pore calcium channel protein 1	GO:0072345,GO:0016021,GO:0005765,GO:0005216,GO:0016020,GO:0006816,GO:0055085,GO:0034220,GO:0005886,GO:0005245,GO:0086010,GO:0006811,GO:0010008	n/a						PF00520					SSF81324									
aly320.4	Proteasome inhibitor PI31 subunit	GO:0005737,GO:0032436,GO:0008584,GO:0006974,GO:0006511,GO:0003674,GO:0043248,GO:0000502,GO:0070864,GO:0007140	CG8979-PA						PF11566,PF08577														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly320.40	Two pore calcium channel protein 1	GO:0072345,GO:0042045,GO:0006936,GO:0034220,GO:0016324,GO:0016021,GO:0070588,GO:0006816,GO:0005765,GO:0016323,GO:0009790,GO:0005891,GO:0005886,GO:0005245,GO:0086010,GO:0010008	CG4894-PC						PF00520				G3DSA:1.20.120.350	SSF81324,SSF81324										
aly320.41	Unknown		n/a																				
aly320.5	Protein tyrosine phosphatase type IVA 3	GO:0005737,GO:0043542,GO:0008138,GO:0004727,GO:0006470,GO:0004725,GO:1900746,GO:0005886,GO:0005769,GO:0043117	CG4993-PA				SM00404		PF00782	PS50056			G3DSA:3.90.190.10	SSF52799										
aly320.6	Deoxyribodipyrimidine photolyase	GO:0003904,GO:0003677,GO:0018298,GO:0006281	CG11205-PA					TIGR00591	PF00875,PF03441	PS51645		PS01084	G3DSA:1.10.579.10,G3DSA:3.40.50.620,G3DSA:1.25.40.80	SSF52425,SSF48173										
aly320.7	Ankyrin repeat and MYND domain-containing protein 1	GO:0046872	n/a				SM00698,SM00698,SM00248,SM00248,SM00248,SM00248		PF00023,PF13637	PS50297,PS50088,PS50297			G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:2.20.110.10	SSF82185,SSF48403,SSF48403										
aly320.8	Phospholipid scramblase 2	GO:0017121,GO:0017128,GO:0016021,GO:0046872,GO:0005886	CG9084-PC						PF03803														

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly320.9	Unknown		n/a							PS51257					571~591								
aly3201.1	Unknown		n/a						PF04500														
aly3201.2	Unknown		n/a						PF04500														
aly3201.3	Unknown	GO:0003677	n/a				SM00614,SM00614,SM00614		PF02892,PF02892	PS50808,PS50808				SSF57667,SSF57667									
aly3201.4	Unknown		n/a						PF04500														
aly3201.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3201.6	Unknown		n/a						PF04500,PF04500														
aly3201.7	Unknown		n/a						PF04500														
aly3201.8	Unknown		n/a																				
aly3201.9	Unknown		n/a						PF04500														
aly32117.1	UDP-glucose 4-epimerase	GO:0050662,GO:0019388,GO:0070062,GO:0044237,GO:0006012,GO:0003974,GO:0003978,GO:0042803	CG12030-PA						PF16363				G3DSA:3.40.50.720	SSF51735									
aly3214.1	Eukaryotic translation initiation factor 3 subunit A	GO:0006446,GO:0005852,GO:0016282,GO:0005829,GO:0007052,GO:0005515,GO:0033290,GO:0000022,GO:0006413,GO:0001731,GO:0003743	CG9805-PA				SM00088		PF01399						359~465,246~284,154~217								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3215.1	Circadian clock-controlled protein	GO:0007623,GO:0005615,GO:0032504	CG10407-PA				SM00700		PF06585														
aly3215.2	Unknown	GO:0008289	CG3246-PA						PF16984,PF06585														
aly3215.3	Unknown	GO:0008289	CG3246-PA				SM00700		PF16984,PF06585				G3DSA:3.15.10.10	SSF55394									
aly3215.4	Protein takeout	GO:0007631,GO:0007623,GO:0005615,GO:0007617,GO:0005576,GO:0042594,GO:0042595,GO:0008343,GO:0008049,GO:0007622	CG2016-PE				SM00700		PF06585														
aly322.1	Uncharacterized protein C15orf26	GO:0005575,GO:0003674,GO:0008150,GO:0004252,GO:0006508	CG5197-PA																				
aly322.10	C-Maf-inducing protein	GO:0005737,GO:0005634	n/a										G3DSA:2.30.29.30,G3DSA:3.80.10.10	SSF50729,SSF52047									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly322.11	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005886,GO:0006508	CG13318-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly322.12	Zinc finger protein 521	GO:0035277,GO:0005634,GO:0030154,GO:0006355,GO:0019904,GO:0003676,GO:0003677,GO:0046872,GO:0007275,GO:0006351	CG42702-PC				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly322.13	F-box/LRR-repeat protein 14	GO:0005737,GO:0005794,GO:0005654,GO:0042787,GO:0005515,GO:0004842	CG8272-PB				SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00256		PF12937,PF00560	PS50181			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:1.20.1280.50	SSF81383,SSF52047,SSF52058,SSF52058									
aly322.14	Heat shock factor protein	GO:0043565,GO:0009408,GO:0006351,GO:0003700,GO:0005634,GO:0031427,GO:0005700,GO:0050832,GO:0042802,GO:0000785,GO:0042742,GO:0005515,GO:0003677,GO:0043388,GO:0045944,GO:0022008,GO:0045892,GO:0045893	CG5748-PD				SM00415		PF00447,PF06546		PR00056,PR00056,PR00056	PS00434	G3DSA:1.10.10.10	SSF46785									
aly322.15	Probable very-long-chain enoyl-CoA reductase art-1	GO:0005737,GO:0006633,GO:0006629,GO:0016021,GO:0005789,GO:0016627	CG10849-PA				SM00213		PF00240,PF02544	PS50244,PS50053			G3DSA:3.10.20.90	SSF54236			REACT_22258						
aly322.16	Cilia- and flagella-associated protein 57	GO:0007605	CG4329-PA				SM00320,SM00320,SM00320,SM00320			PS50082,PS50294,PS50082			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978	609~643,576~596,688~744,883~917,785~826,1063~1107,834~854,973~1000								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly322.17	Unknown		CG5381-PA												235~255								
aly322.18	HEAT repeat-containing protein 3	GO:0005575,GO:0003674,GO:0008150	CG10286-PA										G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371	615~627								
aly322.19	Protein naked cuticle homolog	GO:0005737,GO:0007367,GO:0005634,GO:0016055,GO:0014018,GO:0007275,GO:0030165,GO:0008270,GO:0005886,GO:0030178,GO:0005509	CG11614-PA							PS50222			G3DSA:1.10.238.10	SSF47473									
aly322.2	Uncharacterized protein C15orf26	GO:0005575,GO:0003674,GO:0008150,GO:0004252,GO:0006508	CG5197-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly322.20	Ras GTPase-activating-like protein IQGAP1	GO:0030426,GO:0030424,GO:0048008,GO:0036464,GO:0071902,GO:0005925,GO:0008543,GO:0030054,GO:0005737,GO:0072015,GO:0050796,GO:0070062,GO:0005874,GO:0036120,GO:0005547,GO:0005654,GO:0006112,GO:0005509,GO:0043005,GO:0036057,GO:0044281,GO:0016787,GO:0034260,GO:0016328,GO:1990138,GO:0005096,GO:0031252,GO:0071277,GO:0005095,GO:0019901,GO:0019903,GO:0007173,GO:0005884,GO:0005886,GO:0007264,GO:0035305,GO:0031234,GO:0043539,GO:0043547,GO:0071364,GO:0005829,GO:0030496,GO:0005575,GO:0001817,GO:0005516,GO:0008150,GO:0045860,GO:0007165	CG8455-PB				SM00033,SM00015,SM00015,SM00015,SM00323		PF03836,PF00616,PF00612,PF00612,PF00612,PF00149,PF00307	PS50021,PS50096,PS50096,PS50018			G3DSA:1.10.418.10,G3DSA:3.60.21.10,G3DSA:3.60.21.10,G3DSA:1.10.506.10,G3DSA:1.10.506.10	SSF52540,SSF143885,SSF56300,SSF47576,SSF48350,SSF48350	866~886,1404~1424,1451~1471								
aly322.21	Unknown		n/a																				
aly322.22	GPI ethanolamine phosphate transferase 1	GO:0044267,GO:0016021,GO:0016020,GO:0005789,GO:0006501,GO:0003824,GO:0016740,GO:0008152,GO:0006506,GO:0016254,GO:0043687	CG2292-PA						PF04987,PF01663				G3DSA:3.40.720.10	SSF53649					UPA00196				
aly322.23	CD2 antigen cytoplasmic tail-binding protein 2 homolog	GO:0048749,GO:0006909,GO:0005634,GO:0035220,GO:0022416,GO:0003674,GO:0042060,GO:0005515,GO:0090303,GO:0045742	CG5198-PA				SM00444		PF02213	PS50829			G3DSA:3.30.1490.40	SSF55277	209~236								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly322.24	UPF0585 protein CG18661	GO:0005575,GO:0003674,GO:0008150	CG18661-PA						PF06080				G3DSA:3.40.50.150	SSF53335									
aly322.25	Unknown		n/a																				
aly322.26	Semaphorin-1A	GO:0001700,GO:0007399,GO:0016021,GO:0030154,GO:0004872,GO:0005515,GO:0005886,GO:0007411	CG6446-PA				SM00630,SM00423		PF01437,PF01403	PS51004			G3DSA:2.130.10.10,G3DSA:3.30.1680.10	SSF101912,SSF103575									
aly322.27	Major facilitator superfamily domain-containing protein 12	GO:0005765,GO:0016021,GO:0006810	n/a						PF13347				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly322.28	Unknown		n/a							PS50181			G3DSA:3.80.10.10	SSF52047									
aly322.29	Chromodomain-helicase-DNA-binding protein 1	GO:0008026,GO:0007476,GO:0005634,GO:0005705,GO:0035042,GO:0005703,GO:0004386,GO:0006355,GO:0006351,GO:0003677,GO:0003682,GO:0048477,GO:0005524	CG3733-PB				SM00490,SM00298,SM00298,SM00487		PF00176,PF00385,PF00385,PF00271,PF13907	PS51194,PS50013,PS50013,PS51192		PS00598,PS00690	G3DSA:2.40.50.40,G3DSA:2.40.50.40,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF54160,SSF54160,SSF52540,SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly322.3	Cartilage-associated protein	GO:0032991,GO:0005615,GO:1901874,GO:0005578,GO:0050821,GO:0007283,GO:0032403,GO:0018400,GO:0061077,GO:0005783	n/a										G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452										
aly322.30	Agrin	GO:0043547,GO:2000541,GO:1903277,GO:0008582,GO:0030154,GO:0035374,GO:0031012,GO:0042030,GO:0007009,GO:0002162,GO:0045202,GO:0044325,GO:0043087,GO:0007275,GO:0030054,GO:0005737,GO:0032092,GO:0030548,GO:0070062,GO:0016021,GO:0051491,GO:0007268,GO:0005509,GO:0061098,GO:0010469,GO:0005796,GO:1903407,GO:0009986,GO:0007528,GO:0043395,GO:0045213,GO:0004866,GO:0005886,GO:0055117,GO:0005615,GO:0005605,GO:0005604,GO:0086036,GO:0033691,GO:0045887,GO:0005576,GO:0045944,GO:0043113,GO:0001934,GO:0043525	CG32354-PA				SM00274,SM00274,SM00274,SM00274,SM00274,SM00274,SM00057,SM00057,SM00057,SM00057,SM00180,SM00180,SM00280,SM00280,SM00280,SM00280,SM00280,SM00280,SM00280		PF00053,PF00053,PF07648,PF07648,PF07648,PF07648,PF07648,PF07648,PF07648	PS50027,PS50027,PS51465,PS51257,PS51465,PS51465,PS51465,PS51465,PS51465,PS51465	PR00011,PR00011	PS01248	G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30	SSF100895,SSF100895,SSF100895,SSF100895,SSF57196,SSF100895,SSF100895,SSF57196,SSF100895										
aly322.31	Basement membrane-specific heparan sulfate proteoglycan core protein	GO:0008022,GO:0030204,GO:0030203,GO:0048704,GO:0031012,GO:0008104,GO:0042157,GO:0001525,GO:0001523,GO:0005925,GO:0005615,GO:0005576,GO:0002062,GO:0046872,GO:0022617,GO:0060351,GO:0005796,GO:0007603,GO:0043202,GO:0005886,GO:0070062,GO:0005605,GO:0005975,GO:0007420,GO:0001958,GO:0048738,GO:0030198,GO:0006027,GO:0006024,GO:0044281	n/a				SM00282		PF00054	PS50025			G3DSA:2.60.120.200	SSF49899										
aly322.32	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly322.33	Unknown		n/a										G3DSA:2.40.50.120										
aly322.34	Unknown		n/a																				
aly322.35	Luciferin 4-monooxygenase	GO:0046872,GO:0006637,GO:0045289,GO:0004321,GO:0005777,GO:0004467,GO:0046949,GO:0001676,GO:0008218,GO:0047077,GO:0005524	CG6178-PA						PF13193,PF00501			PS00455	G3DSA:3.40.50.980,G3DSA:3.30.300.30,G3DSA:2.30.38.10,G3DSA:3.40.50.980	SSF56801										
aly322.36	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly322.37	Agrin	GO:0016319,GO:0043547,GO:0006909,GO:0005887,GO:0008582,GO:0030154,GO:0035374,GO:0030425,GO:0030424,GO:0021551,GO:0007419,GO:0007009,GO:0008046,GO:0002162,GO:0070593,GO:0007411,GO:0044325,GO:0007413,GO:0032490,GO:0007275,GO:0030054,GO:1903277,GO:0005737,GO:0032092,GO:0045202,GO:0030548,GO:0070062,GO:0048846,GO:0043087,GO:0016021,GO:0051491,GO:2000541,GO:0007268,GO:0005509,GO:0043005,GO:0061098,GO:0042030,GO:0043025,GO:0042802,GO:0048666,GO:0050976,GO:0005796,GO:1903407,GO:0009986,GO:0007528,GO:0043395,GO:0045213,GO:0003823,GO:0005886,GO:0031012,GO:0055117,GO:0005615,GO:0005605,GO:0005604,GO:0050770,GO:0007422,GO:0010469,GO:0086036,GO:0033691,GO:0045887,GO:0005576,GO:0045944,GO:0048814,GO:0043113,GO:0001934,GO:0043525	CG33950-PAT				SM00180,SM00180,SM00179,SM00179,SM00280,SM00280,SM00280,SM00280,SM00280,SM00280,SM00280,SM00280,SM00274,SM00274,SM00274,SM00274,SM00274,SM00274,SM00274,SM00274,SM00274,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00282,SM00282,SM00282		PF02210,PF00053,PF00053,PF07648,PF07648,PF07648,PF07648,PF07648,PF07648,PF07648,PF07648,PF07648,PF00054,PF00008,PF00008,PF00008	PS50026,PS51465,PS50027,PS50026,PS50026,PS51465,PS51465,PS51465,PS50025,PS51465,PS50027,PS50025,PS50026,PS50026,PS51465,PS50025,PS51465,PS51465,PS51465,PS51465,PS51465		PS00022,PS01186,PS00022,PS00022,PS01186,PS01248,PS00022,PS01186,PS00022	G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:2.60.120.200,G3DSA:2.10.25.10,G3DSA:3.30.60.30,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30	SSF57196,SSF100895,SSF100895,SSF100895,SSF100895,SSF49899,SSF57196,SSF100895,SSF100895,SSF49899,SSF100895,SSF100895,SSF49899,SSF100895								
aly322.38	NADH dehydrogenase [ubiqui] flavoprotein 2, mitochondrial	GO:0007399,GO:0043209,GO:0008137,GO:0051537,GO:0005739,GO:0006120,GO:0048738,GO:0005747,GO:0046872,GO:0003954,GO:0055114,GO:0016491	CG5703-PA			PIRSF000216		TIGR01958	PF01257				G3DSA:3.40.30.10	SSF52833									
aly322.39	PDZ domain-containing protein 2	GO:0048749,GO:0005737,GO:0005911,GO:0016324,GO:0005634,GO:0005576,GO:0003674,GO:0005912,GO:0005515,GO:0007155,GO:0005783	CG6741-PB				SM00228,SM00228		PF00595,PF00595	PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156									
aly322.4	Zinc finger protein 687	GO:0005737,GO:0005819,GO:0043231,GO:0005730,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0005876,GO:0006351	CG8474-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60	SSF57667,SSF57667								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly322.40	PDZ domain-containing protein 2	GO:0048749,GO:0005737,GO:0045177,GO:0043005,GO:0005911,GO:0016324,GO:0005634,GO:0005576,GO:0003674,GO:0005912,GO:0005515,GO:0007155,GO:0014069,GO:0035556,GO:0005783	CG6741-PB				SM00228,SM00228		PF00595	PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156									
aly322.41	Dynein heavy chain 8, axonemal	GO:0036157,GO:0097228,GO:0042623,GO:0007605,GO:0007018,GO:0005858,GO:0003774,GO:0005524,GO:0016887,GO:0030286,GO:0005874,GO:0005875,GO:0003777	CG9492-PG				SM00382,SM00382,SM00382		PF12781,PF03028,PF08393,PF12775,PF08385,PF12780,PF12777,PF12774,PF07728	PS50817			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540	4642~4643,3810~3830,668~688,3445~3486,100~120								
aly322.42	DNA helicase MCM8	GO:0007292,GO:0000724,GO:0004003,GO:0005634,GO:0048232,GO:0097362,GO:0004386,GO:0006974,GO:0005656,GO:0005657,GO:0006260,GO:0007049,GO:0003677,GO:0007131,GO:0005524	CG31293-PA				SM00382,SM00350		PF00493	PS50051	PR01657,PR01657,PR01657,PR01657,PR01657	PS00847	G3DSA:2.20.28.10,G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:3.40.50.300	SSF50249,SSF52540,SSF52540			REACT_152,REACT_383,REACT_1538						
aly322.43	Protein-cysteine N-palmitoyltransferase Rasp	GO:0007367,GO:0007225,GO:0007224,GO:0016021,GO:0016746,GO:0018009,GO:0005886,GO:0046843,GO:0016409,GO:0018345	CG11495-PA						PF03062														
aly322.44	Poly(U)-specific endoribonuclease homolog	GO:0090502,GO:0004521,GO:0016788,GO:0005576,GO:0003723,GO:0046872,GO:0008236	CG2145-PA						PF09412					SSF142877									
aly322.45	5'-nucleotidase domain-containing protein 3	GO:0016787,GO:0046872	CG1814-PA					TIGR02244	PF05761				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF56784	399~419								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly322.46	Poly(U)-specific endoribonuclease homolog	GO:0090502,GO:0004521,GO:0016788,GO:0005576,GO:0003723,GO:0046872,GO:0008236	CG2145-PA						PF09412					SSF142877									
aly322.47	Unknown		n/a								PR01217,PR01217,PR01217												
aly322.48	Unknown		n/a																				
aly322.49	Unknown		n/a																				
aly322.5	E3 ubiquitin-protein ligase RNF4	GO:0050681,GO:0031491,GO:0008270,GO:0003677,GO:0070936,GO:0005737,GO:0016605,GO:0090169,GO:0030521,GO:0070979,GO:0043161,GO:0005634,GO:0003713,GO:0085020,GO:0046685,GO:0070534,GO:0042802,GO:0090234,GO:0004842,GO:0045893,GO:0016874,GO:0003700,GO:0032184,GO:0051865,GO:0045944,GO:0006351,GO:0005515	CG13481-PB				SM00184		PF13639	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly322.50	Mitochondrial cardiolipin hydrolase	GO:0030719,GO:0007126,GO:0034587,GO:0035755,GO:0043046,GO:0016021,GO:0007286,GO:0016042,GO:0008053,GO:0005741,GO:0004519,GO:0046872,GO:0042803	n/a						PF13091				G3DSA:3.30.870.10	SSF56024									
aly322.51	E3 ubiquitin-protein ligase MSL2	GO:0072487,GO:0007549,GO:0006325,GO:0016456,GO:0005634,GO:0000805,GO:0043984,GO:0005654,GO:0016874,GO:0051865,GO:0008270,GO:0046536,GO:0003677,GO:0003682,GO:0005694,GO:0016457,GO:0009047	CG3241-PB						PF16685,PF16682														
aly322.52	Leucine-rich repeat transmembrane neuronal protein 2	GO:0050808,GO:0042734,GO:0007399,GO:0045211,GO:0060291,GO:0016021,GO:0051965,GO:0005515,GO:0060076,GO:0002091,GO:0043025,GO:0030054	CG15658-PA				SM00369,SM00369		PF13855,PF00560	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									
aly322.53	Regulator of nonsense transcripts 3A	GO:0005737,GO:0000184,GO:0043231,GO:0035195,GO:0005829,GO:0006913,GO:0000166,GO:0005654,GO:0010467,GO:0045727,GO:0003723,GO:0005886,GO:0016246,GO:0051028,GO:0005634,GO:0005487	CG11184-PB						PF03467				G3DSA:3.30.70.330	SSF54928									
aly322.54	28S ribosomal protein S28, mitochondrial	GO:0070126,GO:0006996,GO:0070124,GO:0070125,GO:0044822,GO:0005739,GO:0006412,GO:0003735,GO:0005743,GO:0005763,GO:0032543	CG5497-PA						PF10246														
aly322.55	Glutaminase kidney isoform, mitochondrial	GO:0004359,GO:0007476,GO:0005829,GO:0051289,GO:0006541,GO:0005739,GO:0007268,GO:0001967,GO:0006537,GO:0006543,GO:0005515,GO:0002087	CG42708-PH	MF_00313			SM00248	TIGR03814	PF04960,PF12796	PS50297,PS50088			G3DSA:1.25.40.20,G3DSA:3.40.710.10	SSF48403,SSF56601		00250+3.5.1.2,00330+3.5.1.2,00471+3.5.1.2	REACT_13,REACT_13685						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly322.56	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00465,PR00465,PR00465,PR00465,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly322.57	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG3466-PA						PF00067				G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly322.58	Unknown		n/a																				
aly322.6	Patj homolog	GO:0016333,GO:0016332,GO:0016334,GO:0005080,GO:0045196,GO:0034334,GO:0035003,GO:0007163,GO:0007043,GO:0005875,GO:0005737,GO:0002009,GO:0035088,GO:0045176,GO:0005635,GO:0045179,GO:0034332,GO:0032033,GO:0035509,GO:0016324,GO:0016327,GO:0008594,GO:0045186,GO:0005912,GO:0005886,GO:0001736,GO:0005918,GO:0035209,GO:0005515,GO:0045494	CG12021-PC				SM00228,SM00228,SM00228		PF00595,PF00595,PF00595	PS50106,PS51022,PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156,SSF50156									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly322.7	Patj homolog	GO:0016333,GO:0016332,GO:0016334,GO:0005080,GO:0045196,GO:0034334,GO:0035003,GO:0007163,GO:0007043,GO:0005875,GO:0005737,GO:0002009,GO:0035088,GO:0045176,GO:0005635,GO:0045179,GO:0034332,GO:0032033,GO:0035509,GO:0016324,GO:0016327,GO:0008594,GO:0045186,GO:0005912,GO:0005886,GO:0001736,GO:0005918,GO:0035209,GO:0005515,GO:0045494	CG12021-PC				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156										
aly322.8	Long-chain-fatty-acid--CoA ligase ACSBG2	GO:0001676,GO:0005575,GO:0004467,GO:0005524,GO:0005737	CG4501-PA						PF00501				G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.40.50.980,G3DSA:3.40.50.980	SSF56801,SSF56801,SSF56801										
aly322.9	Golgi phosphoprotein 3 homolog rotini	GO:0036089,GO:0070273,GO:0000301,GO:0090307,GO:0003674,GO:0051225,GO:0031985,GO:0010314,GO:0000281,GO:0005794,GO:0070300,GO:0017137,GO:0032154,GO:0007053,GO:0007111,GO:0007110,GO:0007030,GO:0007112,GO:0000915,GO:0007224,GO:0032266,GO:0000139,GO:0015031	CG7085-PD						PF05719				G3DSA:1.10.3630.10										
aly3224.1	Unknown		n/a						PF16009						75~95								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3224.2	Unknown		n/a												202~222,251~308,332~352								
aly323.1	Double-stranded RNA-specific editase Adar	GO:0060964,GO:0030534,GO:0001666,GO:0006397,GO:0005622,GO:0007626,GO:0042391,GO:0016556,GO:0009451,GO:0003726,GO:0006382,GO:0042752,GO:0003725,GO:0046872,GO:0003723,GO:0006979,GO:0009408,GO:0008049,GO:0008344,GO:0006396,GO:0045475	CG12598-PN				SM00552,SM00358,SM00358		PF00035,PF00035,PF02137	PS50137,PS50137,PS50141			G3DSA:3.30.160.20,G3DSA:3.30.160.20	SSF54768,SSF54768									
aly323.2	Aldose reductase	GO:0005737,GO:0004032,GO:0055114,GO:0016491	CG6084-PB			PIRSF000097			PF00248		PR00069,PR00069,PR00069,PR00069,PR00069	PS00062,PS00063,PS00798	G3DSA:3.20.20.100	SSF51430									
aly323.3	Protein SERAC1	GO:0005783,GO:0008654,GO:0016021,GO:0016788,GO:0005578,GO:0005654,GO:0030198,GO:0006505,GO:0005739,GO:0006886	CG5455-PA										G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474									
aly323.4	Transcription factor E4F1	GO:0005737,GO:0006355,GO:0005634,GO:0005654,GO:0016567,GO:0008270,GO:0003677,GO:0007067,GO:0046872,GO:0016874,GO:0040008,GO:0051301,GO:0006351	CG6654-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667	173~200									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly323.5	Lipase member H	GO:0016020,GO:0052689,GO:0016042,GO:0005575,GO:0005576,GO:0016298	CG6472-PB						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly323.6	Unknown		n/a										G3DSA:3.40.50.1820										
aly3232.1	Unknown		n/a												59~79								
aly32341.1	Zinc finger BED domain-containing protein 1	GO:0004803,GO:0003676,GO:0008152,GO:0003677,GO:0000228,GO:0046872	CG16863-PB						PF05699					SSF53098									
aly3235.1	Metal transporter CNNM2	GO:0030554,GO:0016021,GO:0006873,GO:0016323,GO:0005575,GO:0015693,GO:0003674,GO:0010960	CG42595-PE						PF01595	PS50042,PS51371,PS51371			G3DSA:3.10.580.10,G3DSA:2.60.120.10	SSF54631,SSF51206									
aly3235.2	Metal transporter CNNM2	GO:0030554,GO:0016021,GO:0006873,GO:0016323,GO:0005575,GO:0015693,GO:0003674,GO:0010960	CG42595-PE							PS51371,PS51371,PS50042			G3DSA:2.60.120.10,G3DSA:3.10.580.10	SSF54631,SSF51206									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly32384.1	Unknown		n/a																				
aly3239.1	Unknown		n/a																				
aly324.1	Unknown		n/a																				
aly3241.1	Soluble guanylate cyclase 88E	GO:0019826,GO:0019825,GO:0020037,GO:0046982,GO:0001666,GO:0000302,GO:0004383,GO:0016849,GO:0070026,GO:0070025,GO:0008074,GO:0046872,GO:0005525,GO:0006184,GO:0035556,GO:0009190,GO:0006182,GO:0042803	CG4154-PD				SM00044		PF07700,PF00211,PF07701	PS50125		PS00452	G3DSA:3.30.70.1230,G3DSA:3.90.1520.10	SSF111126,SSF55073	360~394	00230+4.6.1.2							
aly3241.2	Amine sulfotransferase	GO:0005737,GO:0047685,GO:0005829,GO:0051923,GO:0008146	CG16733-PA						PF00685				G3DSA:3.40.50.300	SSF52540									
aly3241.3	Transmembrane protein 216	GO:0005737,GO:0005856,GO:0016021,GO:0042995,GO:0042384	CG11760-PB						PF09799														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3241.4	28S ribosomal protein S10, mitochondrial	GO:0003735,GO:0005763,GO:0005761,GO:0006412	CG4247-PB						PF00338				G3DSA:3.30.70.600	SSF54999									
aly3241.5	Dynein light chain roadblock-type 2	GO:0016319,GO:0070062,GO:0042623,GO:0005634,GO:0006810,GO:0007018,GO:0005858,GO:0003774,GO:0048813,GO:0008270,GO:0005868,GO:0030286,GO:0005874,GO:0005875	CG10751-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00960		PF07776,PF03259	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.450.30	SSF103196,SSF57667,SSF57667,SSF57716										
aly3241.6	Dosage compensation regulator	GO:0048675,GO:0072487,GO:0008026,GO:0000785,GO:0003676,GO:0009047,GO:0005737,GO:0031453,GO:0005634,GO:0000805,GO:0005665,GO:0005694,GO:0016457,GO:0005524,GO:0044822,GO:0004004,GO:0004386,GO:0008340,GO:0007549,GO:0045433,GO:0016456,GO:0005700,GO:0003724,GO:0003725,GO:0045944,GO:0003723,GO:0003682,GO:0006396	CG11680-PA				SM00490,SM00487,SM00847,SM00358		PF00271,PF07717,PF04408,PF00035	PS50137,PS51192,PS51194		PS00690	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.30.160.20	SSF52540,SSF52540,SSF54768										
aly3241.7	VIP36-like protein	GO:0005794,GO:0046872,GO:0006888,GO:0016021,GO:0016020,GO:0005789,GO:0015031,GO:0006457,GO:0000139,GO:0030134,GO:0005537	CG5510-PA						PF03388	PS51328			G3DSA:2.60.120.200	SSF49899									
aly3242.1	Dosage compensation regulator	GO:0048675,GO:0072487,GO:0008026,GO:0000785,GO:0003676,GO:0009047,GO:0005737,GO:0031453,GO:0005634,GO:0000805,GO:0005665,GO:0005694,GO:0016457,GO:0005524,GO:0044822,GO:0004004,GO:0004386,GO:0008340,GO:0007549,GO:0045433,GO:0016456,GO:0005700,GO:0003724,GO:0003725,GO:0045944,GO:0003723,GO:0003682,GO:0006396	CG11680-PA						PF00035	PS50137			G3DSA:3.30.160.20	SSF54768									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3246.1	Semaphorin-5B	GO:0016021,GO:0030154,GO:0007399	CG12594-PA				SM00209,SM00210,SM00282		PF02210,PF00090	PS50092			G3DSA:2.20.100.10,G3DSA:2.60.120.200	SSF49899,SSF82895									
aly3246.2	Unknown		n/a																				
aly3246.3	Unknown		n/a																				
aly3248.1	Putative U5 small nuclear ribonucleoprotein 200 kDa helicase	GO:0000381,GO:0030532,GO:0071011,GO:0005634,GO:0004004,GO:0008380,GO:0003724,GO:0000398,GO:0003676,GO:0005681,GO:0007067,GO:0071013,GO:0005682,GO:0005524	CG5931-PA				SM00973,SM00611		PF02889				G3DSA:1.10.3380.10,G3DSA:2.60.40.150,G3DSA:1.10.150.20	SSF158702,SSF46785,SSF81296	285~294								
aly3248.2	Ferritin-2, chloroplastic	GO:0005794,GO:0006879,GO:0042381,GO:0008199,GO:0004322,GO:0008198,GO:0008043,GO:0005576,GO:0006826,GO:0045475,GO:0022416,GO:0009507	CG1469-PE						PF00210	PS50905			G3DSA:1.20.1260.10	SSF47240									
aly3248.3	Ferritin subunit	GO:0008043,GO:0005794,GO:0006879,GO:0008283,GO:0004322,GO:0005623,GO:0045169,GO:0008198,GO:0008199,GO:0005576,GO:0006826,GO:0005875,GO:0009791	CG2216-PI						PF00210	PS50905			G3DSA:1.20.1260.10	SSF47240									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3248.4	Luciferin 4-monooxygenase	GO:0046872,GO:0006637,GO:0045289,GO:0004321,GO:0005777,GO:0004467,GO:0046949,GO:0001676,GO:0008218,GO:0047077,GO:0005524	CG6178-PA						PF00501,PF13193				G3DSA:3.30.300.30,G3DSA:2.30.38.10	SSF56801									
aly3248.5	Luciferin 4-monooxygenase	GO:0046872,GO:0006637,GO:0045289,GO:0004321,GO:0005777,GO:0004467,GO:0046949,GO:0001676,GO:0008218,GO:0047077,GO:0005524	CG6178-PA						PF00501				G3DSA:3.40.50.980,G3DSA:3.40.50.980	SSF56801									
aly3248.6	Myoneurin	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00868,SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF13912,PF13912,PF13912,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57716,SSF57667,SSF57667									
aly3248.7	Unknown		n/a																				
aly3248.8	Zinc finger protein 335	GO:0044212,GO:2000327,GO:0000979,GO:0007420,GO:0048812,GO:0048854,GO:0005634,GO:0006355,GO:0050671,GO:0035097,GO:0040029,GO:0002052,GO:0001701,GO:0006351,GO:0003676,GO:0021895,GO:0051569,GO:0046872,GO:0080182	CG32767-PC				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028		SSF57667										
aly3251.1	Organic cation transporter 1	GO:0016021,GO:0008513,GO:0015695,GO:0008340,GO:0015101,GO:0055085	CG9317-PA						PF07690,PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3251.2	Unknown	GO:0015149,GO:0016021,GO:0006909,GO:0055085	CG14606-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly3254.1	Sodium channel protein 60E	GO:0007608,GO:0042048,GO:0005248,GO:0019228,GO:0006814,GO:0035725,GO:0022843,GO:0005886,GO:0086010,GO:0055085,GO:0001518	CG34405-PM																				
aly3255.1	Juvenile hormone epoxide hydrolase	GO:0008096,GO:0043231,GO:0033961,GO:0016021,GO:0005789,GO:0004301,GO:0019439,GO:0006719	CG15102-PA			PIRSF001112			PF06441		PR00412,PR00412,PR00412,PR00412,PR00412		G3DSA:3.40.50.1820	SSF53474		00980+3.3.2.9							
aly3255.2	Serpin B9	GO:0009617,GO:0004867,GO:0010628,GO:0035009,GO:0005737,GO:0042270,GO:0005615,GO:0005634,GO:0016020,GO:0043066,GO:0002020,GO:0043027,GO:0071391,GO:0033668,GO:0006915,GO:0002448,GO:0006955,GO:0010951,GO:0070062,GO:0005829,GO:0005622,GO:0043154,GO:0045861	CG6680-PA				SM00093		PF00079				G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:2.30.39.10,G3DSA:2.30.39.10	SSF56574										
aly3263.1	Alpha-N-acetylgalactosaminidase	GO:0005737,GO:0008456,GO:0005975,GO:0009311,GO:0016139,GO:0005764,GO:0004557,GO:0046477	CG7997-PB						PF16499		PR00740,PR00740,PR00740,PR00740,PR00740,PR00740	PS00512	G3DSA:3.20.20.70	SSF51445		00052+3.2.1.22,00600+3.2.1.22,00603+3.2.1.22,00561+3.2.1.22		PWY-6527					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3263.10	NADH dehydrogenase [ubiqui] iron-sulfur protein 4, mitochondrial	GO:0007420,GO:0032981,GO:0008137,GO:0072593,GO:0051591,GO:0022900,GO:0045333,GO:0005747,GO:0019933,GO:0048146,GO:0016651	CG12203-PA						PF04800				G3DSA:3.30.160.190										
aly3263.11	Sodium channel protein 60E	GO:0007608,GO:0042048,GO:0005248,GO:0019228,GO:0006814,GO:0035725,GO:0022843,GO:0005886,GO:0086010,GO:0055085,GO:0001518	CG34405-PM						PF00520,PF00520,PF00520,PF06512,PF16905	PS50096	PR00170,PR00170		G3DSA:1.10.287.930,G3DSA:1.10.287.930,G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.5.150	SSF81324,SSF81324,SSF81324,SSF81324,SSF81324,SSF81324	828~848		REACT_18266							
aly3263.12	CD82 antigen	GO:0070062,GO:0016021,GO:0008150,GO:0005887,GO:0005886,GO:0003674	CG4999-PB						PF00335					SSF48652									
aly3263.2	Hydroxymethylglutaryl-CoA synthase 1	GO:0016126,GO:0004421,GO:0001700,GO:0008299,GO:0046331,GO:0022008	CG4311-PF					TIGR01833	PF08540,PF01154				G3DSA:3.40.47.10	SSF53901,SSF53901,SSF53901		00900+2.3.3.10,00072+2.3.3.10,00280+2.3.3.10,00650+2.3.3.10	REACT_22258	PWY-7571,PWY-922,PWY-6174,PWY-7391,PWY-7524	UPA00058				
aly3263.3	Unknown	GO:0003677	CG3838-PA				SM00595		PF02944,PF10545	PS51029,PS51031													
aly3263.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3263.5	Unknown		n/a																				
aly3263.6	Unknown		n/a																				
aly3263.7	Unknown	GO:0022008,GO:0042600,GO:0007304,GO:0005201,GO:0031012	CG32602-PA																				
aly3263.8	Unknown	GO:0005575,GO:0003674,GO:0008150	CG12848-PA											SSF47072									
aly3263.9	Inhibitor of Bruton tyrosine kinase	GO:0005737,GO:0019901,GO:0016020,GO:0051209,GO:0005654,GO:0061099,GO:0001933,GO:0030292	CG8060-PA				SM00248,SM00248,SM00225,SM00225		PF13637,PF00651,PF00415	PS50097,PS50097,PS50088,PS50012,PS50088,PS50297			G3DSA:3.30.710.10,G3DSA:3.30.710.10,G3DSA:3.30.710.10,G3DSA:3.30.710.10,G3DSA:2.130.10.30,G3DSA:1.25.40.20	SSF48403,SSF54695,SSF50985,SSF54695									
aly3266.1	Unknown		n/a						PF03564														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3266.2	Unknown		n/a																				
aly3266.3	Unknown		n/a																				
aly3268.1	Sideroflexin-1	GO:0008324,GO:0016021,GO:0006812,GO:0006811,GO:0016020,GO:0031966,GO:0015075,GO:0055072,GO:0055085,GO:0005371	CG11739-PC						PF03820														
aly3268.10	HIG1 domain family member 1A, mitochondrial	GO:0016021,GO:0090201,GO:0005743,GO:0071456,GO:0042149,GO:0070469,GO:0005634,GO:0055114	CG11825-PC						PF04588	PS51503													
aly3268.11	Centrosomal protein of 295 kDa	GO:0005814,GO:1902117	n/a												1420~1440 ,110~144								
aly3268.12	Unknown		n/a												50~70								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3268.13	Unknown	GO:0005215,GO:0042626,GO:0055085,GO:0005524,GO:0043190	CG4562-PE																				
aly3268.14	Probable multidrug resistance-associated protein lethal(2)03659	GO:0043190,GO:0042626,GO:0005215,GO:0016021,GO:0006810,GO:0007275,GO:0055085,GO:0005524	CG4562-PE				SM00382,SM00382		PF00664,PF00664,PF00005,PF00005	PS50893,PS50929,PS50893,PS50929		PS00211,PS00211	G3DSA:3.40.50.300,G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:3.40.50.300	SSF90123,SSF52540,SSF52540,SSF90123										
aly3268.15	Exocyst complex component 2	GO:0035147,GO:0055037,GO:0000281,GO:0035003,GO:0010629,GO:0003674,GO:0005905,GO:0007298,GO:0030136,GO:0005737,GO:0016028,GO:0000145,GO:0045056,GO:0007349,GO:0043001,GO:0045087,GO:0048599,GO:0016081,GO:0016080,GO:0048215,GO:0017137,GO:0005938,GO:0007269,GO:0005886,GO:0072659,GO:0006893,GO:0072697,GO:0016192,GO:0005642,GO:0032456,GO:0071896	CG8843-PA						PF15469,PF01833				G3DSA:2.60.40.10	SSF81296	313~340,484~504									
aly3268.16	Growth hormone-regulated TBC protein 1-A	GO:0032313,GO:0005096,GO:0005097	CG5916-PA				SM00164		PF00566	PS50086			G3DSA:1.10.8.270	SSF47923,SSF47923									
aly3268.17	Mitochondrial import inner membrane translocase subunit TIM14	GO:0032781,GO:0016021,GO:0001405,GO:0030150,GO:0005744,GO:0022008,GO:0001671	CG7394-PB				SM00271		PF00226	PS50076			G3DSA:1.10.287.110	SSF46565									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3268.18	Importin-5	GO:0006610,GO:0008565,GO:0005875,GO:0005737,GO:0005730,GO:0005634,GO:0016020,GO:0005654,GO:0005794,GO:0071230,GO:0031965,GO:0044822,GO:0006606,GO:0034260,GO:0006607,GO:0008320,GO:0042307,GO:0005095,GO:0043231,GO:0005643,GO:0005829,GO:0008536,GO:0016032	CG1059-PA						PF13646				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371									
aly3268.19	Choline-phosphate cytidylyltransferase B	GO:0005737,GO:0005783,GO:0004105,GO:0007283,GO:0009058,GO:0001541	CG18330-PA					TIGR00125	PF01467				G3DSA:3.40.50.620	SSF52374	241~261								
aly3268.2	Zinc finger protein 79	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG5245-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57716,SSF57667,SSF57667								
aly3268.20	Protein canopy homolog 3	GO:0005575,GO:0008150,GO:0045087,GO:0003674,GO:0005783	CG11577-PA						PF11938						150~170								
aly3268.21	N-acetyltransferase 9-like protein	GO:0005575,GO:0003674,GO:0008150,GO:0008080	CG11539-PA						PF13302				G3DSA:3.40.630.30	SSF55729									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3268.22	Unknown		CG2310-PA												39~40								
aly3268.23	Unknown		n/a																				
aly3268.3	Unknown	GO:0043565,GO:0003677,GO:0046331,GO:0019185,GO:0005515,GO:0065004,GO:0003681,GO:0042795,GO:0042796,GO:0003682	CG2702-PA				SM00717		PF00249	PS50090			G3DSA:1.10.10.60	SSF46689	101~121								
aly3268.4	Division abnormally delayed protein	GO:0019897,GO:0098595,GO:0008101,GO:0008586,GO:0035220,GO:0008315,GO:0008045,GO:0031225,GO:0007472,GO:0016020,GO:0007476,GO:0008407,GO:0005576,GO:2001261,GO:0048749,GO:0048190,GO:0007480,GO:0009986,GO:0043395,GO:0008052,GO:0007409,GO:0005886,GO:0048132,GO:0030513,GO:0007179,GO:0030510,GO:0030718,GO:0040014,GO:0007399,GO:0051726,GO:0016055,GO:0048813,GO:0022416,GO:0005515,GO:0045570,GO:0005578	CG4974-PA						PF01153														
aly3268.5	HBS1-like protein	GO:0045089,GO:0070062,GO:0003746,GO:0005829,GO:0016020,GO:0003924,GO:0007165,GO:0050829,GO:0006415,GO:0003747,GO:0006412,GO:0005525	CG1898-PA						PF03143,PF03144,PF08938,PF00009	PS51722	PR00315,PR00315,PR00315,PR00315,PR00315		G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:3.40.50.300	SSF50465,SSF109732,SSF50447,SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3268.6	Ras-related GTP-binding protein A	GO:0009267,GO:0034448,GO:0019048,GO:0008219,GO:0005737,GO:0005764,GO:0005634,GO:0045919,GO:0030307,GO:0010506,GO:0005525,GO:0005794,GO:0006915,GO:0071230,GO:1990131,GO:0034613,GO:0003924,GO:0042803,GO:0008152,GO:0051219,GO:0005575,GO:0005765,GO:0032008,GO:0046982	CG11968-PA						PF04670				G3DSA:3.40.50.300	SSF52540	126~146								
aly3268.7	HIG1 domain family member 1A, mitochondrial	GO:0016021,GO:0090201,GO:0005743,GO:0071456,GO:0042149,GO:0070469,GO:0005634,GO:0055114	CG11825-PC						PF04588	PS51503													
aly3268.8	Serine/threonine-protein phosphatase 2A activator	GO:0019211,GO:0005737,GO:0032515,GO:0003755,GO:0035308,GO:0005634,GO:0050790,GO:0051721,GO:0000159,GO:0008160,GO:0034047,GO:0043666,GO:0032516,GO:0035307,GO:0008152,GO:0008601,GO:0005524,GO:0042803	CG3289-PA			PIRSF016325			PF03095					SSF140984										
aly3268.9	Beta carbonic anhydrase 1	GO:0006730,GO:0004089,GO:0008270,GO:0005739	CG11967-PA				SM00947		PF00484				G3DSA:3.40.1050.10	SSF53056		00910+4.2.1.1		PWY-6142,PWY-241,PWY-7117,PWY-7115					
aly3269.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3269.2	PCI domain-containing protein 2 homolog	GO:0005737,GO:0005844,GO:0047499,GO:0005829,GO:0006417,GO:0005634,GO:0006406	CG7351-PA																				
aly3269.3	Major facilitator superfamily domain-containing protein 6	GO:0008340,GO:0016021,GO:0016020,GO:0055085	CG7334-PC						PF03825,PF12832	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly3269.4	Unknown		n/a																				
aly3269.5	DENN domain-containing protein 1A	GO:0030665,GO:0045202,GO:0006897,GO:0043547,GO:0042734,GO:0017124,GO:0017112,GO:0032483,GO:0030425,GO:0048488,GO:0015031,GO:0043025,GO:0030054,GO:0030136	CG18659-PA				SM00801,SM00800,SM00799		PF03455,PF02141,PF03456	PS50211,PS50947,PS50946													
aly3269.6	Unknown		n/a																				
aly327.1	Unknown		CG12164-PA						PF16086,PF16086,PF16086,PF16086,PF16086														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly327.2	Alpha-1,3-mannosyl-glycoprotein 4 beta-N-acetylglucosaminyltransferase A	GO:0008454,GO:0005975,GO:0070062,GO:0006487,GO:0016021,GO:0016020,GO:0000139,GO:0008375,GO:0016758,GO:0046872	CG9384-PA						PF04666							00510+2.4.1.145,00513+2.4.1.145		PWY-7426	UPA00378				
aly327.3	Probable cytochrome P450 303a1	GO:0004497,GO:0016705,GO:0020037,GO:0007423,GO:0016020,GO:0005789,GO:0005506,GO:0009055,GO:0055114,GO:0043231	CG4163-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385		G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly327.4	Krueppel-like factor 7	GO:0043565,GO:0008270,GO:0003700,GO:0005634,GO:0003713,GO:0006355,GO:0048813,GO:0006357,GO:0045893,GO:0003677,GO:0007411,GO:0046872,GO:0006351	CG33473-PB				SM00355,SM00355,SM00355			PS50157,PS50157,PS50157	PR01217,PR01217,PR01217,PR01217,PR01217	PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly327.5	Unknown		n/a																				
aly327.6	Unknown	GO:0006909	CG6091-PE						PF02338	PS50802				SSF54001									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly32716.1	Unknown	GO:0050660,GO:0005615,GO:0032504,GO:0004466,GO:0001745,GO:0006979,GO:0055114	CG9006-PA																				
aly32760.1	Synaptic vesicle glycoprotein 2A	GO:0030672,GO:0005783,GO:0006874,GO:0016021,GO:0048786,GO:0005215,GO:0031594,GO:0022857,GO:0004872,GO:0005911,GO:0006836,GO:0043195,GO:0055085,GO:0045202	CG3168-PC						PF07690	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly3277.1	Bombyxin C-1	GO:0005179,GO:0060180,GO:0008286,GO:0005615,GO:0005158,GO:0005576	CG14167-PA				SM00078		PF00049		PR00276,PR00276	PS00262	G3DSA:1.10.100.10	SSF56994									
aly3277.10	SUZ domain-containing protein 1		CG31908-PA						PF12901,PF12752	PS51673													
aly3277.11	DNA-directed RNA polymerase I subunit RPA1	GO:0005737,GO:0005736,GO:0005730,GO:0005634,GO:0040029,GO:0005654,GO:0006360,GO:0010467,GO:0006362,GO:0006363,GO:0008270,GO:0003677,GO:0003899,GO:0045814,GO:0006361	CG10122-PA				SM00663		PF04997,PF04998,PF04983,PF00623,PF05000				G3DSA:3.30.1490.180,G3DSA:2.40.40.20,G3DSA:2.40.40.20	SSF64484,SSF64484,SSF64484,SSF64484,SSF64484	1246~1266,1038~1058	00240+2.7.7.6,00230+2.7.7.6	REACT_1788						
aly3277.12	Putative inorganic phosphate cotransporter	GO:0015293,GO:0035435,GO:0006817,GO:0015114,GO:0005316,GO:0022857,GO:0006820,GO:0005886,GO:0055085,GO:0006814,GO:0016021	CG8098-PB						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	490~517								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3277.13	BUB3-interacting and GLEBS motif-containing protein ZNF207	GO:0050821,GO:0000070,GO:0005634,GO:0008608,GO:0048813,GO:0051983,GO:0000776,GO:0003677,GO:0007094,GO:0046872,GO:0005874,GO:0051301,GO:0000777	CG17912-PF				SM00355,SM00355			PS50808		PS00028,PS00028	G3DSA:3.90.10.10										
aly3277.14	Unknown		n/a																				
aly3277.15	WAS/WASL-interacting protein family member 3	GO:0005737,GO:0030154,GO:0017124,GO:0003779,GO:0007283,GO:0007275	n/a				SM00246		PF02205	PS51082													
aly3277.16	Unknown		n/a												208~228,234~261,532~552								
aly3277.17	26S proteasome non-ATPase regulatory subunit 11	GO:0004175,GO:0005838,GO:0043161,GO:0000502,GO:0006508,GO:0005875,GO:0008541	CG10149-PA				SM00088,SM00753		PF01399				G3DSA:1.10.10.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF46785									
aly3277.18	Protein gamma response 1	GO:0000014,GO:0010212,GO:0006281,GO:0005634,GO:0006974,GO:0000077,GO:0007276	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3277.19	Unknown		n/a												78~91								
aly3277.2	Bombyxin A-3 homolog	GO:0005615	n/a				SM00078		PF00049		PR00276,PR00276	PS00262	G3DSA:1.10.100.10	SSF56994									
aly3277.20	Unknown		n/a																				
aly3277.21	Zinc finger protein 768	GO:0031936,GO:0043565,GO:0006355,GO:0005634,GO:0006366,GO:0005700,GO:0005665,GO:0045892,GO:0005515,GO:0003677,GO:0000785,GO:0046872,GO:0044822,GO:0043035	CG8573-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF13912	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										
aly3277.22	Protein yippee like 2	GO:0005575,GO:0003674,GO:0007476,GO:0005730	CG15309-PA						PF03226														
aly3277.23	COP9 signalosome complex subunit 7b	GO:0005737,GO:0034399,GO:0051726,GO:0005654,GO:0050821,GO:0046331,GO:0005515,GO:0007095,GO:0010388,GO:0008180	CG2038-PA				SM00088																

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3277.24	Zinc finger protein 268	GO:0008588,GO:0015629,GO:0030154,GO:0046022,GO:0003676,GO:0003677,GO:0005737,GO:0007346,GO:0000122,GO:0071356,GO:0005634,GO:0007476,GO:0043065,GO:0043066,GO:0046872,GO:0071157,GO:0008284,GO:0008285,GO:0030335,GO:0045597,GO:0003700,GO:0090073,GO:0006355,GO:0043497,GO:0045732,GO:0045944,GO:0006351,GO:0001934	CG8367-PL				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	684~704,650~674								
aly3277.25	Unknown		n/a																				
aly3277.26	Probable cytochrome P450 49a1	GO:0004497,GO:0016705,GO:0020037,GO:0016020,GO:0005739,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG18377-PA						PF00067		PR00463,PR00463,PR00463,PR00463		G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264,SSF48264			REACT_13433						
aly3277.3	Bombyxin C-1	GO:0005615	n/a				SM00078		PF00049		PR00276,PR00276	PS00262	G3DSA:1.10.100.10	SSF56994									
aly3277.4	Bombyxin A-2 homolog	GO:0005615	n/a				SM00078		PF00049	PS51257	PR00276,PR00276	PS00262	G3DSA:1.10.100.10	SSF56994									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3277.5	Bombyxin A-1 homolog	GO:0005179,GO:0005576,GO:0005615	n/a				SM00078		PF00049	PS51257	PR00276,PR00276	PS00262	G3DSA:1.10.100.10	SSF56994	90~103								
aly3277.6	Bombyxin A-2 homolog	GO:0005615	n/a				SM00078		PF00049		PR00276,PR00276	PS00262	G3DSA:1.10.100.10	SSF56994									
aly3277.7	Bombyxin A-1 homolog	GO:0005179,GO:0005576,GO:0005615	n/a				SM00078		PF00049		PR00276,PR00276	PS00262	G3DSA:1.10.100.10	SSF56994									
aly3277.8	Protein kinase C, brain isozyme	GO:0006468,GO:0035206,GO:0019992,GO:2000370,GO:0005622,GO:0004674,GO:0004698,GO:0008270,GO:0035556,GO:0004697,GO:0005524	CG6622-PB				SM00220,SM00109,SM00133,SM00239		PF00433,PF00069,PF00168,PF00130	PS51285,PS50081,PS50011,PS50004	PR00008,PR00008,PR00008,PR00008,PR00360,PR00360,PR00360	PS00108	G3DSA:3.30.60.20,G3DSA:1.10.510.10,G3DSA:3.30.60.20,G3DSA:2.60.40.150,G3DSA:3.30.200.20	SSF57889,SSF49562,SSF56112									
aly3277.9	Tetratricopeptide repeat protein 36	GO:0005575,GO:0003674,GO:0008150,GO:0005515	CG14105-PA				SM00028,SM00028,SM00028		PF07719,PF13414	PS50005,PS50005,PS50293,PS50005			G3DSA:1.25.40.10	SSF48452									
aly32782.1	GATA-binding factor C	GO:0043565,GO:0009887,GO:0005634,GO:0009888,GO:0006357,GO:0008270,GO:0008045,GO:0000981,GO:0006351	CG9656-PC																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly32798.1	Unknown		n/a																				
aly3282.1	Unknown		n/a						PF13358														
aly3283.1	Unknown		n/a																				
aly3283.2	Phosphate carrier protein, mitochondrial	GO:0016021,GO:0006810,GO:0006817,GO:0005740,GO:0005743,GO:0022857,GO:0015114	CG9090-PC						PF00153,PF00153	PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly3283.3	Transcription initiation factor TFIID subunit 10	GO:0003713,GO:0000082,GO:0019899,GO:0001075,GO:0001889,GO:0035264,GO:0003677,GO:0005737,GO:0000124,GO:0070063,GO:0043966,GO:0000123,GO:0010468,GO:0005634,GO:0051260,GO:0030914,GO:0033276,GO:0006367,GO:0048471,GO:0016578,GO:0000125,GO:0030331,GO:0051101,GO:0006915,GO:0043623,GO:0070365,GO:0006355,GO:0006352,GO:0005669	CG2859-PA			PIRSF017246			PF03540		PR01443,PR01443,PR01443												

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3283.4	ADP,ATP carrier protein	GO:0051124,GO:0046716,GO:0005739,GO:0001508,GO:0048489,GO:0016021,GO:0005811,GO:0005740,GO:0009612,GO:0015867,GO:0051560,GO:0048477,GO:0010507,GO:0015866,GO:0005215,GO:0006810,GO:0007629,GO:2001171,GO:0007268,GO:0006839,GO:0008340,GO:0034599,GO:0055085,GO:0040011,GO:0051480,GO:0005829,GO:0070050,GO:0005743,GO:0022857,GO:0005471	CG16944-PC						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920	PR00927,PR00927,PR00927,PR00927,PR00926,PR00926,PR00926,PR00926,PR00926,PR00926		G3DSA:1.50.40.10	SSF103506									
aly3289.1	Protein prune homolog	GO:0005737,GO:0046872,GO:0004427,GO:0019889,GO:0005634,GO:0030145,GO:0048072,GO:0016462,GO:0004309,GO:0005925,GO:0006798	CG3461-PA										G3DSA:3.90.1640.10										
aly3299.1	Angiotensin-converting enzyme	GO:0009897,GO:0016020,GO:0008144,GO:0008238,GO:0010629,GO:0060047,GO:0008217,GO:0043171,GO:0008233,GO:0050435,GO:0008237,GO:0005737,GO:1903597,GO:0032092,GO:0042447,GO:0070062,GO:0031434,GO:0010608,GO:0016021,GO:0004180,GO:0001822,GO:0003779,GO:2000170,GO:1902033,GO:0061098,GO:0006508,GO:1900086,GO:0051019,GO:0032091,GO:0008240,GO:0008241,GO:0007283,GO:0071838,GO:0005886,GO:0060177,GO:0002446,GO:0005615,GO:0005768,GO:0003084,GO:0050482,GO:0031404,GO:0005764,GO:0031711,GO:0004175,GO:0003081,GO:0008270	CG17988-PB						PF01401					SSF55486									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3299.2	Facilitated trehalose transporter Tret1	GO:0022891,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG4607-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly3299.3	Chromobox protein homolog 3	GO:0035064,GO:0000785,GO:0031618,GO:0005819,GO:0005719,GO:0005634,GO:0005635,GO:0005654,GO:0048511,GO:0005720,GO:0031940,GO:0000779,GO:0000791,GO:0045892,GO:0019904,GO:0043234,GO:0005705,GO:0010369,GO:0006357,GO:0006351,GO:0005515,GO:0003682,GO:0016568	CG6990-PA				SM00298		PF00385	PS50013	PR00504,PR00504,PR00504	PS00598	G3DSA:2.40.50.40	SSF54160									
aly3299.4	Eclosion hormone	GO:0030534,GO:0007218,GO:0005184,GO:0018990,GO:0008031,GO:0008255,GO:0007562,GO:0007563,GO:0005576	CG5400-PA			PIRSF001859			PF04736														
aly3299.5	Tektin-2	GO:0005737,GO:0005634,GO:0036159,GO:0000226,GO:0005929,GO:0005874,GO:0030317	CG3085-PA						PF03148		PR00511,PR00511,PR00511,PR00511				337~371,278~305,77~104									
aly330.1	Pogo transposable element with KRAB domain	GO:0006355,GO:0005634,GO:0007275,GO:0003676,GO:0003677	n/a						PF03184														
aly330.10	Nucleoplasmin like protein	GO:0005737,GO:0042393,GO:0006338,GO:0005634,GO:0035041,GO:0005654,GO:0003676	CG7911-PA						PF03066				G3DSA:2.60.120.340	SSF69203	109~133								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly330.11	Unknown		n/a				SM00595,SM00595,SM00595		PF13837,PF13837,PF10545	PS51029,PS51029,PS51029													
aly330.12	Antigen KI-67	GO:0005201,GO:0034605,GO:0008022,GO:0031012,GO:0014070,GO:0005737,GO:0007126,GO:0040005,GO:0005634,GO:0016020,GO:0007475,GO:0005509,GO:0005524,GO:0030212,GO:0008283,GO:0044822,GO:0008362,GO:0046331,GO:0031100,GO:0000775,GO:0007424,GO:0051539,GO:0000793,GO:0005730,GO:0005515,GO:0006259,GO:0005578	CG33196-PQ				SM00240		PF00498	PS50006			G3DSA:2.60.200.20	SSF49879										
aly330.13	Protein C12orf4 homolog	GO:0005575,GO:0008150,GO:0043304,GO:0003674,GO:0005737	CG9986-PA						PF10154														
aly330.14	Myosin regulatory light chain 2	GO:0000146,GO:0030239,GO:0060361,GO:0005859,GO:0030016,GO:0003012,GO:0016459,GO:0005509	CG2184-PA				SM00054,SM00054		PF13833,PF13405	PS50222,PS50222,PS50222		PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly330.15	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly330.16	Unknown	GO:0046872,GO:0006801,GO:0055114	CG31028-PC						PF00080,PF00080,PF00080				G3DSA:2.60.40.200,G3DSA:2.60.40.200,G3DSA:2.60.40.200,G3DSA:2.60.40.200,G3DSA:2.60.40.200	SSF49329,SSF49329,SSF49329,SSF49329				PWY-6854					
aly330.17	V-type proton ATPase subunit S1	GO:0045780,GO:0045851,GO:0070062,GO:2001206,GO:0015991,GO:0016021,GO:0046933,GO:0017137,GO:0005774,GO:0033180,GO:0070374,GO:0045921,GO:0046961,GO:0051656,GO:0045669,GO:0005524	CG31030-PB																				
aly330.18	Unknown		CG11498-PB						PF16026						173~193								
aly330.19	Unknown	GO:0005737,GO:0019010	CG10527-PA				SM00696,SM00696		PF11901														
aly330.2	Unknown	GO:0008270,GO:0003676	n/a							PS50158				SSF57756									
aly330.20	Unknown		CG15529-PA				SM00252		PF00017	PS50001			G3DSA:3.30.505.10	SSF55550									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly330.21	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0046427,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG10960-PB						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						
aly330.22	Unknown		n/a																				
aly330.3	Cytochrome P450 4d2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG3466-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385		G3DSA:1.10.630.10	SSF48264	421~421,159~186		REACT_13433						
aly330.4	Cytochrome P450 4d2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG3466-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385		G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly330.5	Probable tubulin polyglutamylase TTLL2	GO:0016874,GO:0004835,GO:0006464	CG31108-PA						PF03133	PS51221				SSF56059,SSF56059									
aly330.6	Unknown		n/a												54~74								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly330.7	Unknown		n/a																				
aly330.8	Unknown		n/a												24~68								
aly330.9	Ubiquitin thioesterase trabid	GO:0005737,GO:0005634,GO:0016055,GO:0030177,GO:0008270,GO:0016579,GO:0004843,GO:0070536	CG9448-PA				SM00547,SM00547		PF00641,PF00641,PF02338	PS50802,PS50199,PS50199		PS01358,PS01358	G3DSA:4.10.1060.10	SSF90209,SSF90209									
aly331.1	Unknown		n/a																				
aly331.10	Broad-complex core protein isoforms 1/2/3/4/5	GO:0010629,GO:0003677,GO:0008219,GO:0007458,GO:0005634,GO:0007552,GO:0048808,GO:0046872,GO:0048477,GO:0071390,GO:0035075,GO:0035072,GO:0035071,GO:0035070,GO:0006914,GO:0048747,GO:0042332,GO:0040034,GO:0001752,GO:0003700,GO:0009608,GO:0007562,GO:0035193,GO:0006355,GO:0048813,GO:0045944,GO:0000977	CG11491-PP				SM00225,SM00355,SM00355		PF00651	PS50097,PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.710.10	SSF54695									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly331.11	Unknown		n/a																				
aly331.12	Protein still life, isoform SIF type 1	GO:0005089,GO:0030676,GO:0050770,GO:0050803,GO:0005057,GO:0007268,GO:0005085,GO:0043547,GO:0051491,GO:0032314,GO:0030036,GO:0035023,GO:0005622,GO:0043087,GO:0030054,GO:0045202	CG34418-PJ				SM00228,SM00325,SM00045,SM00233,SM00233		PF02196,PF00169,PF00621	PS50003,PS50010,PS50898,PS50106		PS00741	G3DSA:2.30.29.30,G3DSA:2.30.29.30,G3DSA:3.10.20.90,G3DSA:1.20.900.10,G3DSA:2.30.42.10	SSF48065,SSF50729,SSF50729,SSF50156	1472~1472,421~441		REACT_14797,REACT_11044,REACT_11061						
aly331.13	Protein still life, isoform SIF type 1	GO:0005089,GO:0030676,GO:0050770,GO:0050803,GO:0005057,GO:0043547,GO:0005085,GO:0051491,GO:0032314,GO:0030036,GO:0007268,GO:0005622,GO:0043087,GO:0030054,GO:0045202	CG5406-PB				SM00461			PS50229			G3DSA:2.30.29.30	SSF50729									
aly331.14	Protein lin-28 homolog	GO:0005737,GO:0001708,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:2000632,GO:0048477	CG17334-PA				SM00343,SM00343		PF00098				G3DSA:4.10.60.10	SSF57756									
aly331.15	B lymphocyte-induced maturation protein 1 homolog	GO:0005737,GO:0035152,GO:1903355,GO:0000122,GO:0003700,GO:0048869,GO:0005634,GO:0043053,GO:0006351,GO:0003676,GO:0008340,GO:0046872,GO:0001078,GO:0071390,GO:0040035,GO:0045684	CG5249-PB				SM00355,SM00355,SM00035,SM00355,SM00355		PF13912,PF13912,PF00856	PS50157,PS50157,PS50157,PS50280,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:2.170.270.10	SSF57667,SSF57667,SSF82199,SSF57667										
aly331.16	Zinc finger and SCAN domain-containing protein 22	GO:0003700,GO:0005634,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG15269-PA				SM00355,SM00355,SM00035,SM00355,SM00355,SM00355,SM00355,SM00225		PF00651,PF00096,PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50097		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.710.10,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF54695,SSF57667,SSF57667										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly331.17	tRNA-dihydrouridine (20a/20b) synthase [NAD(P)+]-like	GO:0017150,GO:0050660,GO:0008033,GO:0055114	CG10495-PA						PF01207			PS01136	G3DSA:3.20.20.70	SSF51395									
aly331.18	Programmed cell death protein 2	GO:0005737,GO:0070062,GO:0008283,GO:1901532,GO:0005634,GO:0006919,GO:0035162,GO:0048103,GO:0012501,GO:1902035,GO:0003677,GO:0046872,GO:0048477	CG3260-PA						PF01753,PF04194	PS50865		PS01360		SSF144232									
aly331.19	Transmembrane protein 242	GO:0016021	CG11699-PA						PF07096														
aly331.2	Unknown		n/a																				
aly331.20	Sentrin-specific protease 7	GO:0060548,GO:0005634,GO:0016929,GO:0060997,GO:0007411,GO:0016926,GO:0006508,GO:0005622,GO:0008234,GO:0021952	CG10107-PA						PF02902	PS50600			G3DSA:3.30.310.130,G3DSA:3.30.310.130	SSF54001,SSF54001									
aly331.21	Unknown		n/a							PS51257													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly331.22	Unknown		n/a																				
aly331.23	Coiled-coil domain-containing protein 6	GO:0005737,GO:0005856	CG6664-PA						PF09755						148~168,51~146,188~215,4~38								
aly331.24	T-related protein	GO:0007443,GO:0007442,GO:0001700,GO:0007494,GO:0007280,GO:0003700,GO:0005634,GO:0001709,GO:0007509,GO:0006355,GO:0045944,GO:0006351,GO:0003677,GO:0000981,GO:0042803	CG7260-PB				SM00425		PF00907	PS50252	PR00937,PR00937,PR00937,PR00937,PR00937,PR00937,PR00938,PR00938,PR00938,PR00938,PR00938,PR00938	PS01264,PS01283	G3DSA:2.60.40.820	SSF49417									
aly331.25	Unknown		n/a																				
aly331.26	Origin recognition complex subunit 3	GO:0030536,GO:0051298,GO:0051297,GO:0006270,GO:0007612,GO:0007611,GO:0072686,GO:0006260,GO:0005664,GO:0003677,GO:0007298,GO:0008355	CG4088-PA						PF07034														
aly331.27	Larval cuticle protein LCP-17	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG8505-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly331.28	Larval cuticle protein LCP-17	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG30045-PB						PF00379	PS51155													
aly331.29	Larval cuticle protein LCP-30	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG30042-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly331.3	Carboxypeptidase N subunit 2	GO:0070062,GO:0072562	CG7509-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00365,SM00365,SM00365,SM00365,SM00365		PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS50176,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly331.30	Unknown		CG13024-PC																				
aly331.31	Protein still life, isoforms C/SIF type 2	GO:0030676,GO:0043547,GO:0050803,GO:0005057,GO:0051491,GO:0005622,GO:0030036,GO:0045202,GO:0043087,GO:0030054,GO:0050770	n/a																				
aly331.32	tRNA-dihydrouridine (20a/20b) synthase [NAD(P)+]-like	GO:0017150,GO:0050660,GO:0008033,GO:0055114	CG10495-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly331.33	Endocuticle structural glycoprotein SgAbd-2	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG13222-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly331.4	Tachykinin-like peptides receptor 99D	GO:0050911,GO:0007218,GO:0042048,GO:0016021,GO:0002520,GO:0042071,GO:0007204,GO:0050805,GO:0016323,GO:0004983,GO:0007217,GO:0005887,GO:0008188,GO:0004995,GO:0005886,GO:0007186	CG10626-PA						PF00001	PS50262	PR01012,PR01012,PR01012,PR01012,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797							
aly331.5	Glutamine synthetase	GO:0005737,GO:0004356,GO:0005739,GO:0006542,GO:0003824,GO:0045213,GO:0005524,GO:0004351,GO:0006538,GO:0007416	CG1743-PD						PF00120				G3DSA:3.30.590.10	SSF55931		00330+6.3.1.2,00630+6.3.1.2,00250+6.3.1.2,00910+6.3.1.2	REACT_13	PWY-6964,PWY-6963,PWY-5675,PWY-381,PWY-6549					
aly331.6	Chymotrypsinogen 2	GO:0007586,GO:0004252,GO:0005615,GO:0006508	CG10663-PB				SM00020		PF00089	PS50092,PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly331.7	Unknown	GO:0005515	CG10660-PA						PF00168	PS50004			G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly331.8	Protein odr-4 homolog	GO:0005575,GO:0003674,GO:0016021,GO:0008150,GO:0012505	CG10616-PB						PF14778														
aly331.9	Nuclear migration protein nudC	GO:0005737,GO:0007264,GO:0000278,GO:0008283,GO:0005874,GO:0005829,GO:0007275,GO:0005654,GO:0007067,GO:0007097,GO:0048477,GO:0005875,GO:0051301	CG9710-PA						PF14050,PF04969	PS51203			G3DSA:2.60.40.790	SSF49764	61~95								
aly3312.1	Unknown		n/a																				
aly3312.2	Proton-coupled amino acid transporter 4	GO:0016021,GO:0006865,GO:0015293	CG43693-PG						PF01490														
aly3312.3	Proton-coupled amino acid transporter 1	GO:0005280,GO:0015992,GO:0005783,GO:0055085,GO:0035524,GO:1902600,GO:0016021,GO:0006865,GO:0015816,GO:0015193,GO:0005765,GO:0015078,GO:0005886,GO:0006811,GO:0015187,GO:0015808,GO:0015180	CG43693-PG						PF01490														
aly3312.4	Proton-coupled amino acid transporter 4	GO:0016021,GO:0006865,GO:0015293	CG43693-PG						PF01490														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3312.5	Zinc finger matrin-type protein 5	GO:0030532,GO:0000398,GO:0005654,GO:0003674,GO:0008270,GO:0005689,GO:0008380,GO:0006397	CG31922-PA				SM00451		PF06220	PS50103			G3DSA:4.10.1000.10	SSF57667									
aly3312.6	Unknown		n/a																				
aly3312.7	UV radiation resistance-associated gene protein	GO:0046718,GO:0005783,GO:0032801,GO:0003674,GO:0048260,GO:0071900,GO:0005737,GO:0005764,GO:0005813,GO:0000149,GO:0005770,GO:0045746,GO:0048803,GO:0010508,GO:0032465,GO:0006914,GO:0008285,GO:0006281,GO:0051297,GO:0060627,GO:0045335,GO:0000775,GO:0043234,GO:0006890,GO:0030496,GO:0005575,GO:0035493,GO:0097680,GO:0005769,GO:0051684	CG6116-PA												485~512,244~264,885~905								
aly3312.8	Unknown		n/a																				
aly33174.1	Nef-associated protein 1	GO:0016787	CG12822-PA						PF01980	PS51668			G3DSA:2.40.30.70	SSF118196									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3319.1	Neuropilin and tolloid-like protein 2	GO:0040011,GO:0031594,GO:0035187,GO:0032983,GO:0008328,GO:0097482,GO:0051726,GO:0060361,GO:0097106,GO:0035255,GO:0007528,GO:0046331,GO:0003674,GO:0045202,GO:0014069,GO:0043113,GO:0007274,GO:2000312	CG44328-PB				SM00042,SM00042		PF00431,PF00431	PS01180,PS01180			G3DSA:2.60.120.290,G3DSA:2.60.120.290	SSF49854,SSF49854	76~96								
aly3319.2	Unknown		n/a																				
aly33249.1	Unknown		n/a										G3DSA:1.10.287.80		41~75								
aly33331.1	Unknown		n/a																				
aly334.1	Unknown		n/a																				
aly3342.1	Cytochrome b5-related protein	GO:0006633,GO:0006629,GO:0020037,GO:0016717,GO:0005811,GO:0005739,GO:0016491,GO:0005506,GO:0046872,GO:0016021,GO:0055114,GO:0009055	CG13279-PA						PF00487,PF00173	PS50255		PS00191	G3DSA:3.10.120.10	SSF55856									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3342.2	Cytochrome b5-related protein	GO:0006633,GO:0006629,GO:0020037,GO:0016717,GO:0005811,GO:0005739,GO:0046331,GO:0005506,GO:0046872,GO:0016021,GO:0055114,GO:0016491	CG17928-PA						PF00173,PF00487	PS50255		PS00191	G3DSA:3.10.120.10	SSF55856									
aly3345.1	U6 snRNA-associated Sm-like protein LSm4	GO:0000288,GO:0030532,GO:0005829,GO:0044822,GO:0098779,GO:0010467,GO:0002230,GO:0005688,GO:0006397,GO:0043928,GO:0008380,GO:0005681,GO:0017070	CG17768-PA				SM00651		PF01423				G3DSA:2.30.30.100	SSF50182									
aly3346.1	Chorion class A protein Ld5	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														
aly3346.2	Chorion class A protein Ld19	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														
aly3346.3	Unknown	GO:0000902,GO:0045475	CG13432-PA				SM00241		PF00100	PS51034													
aly33495.1	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	GO:0016020,GO:0070062,GO:0006635,GO:0005811,GO:0005777,GO:0005739,GO:0008416,GO:0008152,GO:0046872,GO:0016853	CG9577-PA						PF00378				G3DSA:3.90.226.10	SSF52096									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly33528.1	Unknown		n/a												13~33								
aly33537.1	Unknown		n/a																				
aly33542.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly33571.1	Lethal(2) giant larvae protein	GO:0016333,GO:0008021,GO:0008105,GO:0008104,GO:0016336,GO:0016335,GO:0016334,GO:0060429,GO:0030154,GO:0045197,GO:0045196,GO:0017022,GO:0016332,GO:0007293,GO:0006469,GO:0007391,GO:0045159,GO:0045200,GO:0005920,GO:0035072,GO:0005856,GO:0002009,GO:0001738,GO:0005614,GO:0016082,GO:0019991,GO:0090163,GO:0045746,GO:0098725,GO:0055059,GO:0042127,GO:0008285,GO:0007559,GO:0000149,GO:0035212,GO:0035070,GO:0016325,GO:0016327,GO:0045175,GO:0004860,GO:0007314,GO:0005938,GO:0007269,GO:0005886,GO:0051668,GO:0007406,GO:0016323,GO:0035293,GO:0007179,GO:0005918,GO:0045184,GO:0008283,GO:0000132,GO:0007399,GO:0007423,GO:0051726,GO:0030863,GO:0030036,GO:0005829,GO:0045167,GO:0005737,GO:0008360,GO:0005515,GO:0048730,GO:0005578	CG2671-PC										SSF50978										
aly33596.1	Etoposide-induced protein 2.4 homolog	GO:0005737,GO:0005794,GO:0016020,GO:0005783,GO:0030308,GO:0006914,GO:0006915,GO:0031965,GO:0005789,GO:1901418,GO:0016021	CG15626-PB						PF07264														
aly336.1	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0030672,GO:0016021,GO:0016020,GO:0043195,GO:0022857,GO:0046331,GO:0001669,GO:0001504,GO:0055085,GO:0030054	CG3690-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly336.2	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0016020,GO:0030672,GO:0006629,GO:0005215,GO:0016021,GO:0006810,GO:0043195,GO:0022857,GO:0001669,GO:0001504,GO:0016298,GO:0055085,GO:0030054	CG31272-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly336.3	Unknown		n/a																				
aly33617.1	Unknown		n/a							PS51139													
aly3367.1	Unknown		n/a						PF00001	PS50262	PR00237,PR00237,PR00237		G3DSA:1.20.1070.10,G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly3367.10	Peroxisomal targeting signal 2 receptor	GO:0007031,GO:0006909,GO:0006635,GO:0001958,GO:0006625,GO:0005829,GO:0016558,GO:0005777,GO:0005053,GO:0019899,GO:0001764,GO:0005515,GO:0005782,GO:0008611,GO:0042803	CG6486-PA				SM00320,SM00320,SM00320			PS50294,PS50082,PS50082		PS00678,PS00678	G3DSA:2.130.10.10	SSF50978									
aly3367.11	Arrestin homolog	GO:0005737,GO:0016029,GO:0016028,GO:0016062,GO:0016059,GO:0007605,GO:0016060,GO:0007602,GO:0007165,GO:0005515,GO:0002046,GO:0045494	CG5962-PA				SM01017		PF02752,PF00339		PR00309,PR00309,PR00309,PR00309,PR00309		G3DSA:2.60.40.840,G3DSA:2.60.40.640	SSF81296,SSF81296									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3367.12	Unknown		CG13305-PB												210~230								
aly3367.13	Larval cuticle protein A3A	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG32029-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly3367.14	Unknown		n/a											SSF57501									
aly3367.15	Metal regulatory transcription factor 1	GO:0001047,GO:0055076,GO:0001077,GO:0003677,GO:0005737,GO:0005634,GO:0005654,GO:0046688,GO:0006366,GO:0046686,GO:0000976,GO:0046872,GO:0006875,GO:0035035,GO:0006950,GO:0045893,GO:0010038,GO:0055069,GO:0006979,GO:0003700,GO:0045944,GO:0006351,GO:0000978,GO:0000979	CG3743-PC				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly3367.16	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3367.17	PiggyBac transposable element-derived protein 3		n/a						PF13843														
aly3367.18	KRAB-A domain-containing protein 2	GO:0015074,GO:0006355,GO:0003676,GO:0005622	n/a							PS50994			G3DSA:3.30.420.10	SSF53098									
aly3367.2	Unknown		n/a						PF01826,PF01826				G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57567									
aly3367.3	Aspartate--tRNA ligase, mitochondrial	GO:0005737,GO:0004812,GO:0006422,GO:0050560,GO:0000166,GO:0005654,GO:0003676,GO:0006418,GO:0005759,GO:0004815,GO:0005524	CG31739-PA	MF_00044					PF00152	PS50862	PR01042,PR01042,PR01042,PR01042		G3DSA:2.40.50.140,G3DSA:3.30.930.10,G3DSA:3.30.930.10	SSF50249,SSF55681,SSF55681			REACT_71						
aly3367.4	APOBEC1 complementation factor	GO:0005737,GO:0030895,GO:0035770,GO:0005783,GO:0046011,GO:0006397,GO:0071011,GO:0000398,GO:0000166,GO:0050821,GO:0003727,GO:0003676,GO:0007310,GO:0022008,GO:0003729,GO:0046843	CG17838-PJ				SM00360,SM00360,SM00360	TIGR01648	PF00076,PF00076,PF00076	PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3367.5	Vesicular glutamate transporter 1	GO:0042137,GO:0007616,GO:0035435,GO:0060076,GO:0043229,GO:0045202,GO:0008068,GO:0035249,GO:0030054,GO:0051938,GO:0044300,GO:0044341,GO:0015319,GO:0016021,GO:0048786,GO:0035725,GO:0005315,GO:0006817,GO:0005316,GO:0034592,GO:0006836,GO:0060079,GO:0055085,GO:0030672,GO:0007420,GO:0015321,GO:0003407,GO:0097401	CG4288-PB						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly3367.6	Cardioacceleratory peptide receptor	GO:0007218,GO:0018990,GO:0016021,GO:0005000,GO:0005887,GO:0008188,GO:0007186	CG33344-PC						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00896,PR00896,PR00896,PR00896	PS00237	G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly3367.7	Cardioacceleratory peptide receptor	GO:0004930,GO:0018990,GO:0016021,GO:0007218,GO:0005000,GO:0005887,GO:0008188,GO:0007186	CG33344-PC						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly3367.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3367.9	Unknown		n/a												119~154								
aly3370.1	Methionine--tRNA ligase, cytoplasmic	GO:0005737,GO:0004825,GO:0000049,GO:0006431,GO:0070062,GO:0005730,GO:0005829,GO:0016020,GO:0009303,GO:0005739,GO:0022008,GO:0005875,GO:0005524	CG15100-PA				SM00991,SM00991		PF00458,PF00458,PF09334	PS51185,PS51185			G3DSA:1.10.730.10,G3DSA:3.40.50.620,G3DSA:1.10.287.10,G3DSA:1.10.287.10	SSF47060,SSF52374,SSF47323,SSF47060	254~274		REACT_71						
aly3370.2	Zinc finger protein 320	GO:0031935,GO:0003700,GO:0005634,GO:0006355,GO:0048813,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG11352-PF				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	424~444,346~366								
aly3370.3	Zinc finger protein 436	GO:0005737,GO:0003700,GO:0005634,GO:0005654,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG6654-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776,PF00096,PF00096,PF12874,PF13912,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57716									
aly3370.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3370.5	Unknown		CG32813-PH						PF13873														
aly340.1	Unknown	GO:0003674,GO:0005576,GO:0008150,GO:0005515	CG13532-PA							PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly3404.1	ATP-citrate synthase	GO:0046912,GO:0005737,GO:0016020,GO:0044262,GO:0070062,GO:0006085,GO:0048037,GO:0005811,GO:0005739,GO:0005622,GO:0005654,GO:0003878,GO:0006101,GO:0005886,GO:0004775,GO:0046872,GO:0005524,GO:0008610	CG8322-PD						PF00285,PF00549,PF16114		PR01798,PR01798,PR01798,PR01798	PS01216,PS01217	G3DSA:3.30.470.20,G3DSA:3.40.50.720,G3DSA:3.40.50.261,G3DSA:1.10.580.10,G3DSA:3.40.50.261,G3DSA:1.10.230.10	SSF48256,SSF48256,SSF51735,SSF56059,SSF52210		00640+6.2.1.5,00660+6.2.1.5,00020+6.2.1.5,00720+6.2.1.5		PWY-5913,PWY-7384,PWY-5392,PWY-6969,PWY-5537,PWY-6728,PWY-5538,PWY-5690	UPA00223				
aly34048.1	Unknown		n/a						PF10168						109~129,3~23								
aly34048.2	Sarcoplasmic calcium-binding protein	GO:0050829,GO:0016529,GO:0005509	CG1435-PC				SM00054,SM00054,SM00054		PF13499	PS50222,PS50222,PS50222		PS00018,PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly34048.3	Vacuolar protein sorting associated protein 29	GO:0006886,GO:0030904,GO:0008270,GO:0042147,GO:0005768,GO:0010008	CG4764-PA					TIGR00040	PF12850				G3DSA:3.60.21.10	SSF56300									
aly34093.1	Unknown		n/a																				
aly3411.1	Ankyrin-3	GO:0050808,GO:0034112,GO:0032418,GO:0030425,GO:0014704,GO:1900827,GO:0018105,GO:0007165,GO:0043266,GO:0044325,GO:0010960,GO:0030018,GO:0030507,GO:0072659,GO:1900242,GO:0014731,GO:0004674,GO:0016529,GO:0043005,GO:0004672,GO:0045838,GO:0071709,GO:0031902,GO:0005524,GO:0005525,GO:0042383,GO:1902260,GO:0030315,GO:0009986,GO:0017137,GO:0090314,GO:0007528,GO:0045211,GO:0005886,GO:0007264,GO:0010650,GO:0031594,GO:0030674,GO:0043194,GO:0071286,GO:0008092,GO:0045296,GO:0005764,GO:0005765,GO:0010628,GO:0005515,GO:2001259,GO:0033268,GO:0010765,GO:2000651,GO:0043034	CG5483-PD				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796	PS50088,PS50088,PS50088,PS50297			G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:3.80.10.10	SSF48403,SSF48403									
aly3415.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3415.2	Unknown	GO:0004252,GO:0005576,GO:0006508	CG8586-PA				SM00020		PF00089	PS50240			G3DSA:2.40.10.10	SSF50494									
aly34316.1	Unknown	GO:0015020,GO:0008152	CG6475-PD											SSF53756									
aly34316.2	Unknown	GO:0015020,GO:0008152	CG6633-PB											SSF53756									
aly34316.3	Unknown		n/a																				
aly34359.1	Alpha-mannosidase 2	GO:0005795,GO:0004572,GO:0005975,GO:0005783,GO:0006486,GO:0006487,GO:0006491,GO:0016021,GO:0030246,GO:0000139,GO:0006013,GO:0003824,GO:0008270,GO:0016063,GO:0015923,GO:0035010,GO:0006517	CG18802-PB										G3DSA:2.60.40.1180	SSF74650									
aly344.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly344.2	Unknown	GO:0046872	n/a							PS50157		PS00028											
aly344.3	Protein neuralized	GO:0008104,GO:0007616,GO:0051260,GO:0008593,GO:0008270,GO:0003677,GO:0002121,GO:0008356,GO:0000209,GO:0005737,GO:0045747,GO:0061630,GO:0005634,GO:0007476,GO:0030707,GO:0007498,GO:0001964,GO:0016360,GO:0048471,GO:0048749,GO:0031987,GO:0042048,GO:0046331,GO:0005886,GO:0045314,GO:0004842,GO:0030718,GO:0007423,GO:0007399,GO:0007422,GO:0048854,GO:0005829,GO:0007398,GO:1901981,GO:0046532,GO:0005515,GO:0005768	CG11988-PA				SM00184,SM00588,SM00588		PF07177,PF07177,PF13920	PS51065,PS51065,PS50089			G3DSA:3.30.40.10	SSF57850										
aly344.4	1,5-anhydro-D-fructose reductase	GO:0016319,GO:0004032,GO:0050571,GO:0055114,GO:0016491	CG6083-PA						PF00248		PR00069,PR00069,PR00069,PR00069,PR00069		G3DSA:3.20.20.100	SSF51430	48~68								
aly344.5	Unknown		n/a																				
aly34442.1	Caytaxin	GO:0005737,GO:0048311,GO:2000212,GO:0006810,GO:0030425,GO:0031966,GO:0045202,GO:0043005,GO:0031175,GO:0030424,GO:0035418,GO:0030054,GO:0032880	CG11593-PB						PF13716	PS50191			G3DSA:3.40.525.10	SSF52087									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3446.1	V-type proton ATPase 116 kDa subunit a isoform 1	GO:0005737,GO:0005794,GO:0070072,GO:0015986,GO:0070062,GO:0015991,GO:0042470,GO:0051117,GO:0016021,GO:0005654,GO:0030659,GO:1901998,GO:0033181,GO:0033179,GO:0000220,GO:0007035,GO:0046961,GO:0005886,GO:0016471,GO:0015078,GO:0043231	CG18617-PB			PIRSF001293			PF01496						191~211,231~65								
aly3446.10	Unknown		n/a												122~156,206~233								
aly3446.11	Set1/Ash2 histone methyltransferase complex subunit ASH2	GO:0044212,GO:0006351,GO:0048096,GO:0005634,GO:0007476,GO:0005700,GO:0007474,GO:0048813,GO:0048188,GO:0008270,GO:0051568,GO:0044666,GO:0044665	CG6677-PC				SM00449,SM00249		PF00622	PS50188		PS01359	G3DSA:3.30.40.10	SSF49899,SSF49899,SSF57903									
aly3446.12	BolA-like protein DDB_G0274169	GO:0005575,GO:0048812,GO:0003674	CG31126-PA			PIRSF003113			PF01722				G3DSA:3.30.300.90	SSF82657									
aly3446.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3446.14	Bile salt-activated lipase	GO:0005737,GO:0005794,GO:0004771,GO:0005791,GO:0005615,GO:0043208,GO:0005829,GO:0045121,GO:0052689,GO:0016042,GO:0005575,GO:0032403,GO:0008150,GO:0008152,GO:0042588,GO:0004622,GO:0043234,GO:0042572,GO:0004806,GO:0050253,GO:0043231	CG10175-PD						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474	319~339								
aly3446.15	Unknown		n/a																				
aly3446.16	Unknown		n/a																				
aly3446.2	Katanin p60 ATPase-containing subunit A1	GO:0050775,GO:0005737,GO:0007017,GO:0005783,GO:0051013,GO:0005813,GO:0008017,GO:0030496,GO:0008568,GO:0016322,GO:0031122,GO:0008152,GO:0005819,GO:0051301,GO:0016887,GO:0008352,GO:0007067,GO:0000922,GO:0005874,GO:0005875,GO:0005524	CG1193-PE	MF_03023			SM00382		PF09336,PF00004			PS00674	G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540									
aly3446.3	Sphingosine-1-phosphate lyase	GO:0030149,GO:0030176,GO:0008117,GO:0016021,GO:0016831,GO:0019752,GO:0005789,GO:0046331,GO:0030170,GO:0007275,GO:0007527	CG8946-PB						PF00282				G3DSA:3.40.640.10	SSF53383									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3446.4	Ras suppressor protein 1	GO:0043547,GO:0005829,GO:0005515,GO:0010811,GO:0005083,GO:0007165,GO:0007475,GO:0034329,GO:0043508,GO:0046329,GO:2000179,GO:0007265,GO:0005925,GO:0007229,GO:0070062	CG9031-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058										
aly3446.5	Nuclear envelope integral membrane protein 1b	GO:0016021	CG9723-PA						PF10225						186~186								
aly3446.6	Myosin heavy chain 95F	GO:0016333,GO:0055059,GO:0008104,GO:0070856,GO:0070865,GO:0030589,GO:0045217,GO:0055057,GO:0032027,GO:0030036,GO:0030139,GO:0061024,GO:0007291,GO:0007297,GO:0031476,GO:0007298,GO:0070864,GO:0005875,GO:0032880,GO:0005737,GO:0040001,GO:0000146,GO:0042623,GO:0008017,GO:0007552,GO:0045921,GO:0045178,GO:0003779,GO:0016459,GO:0048477,GO:0003774,GO:0005524,GO:0045175,GO:0031941,GO:0045167,GO:0047497,GO:0019749,GO:0032970,GO:0051015,GO:0008363,GO:0007051,GO:0007283,GO:0005938,GO:0008152,GO:0032956,GO:0051647,GO:0043234,GO:0007015,GO:0030048,GO:0006997,GO:0045172,GO:0007560,GO:0007391,GO:0016461,GO:0005516,GO:0005515,GO:0007286,GO:0030317	CG5695-PH				SM00242		PF16521,PF00063,PF02736	PS50096,PS51456	PR00193,PR00193,PR00193,PR00193,PR00193			SSF52540,SSF52540	901~984,847~881									
aly3446.7	Myophilin	GO:0035626,GO:0006939,GO:0003779,GO:0005515,GO:0005865,GO:0070594	CG14996-PB				SM00033		PF00307,PF00402	PS50021	PR00888,PR00888,PR00888,PR00888,PR00888,PR00888,PR00888		G3DSA:1.10.418.10	SSF47576									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3446.8	Putative protein disulfide-isomerase C1F5.02	GO:0006457,GO:0005783,GO:0005788,GO:0003756,GO:0005886,GO:0045454,GO:0015035,GO:0055114,GO:0034976	CG9432-PF						PF00085,PF00085	PS51352,PS51352,PS51352,PS51352			G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10	SSF52833,SSF52833,SSF52833,SSF52833,SSF52833,SSF52833,SSF52833,SSF52833,SSF52833,SSF52833,SSF52833	296~316									
aly3446.9	2-acylglycerol O-acyltransferase 1	GO:0006651,GO:0007498,GO:0016021,GO:0005789,GO:0019432,GO:0006071,GO:0016747,GO:0004144,GO:0003846	CG1942-PA						PF03982														
aly34468.1	Unknown		n/a																				
aly34499.1	Unknown		n/a																				
aly345.1	ATP-binding cassette sub-family G member 1	GO:0009897,GO:0034375,GO:0034374,GO:0055037,GO:0017127,GO:0030301,GO:0034041,GO:0055099,GO:0042987,GO:1901998,GO:0055091,GO:0005548,GO:0042626,GO:0033993,GO:0016021,GO:0005739,GO:0005654,GO:0034436,GO:0034437,GO:0010745,GO:0010875,GO:0005524,GO:0033700,GO:0005794,GO:0005215,G	CG4822-PA				SM00382		PF01061,PF00005	PS50893		PS00211	G3DSA:3.40.50.300	SSF52540	266~286								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly345.10	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0002121,GO:0008152	CG17323-PA						PF00201,PF00201					SSF53756									
aly345.11	Spermidine synthase	GO:0005575,GO:0004766,GO:0008295,GO:0042803	CG8327-PC	MF_00198				TIGR00417	PF01564	PS51006		PS01330	G3DSA:2.30.140.10,G3DSA:3.40.50.150	SSF53335		00480+2.5.1.16,00410+2.5.1.16,00330+2.5.1.16,00270+2.5.1.16			UPA00248				
aly345.12	Ubiquitin-like-conjugating enzyme ATG10	GO:0005737,GO:0006497,GO:0006914,GO:0031401,GO:0019777,GO:0034263,GO:0005622,GO:0032446,GO:0015031,GO:0016874	CG12821-PB						PF03987														
aly345.13	Probable phospholipid-transporting ATPase IF	GO:0016020,GO:0005783,GO:0015917,GO:0055037,GO:0004012,GO:0055038,GO:0005637,GO:0016021,GO:0000287,GO:0015914,GO:0005524,GO:0005794,GO:0006812,GO:0006811,GO:0034220,GO:0045332,GO:0005886,GO:0055085,GO:0019829,GO:0015075,GO:0015662,GO:0005769	CG9981-PA					TIGR01652	PF16209,PF16212,PF13246,PF00122			PS00154	G3DSA:2.70.150.10,G3DSA:2.70.150.10,G3DSA:3.40.50.1000,G3DSA:3.40.50.1000,G3DSA:3.40.1110.10,G3DSA:3.40.1110.10	SSF81665,SSF81665,SSF81665,SSF81660,SSF81660,SSF56784,SSF56784,SSF81653,SSF81653										
aly345.14	Unknown		CG13392-PA						PF07114														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly345.15	Uncharacterized protein CG5902	GO:0005575,GO:0008150,GO:0003674	CG5902-PB					TIGR00296	PF01871	PS51112			G3DSA:3.30.700.20,G3DSA:3.30.1490.150	SSF143447									
aly345.16	Remodeling and spacing factor 1	GO:0016584,GO:0034080,GO:0042393,GO:0006338,GO:0045893,GO:0005634,GO:0005705,GO:0005700,GO:0031213,GO:0045892,GO:0008270,GO:0006352,GO:0070868,GO:0050434,GO:0005654,GO:0006334,GO:0043392	CG8677-PB				SM00249		PF00628	PS50827,PS50016		PS01359	G3DSA:3.30.40.10	SSF57903	1133~1153,1378~1398,36~56,1023~1043,263~283									
aly345.17	Retinoblastoma-binding protein 5 homolog	GO:0006355,GO:0048188,GO:0006351,GO:0051568,GO:0044666,GO:0044665	CG5585-PA				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400	PS50294,PS50082		PS00678	G3DSA:2.130.10.10	SSF117289									
aly345.18	Poly(ADP-ribose) glycohydrolase	GO:0004649,GO:0005975,GO:0035065,GO:0006342,GO:0005634,GO:0043484,GO:0030576,GO:0005654,GO:0009408,GO:0051457,GO:0036099,GO:0006909	CG2864-PB						PF05028														
aly345.19	Poly(ADP-ribose) glycohydrolase	GO:0004649,GO:0005975,GO:0035065,GO:0006342,GO:0005634,GO:0043484,GO:0030576,GO:0005654,GO:0009408,GO:0051457,GO:0036099,GO:0006909	CG2864-PB						PF05028						230~230,249~250								
aly345.2	Polypeptide N-acetylgalactosaminyltransferase 2	GO:0005795,GO:0046872,GO:0006486,GO:0016021,GO:0004653,GO:0030246,GO:0000139,GO:0009312	CG3254-PA				SM00458		PF02709,PF00652,PF00535	PS50231			G3DSA:3.90.550.10,G3DSA:2.80.10.50	SSF50370,SSF53448					UPA00378				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly345.20	CUGBP Elav-like family member 4	GO:0043234,GO:0005737,GO:0006397,GO:0005634,GO:0000166,GO:0003723,GO:0017148,GO:0048026,GO:0003729,GO:0008380,GO:0042803	CG43744-PA						PF00076,PF00076	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									
aly345.21	PiggyBac transposable element-derived protein 1	GO:0003700,GO:0005044,GO:0016020	n/a						PF13843														
aly345.22	Unknown		n/a																				
aly345.23	Parkin coregulated gene protein homolog	GO:0097225,GO:0043005,GO:0030544,GO:0031072,GO:0005829,GO:0051087,GO:0044297,GO:0005739,GO:0003779,GO:0048487,GO:0031625,GO:0034620,GO:0060548,GO:0005929,GO:0043014,GO:0001664,GO:0007286,GO:0051879,GO:0005634,GO:0031982	CG15120-PA						PF10274				G3DSA:1.25.10.10	SSF48371									
aly345.24	Unknown		n/a												12~67								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly345.3	Unknown		n/a																				
aly345.4	Kinesin-like protein CG14535	GO:0005737,GO:0008017,GO:0007018,GO:0005575,GO:0048812,GO:0003674,GO:0005524,GO:0008152,GO:0005871,GO:0005874,GO:0003777	CG14535-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380		G3DSA:3.40.850.10	SSF52540									
aly345.5	Transmembrane protein 50A	GO:0004563,GO:0016021,GO:0005783	CG15012-PC						PF05255														
aly345.6	Nidogen-1	GO:0005605,GO:0005604,GO:0070062,GO:0032836,GO:0010811,GO:0043236,GO:0031012,GO:0007160,GO:0071944,GO:0005509,GO:0043394,GO:0071711,GO:0005576,GO:0005518,GO:0022617,GO:0030198	CG12908-PA				SM00179,SM00179,SM00179,SM00135,SM00135,SM00135,SM00135,SM00135,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00539,SM00682		PF12947,PF00058,PF00058,PF07474,PF07645,PF06119	PS50026,PS50026,PS50026,PS50026,PS50993,PS51220,PS51120,PS51120,PS50026,PS50026,PS50026,PS51120,PS51120,PS50026,PS50026,PS50026,PS51120		PS01186,PS01186,PS01186,PS01186,PS01187,PS01186,PS00010,PS01186,PS01186,PS01186,PS01186,PS01186	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.40.155.10,G3DSA:2.40.155.10,G3DSA:2.40.155.10,G3DSA:2.40.155.10,G3DSA:2.40.155.10,G3DSA:2.120.10.30	SSF54511,SSF63825,SSF57184,SSF57184,SSF57184,SSF57184									
aly345.7	Chorion class CB protein PC404 (Fragment)	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly345.8	Chitooligosaccharidolytic beta-N-acetylglucosaminidase	GO:0005975,GO:0016231,GO:0000272,GO:0004563,GO:0005886,GO:0006032	CG1318-PA			PIRSF001093			PF14845,PF00728		PR00738,PR00738,PR00738,PR00738,PR00738,PR00738,PR00738		G3DSA:3.30.379.10,G3DSA:3.20.20.80	SSF51445,SSF55545		00604+3.2.1.52,00520+3.2.1.52,00511+3.2.1.52,00603+3.2.1.52,00513+3.2.1.52,00531+3.2.1.52		PWY-6902					
aly345.9	General transcription factor IIE subunit 2	GO:0006355,GO:0005634,GO:0005673,GO:0045944,GO:0006367,GO:0003677,GO:0022008	CG1276-PA				SM00225		PF04500,PF00651,PF02186	PS50097,PS51351			G3DSA:1.10.10.10,G3DSA:3.30.710.10	SSF54695,SSF46785	162~182								
aly34516.1	Unknown		n/a																				
aly34555.1	Unknown		n/a																				
aly34680.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly34683.1	Calcium-dependent protein kinase C	GO:0005737,GO:0006468,GO:0035206,GO:0019992,GO:0004674,GO:0004698,GO:0008270,GO:0035556,GO:0004697,GO:0005524	CG6622-PB						PF00069	PS50011			G3DSA:3.30.200.20	SSF56112									
aly347.1	Unknown		n/a																				
aly347.10	Translation initiation factor IF-2, mitochondrial	GO:0070124,GO:0032790,GO:0044822,GO:0008135,GO:0003924,GO:0005739,GO:0043024,GO:0005654,GO:0003743,GO:0006413,GO:0006412,GO:0005525	CG12413-PA					TIGR00231	PF00009,PF11987	PS51722			G3DSA:3.40.50.300,G3DSA:2.40.30.10,G3DSA:3.40.50.10050	SSF50447,SSF52156,SSF50447,SSF52540									
aly347.11	WD repeat-containing protein 20	GO:0005515	CG6420-PA				SM00320,SM00320,SM00320,SM00320,SM00320			PS50294,PS50082			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978									
aly347.12	HIV Tat-specific factor 1	GO:0030182,GO:0019079,GO:0005634,GO:0032784,GO:0000166,GO:0005654,GO:0006357,GO:0006351,GO:0003676,GO:0022008,GO:0044822,GO:0003729	CG6049-PC				SM00360,SM00360		PF13893,PF00076	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928	195~215								
aly347.13	Uridine diphosphate glucose pyrophosphatase	GO:0005737,GO:0016787,GO:0016818,GO:0070062,GO:0008768,GO:0046872,GO:0047631	CG42813-PA					TIGR00052	PF00293	PS51462			G3DSA:3.90.79.10	SSF55811									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly347.14	DNA damage-binding protein 1	GO:0035518,GO:1902188,GO:0007307,GO:0035220,GO:0070914,GO:0042769,GO:1901990,GO:0003677,GO:0005737,GO:0070062,GO:0080008,GO:0043161,GO:0005634,GO:0045070,GO:0005654,GO:0043066,GO:0042787,GO:0016032,GO:0006281,GO:0006289,GO:0006974,GO:0046726,GO:0051702,GO:0031464,GO:0031465,GO:0005615,GO:0050832,GO:0000718,GO:0016055,GO:0019985,GO:0005515,GO:0007095,GO:0003684	CG7769-PA							PF10433,PF03178,PF03178			G3DSA:2.130.10.10,G3DSA:2.130.10.10										
aly347.15	b(0,+)-type amino acid transporter 1	GO:0015804,GO:0015297,GO:0016020,GO:0006461,GO:0055085,GO:0042605,GO:0016324,GO:0003333,GO:0006865,GO:0031526,GO:0007596,GO:0050900,GO:0005887,GO:0015175,GO:0006811,GO:0015184,GO:0005886,GO:0015171,GO:0015811	CG9413-PB			PIRSF006060			PF13520														
aly347.16	Protein arginine N-methyltransferase 8	GO:0016274,GO:0042054,GO:0046982,GO:0018216,GO:0008757,GO:0005829,GO:0006355,GO:0043985,GO:0044020,GO:0008469,GO:0034969,GO:0016571,GO:0035241,GO:0035242,GO:0005886,GO:0019919,GO:0042802,GO:0042803	CG6554-PA						PF06325	PS51678			G3DSA:3.40.50.150,G3DSA:2.70.160.11	SSF53335									
aly347.17	Unknown		CG12540-PA																				
aly347.18	Unknown		n/a												136~156,100~120								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly347.2	Eclosion hormone	GO:0030534,GO:0007218,GO:0005184,GO:0018990,GO:0008031,GO:0008255,GO:0007562,GO:0007563,GO:0005576	CG5400-PA						PF04736														
aly347.3	Glutamate receptor ionotropic, kainate 3	GO:0042391,GO:0009593,GO:0007216,GO:0007268,GO:0030425,GO:0030424,GO:0008066,GO:0001640,GO:0035249,GO:0004970,GO:0032983,GO:0016021,GO:0015277,GO:0015276,GO:0007215,GO:0030054,GO:0032839,GO:0035235,GO:0005234,GO:0034220,GO:0005887,GO:0005886,GO:0043204,GO:0043195,GO:0042734,GO:0045211,GO:0051967,GO:0007196	CG13576-PA						PF00060				G3DSA:1.10.287.70,G3DSA:3.40.190.10	SSF53850,SSF53850										
aly347.4	Neurexin-1	GO:0051124,GO:0005783,GO:0042297,GO:0005886,GO:0033130,GO:0031594,GO:0090129,GO:0050808,GO:0004872,GO:0060134,GO:0007411,GO:0007274,GO:0007416,GO:0097109,GO:2000821,GO:0031982,GO:0050885,GO:1900244,GO:0097116,GO:0097104,GO:0005509,GO:0007269,GO:0043025,GO:0009986,GO:0071625,GO:2000463,GO:0051965,GO:0061178,GO:2000331,GO:0035176,GO:0007612,GO:0030054,GO:0031965,GO:0008306,GO:0007158,GO:0005887,GO:0007268,GO:0050839,GO:0034185,GO:0043234,GO:0030534,GO:0040012,GO:0042734,GO:0071938,GO:1900073,GO:0030198,GO:0005515,GO:0005246,GO:0051968,GO:0097118,GO:0097119	CG7050-PF				SM00181,SM00181,SM00181,SM00282,SM00282,SM00282,SM00282,SM00282,SM00282		PF00008,PF02210,PF02210,PF02210,PF02210,PF02210,PF02210	PS50026,PS50025,PS50026,PS50025,PS50026,PS50025,PS50025,PS50025			G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200	SSF49899,SSF49899,SSF49899,SSF49899,SSF49899,SSF49899										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly347.5	Prostaglandin reductase 1	GO:0005737,GO:0036132,GO:0008270,GO:0070062,GO:2001300,GO:0009636,GO:0006691,GO:0019369,GO:0044281,GO:0047522,GO:0032440,GO:0019371	n/a				SM00829		PF16884,PF00107				G3DSA:3.90.180.10,G3DSA:3.40.50.720	SSF50129,SSF51735									
aly347.6	Probable methyltransferase-like protein 15 homolog	GO:0071424,GO:0005575,GO:0003674,GO:0008150,GO:0008168,GO:0070475	CG14683-PA	MF_01007				TIGR00006	PF01795				G3DSA:3.40.50.150,G3DSA:3.40.50.150,G3DSA:1.10.150.170	SSF81799,SSF53335,SSF53335,SSF53335									
aly347.7	Protein preli-like	GO:0070584,GO:0015914,GO:0048813,GO:0005739,GO:0030061,GO:0043066,GO:0003674,GO:1990050,GO:0005758	CG8806-PC						PF04707	PS50904													
aly347.8	Unknown		n/a						PF05186						54~81,106~126								
aly347.9	Protein phosphatase 1B	GO:0016020,GO:0019221,GO:0006470,GO:0050687,GO:0043407,GO:0006499,GO:0046329,GO:0001745,GO:0000287,GO:0007476,GO:0035970,GO:0043124,GO:0046529,GO:0000278,GO:0070303,GO:0030145,GO:0032873,GO:0046580,GO:0008340,GO:0010225,GO:0006979,GO:1901562,GO:0042347,GO:0007391,GO:0005829,GO:0004722,GO:0004721,GO:1900744,GO:0032688,GO:0045678	CG1906-PE				SM00332		PF00481,PF07830	PS51746		PS01032	G3DSA:1.10.10.430,G3DSA:3.60.40.10	SSF81606,SSF81601									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3478.1	Cecropin-A	GO:0005615,GO:0019731,GO:0045087,GO:0050832,GO:0050830,GO:0005576,GO:0042742,GO:0050829,GO:0006959	CG1367-PA						PF00272														
aly3478.2	Cecropin-A	GO:0045087,GO:0005576,GO:0042742	n/a						PF00272														
aly3478.3	Cecropin-A	GO:0005615,GO:0019731,GO:0045087,GO:0050832,GO:0050830,GO:0005576,GO:0042742,GO:0050829,GO:0006959	CG1367-PA						PF00272			PS00268											
aly3478.4	Cecropin-A	GO:0045087,GO:0005576,GO:0042742	n/a						PF00272			PS00268											
aly3478.5	Cecropin-D	GO:0045087,GO:0005576,GO:0042742	n/a						PF00272														
aly3478.6	Neuropeptide F receptor	GO:0004930,GO:0030536,GO:0016021,GO:0007218,GO:0007217,GO:0004983,GO:0005887,GO:0008188,GO:0004995,GO:0042263,GO:0007186,GO:0007194	CG1147-PD						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly348.1	Unknown		n/a																				
aly348.2	Iodotyrosine dehalogenase 1	GO:0016021,GO:0016491	n/a										G3DSA:3.40.109.10	SSF55469									
aly348.3	Scavenger receptor class B member 1	GO:0006898,GO:0016324,GO:0005044,GO:0016021,GO:0016020,GO:0045056,GO:0016323,GO:0006952,GO:0005901,GO:0005887,GO:0005886,GO:0007155,GO:0070506	CG10345-PA						PF01130														
aly348.4	Sensory neuron membrane protein 1	GO:0007608,GO:0016021,GO:0016020,GO:0005886,GO:0007155,GO:0050896	CG40006-PA						PF01130														
aly3482.1	Acetyl-CoA carboxylase 2	GO:0006633,GO:0005737,GO:0006084,GO:0000902,GO:0051289,GO:0005634,GO:0005811,GO:0005739,GO:0016020,GO:0046322,GO:0012505,GO:0003989,GO:0060421,GO:0004075,GO:0046872,GO:0010884,GO:0005524,GO:2001295	CG11198-PA				SM00878		PF02785,PF00289,PF08326,PF00364,PF02786	PS50979,PS50975,PS50968		PS00866,PS00188,PS00887	G3DSA:3.30.470.20,G3DSA:2.40.50.100,G3DSA:3.40.50.20,G3DSA:3.30.1490.20	SSF51230,SSF56059,SSF51246,SSF52440		00253+6.4.1.2,00620+6.4.1.2,00640+6.4.1.2,00061+6.4.1.2,00254+6.4.1.2,00720+6.4.1.2	REACT_15105,REACT_22258	PWY-7388,PWY-5789,PWY-5743,PWY-5744,PWY-6722,PWY-6679,PWY-4381	UPA00655				
aly3482.2	Odorant receptor 4	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0004984	CG11735-PA						PF02949														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3486.1	Potassium voltage-gated channel subfamily H member 6	GO:0042391,GO:0005267,GO:0004871,GO:0071805,GO:0005221,GO:0006812,GO:0005249,GO:0051291,GO:0005242,GO:0019934,GO:0006813,GO:0086091,GO:0005887,GO:0001666,GO:0055085,GO:0017071	CG42701-PB				SM00100,SM00100,SM00100		PF00027,PF07885,PF07885	PS50042,PS50042,PS50042	PR01463,PR01463,PR01463,PR01463		G3DSA:2.60.120.10,G3DSA:2.60.120.10,G3DSA:2.60.120.10,G3DSA:1.10.287.630,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF51206,SSF51206,SSF81324,SSF51206,SSF81324,SSF81324	1243~1244								
aly3486.2	Protein held out wings	GO:0007498,GO:0030154,GO:0009790,GO:0003676,GO:0005737,GO:0007517,GO:0000381,GO:0005634,GO:0007438,GO:0007475,GO:0003730,GO:0016477,GO:0008366,GO:0016203,GO:0008078,GO:0008016,GO:0045214,GO:0007284,GO:0045995,GO:0007155,GO:0007521,GO:0007525,GO:0008347,GO:0030718,GO:0003729	CG10293-PF				SM00322		PF00013,PF16544	PS50084			G3DSA:3.30.1370.10	SSF54791										
aly3486.3	Unknown		n/a						PF15868														
aly3487.1	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9512-PA			PIRSF000137			PF05199,PF00732			PS00624,PS00623	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly3487.2	Protein eva-1 homolog C	GO:0016021,GO:0030246,GO:0005886	CG42402-PE						PF02140,PF02140	PS50228													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3487.3	PiggyBac transposable element-derived protein 3		n/a						PF13843						578~598								
aly349.1	Leucine-rich repeat and calponin homology domain-containing protein 1	GO:0007265,GO:0005938,GO:0005515,GO:0032154	CG6860-PB				SM00033,SM00369,SM00369,SM00364,SM00364,SM00364,SM00364		PF00560,PF00307,PF13855	PS51450,PS51450,PS50021,PS51450,PS51450,PS51450,PS51450,PS51450	PR00019,PR00019		G3DSA:1.10.418.10,G3DSA:3.80.10.10	SSF52058,SSF47576	382~402								
aly349.10	Neither inactivation nor afterpotential protein C	GO:0008104,GO:0042385,GO:1990146,GO:0033227,GO:0009416,GO:0005875,GO:0023014,GO:0005737,GO:0016028,GO:0016062,GO:0042623,GO:0006886,GO:0016027,GO:0004674,GO:0016459,GO:0004713,GO:0004672,GO:0003774,GO:0005524,GO:0005856,GO:0006468,GO:0007604,GO:0007601,GO:0007603,GO:0007010,GO:0016059,GO:0035091,GO:0016461,GO:0005516,GO:0004702,GO:0045494	CG5125-PB				SM00242,SM00220		PF00069,PF00063	PS51456,PS50096,PS50011	PR00193,PR00193,PR00193	PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF52540,SSF52540,SSF56112									
aly349.11	Neither inactivation nor afterpotential protein C	GO:0008104,GO:0042385,GO:1990146,GO:0033227,GO:0009416,GO:0005875,GO:0023014,GO:0005737,GO:0016028,GO:0016062,GO:0042623,GO:0006886,GO:0016027,GO:0004674,GO:0016459,GO:0004713,GO:0004672,GO:0003774,GO:0005524,GO:0005856,GO:0006468,GO:0007604,GO:0007601,GO:0007603,GO:0007010,GO:0016059,GO:0035091,GO:0016461,GO:0005516,GO:0004702,GO:0045494	CG5125-PB				SM00220		PF00069	PS50011			G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly349.12	Neither inactivation nor afterpotential protein C	GO:0008104,GO:0042385,GO:1990146,GO:0033227,GO:0009416,GO:0005875,GO:0023014,GO:0005737,GO:0016028,GO:0016062,GO:0042623,GO:0006886,GO:0016027,GO:0004674,GO:0016459,GO:0004713,GO:0004672,GO:0003774,GO:0005524,GO:0005856,GO:0006468,GO:0007604,GO:0007601,GO:0007603,GO:0007010,GO:0016059,GO:0035091,GO:0016461,GO:0005516,GO:0004702,GO:0045494	CG5125-PB				SM00242,SM00015,SM00015		PF00063,PF00612	PS51456,PS50096,PS50096	PR00193,PR00193,PR00193,PR00193		G3DSA:1.10.510.10	SSF52540,SSF52540									
aly349.13	Longitudinals lacking protein like	GO:0006351,GO:0001700,GO:0007435,GO:0031519,GO:0006357,GO:0003700,GO:0006342,GO:0005634,GO:0000794,GO:0005700,GO:0016458,GO:0007426,GO:0031208,GO:0045893,GO:0005515,GO:0003677,GO:0045892,GO:0035167,GO:0016568,GO:0042803	CG5738-PB				SM00355,SM00355,SM00225		PF00651	PS50097		PS00028,PS00028	G3DSA:3.30.710.10	SSF54695									
aly349.14	Lipase 3	GO:0004806,GO:0006629,GO:0016788,GO:0016042	CG6113-PC			PIRSF000862			PF04083				G3DSA:3.40.50.1820	SSF53474									
aly349.15	Unknown		n/a												172~206								
aly349.16	Unknown		n/a												344~364,438~472,76~103,310~333,399~426								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly349.17	Laminin subunit alpha-3	GO:0005610,GO:0005604,GO:0070062,GO:0022617,GO:0031581,GO:0030334,GO:0005198,GO:0030198,GO:0045995,GO:0007155,GO:0030155,GO:0008544,GO:0035987,GO:0034329,GO:0005576	n/a												149~169,180~221,24~72,362~441,233~253,124~144,306~354,268~298								
aly349.18	Unknown		n/a												33~60,820~847,1041~1061,233~253,875~916,113~211,1084~1111								
aly349.19	Integrin beta-PS	GO:0016203,GO:0007494,GO:0030336,GO:0016339,GO:0035160,GO:0007160,GO:0035001,GO:0004872,GO:0005927,GO:0007411,GO:0007298,GO:0005925,GO:0003344,GO:0007417,GO:0007517,GO:0007431,GO:0034446,GO:0051492,GO:0007475,GO:0048803,GO:0009925,GO:0016477,GO:0021551,GO:0033627,GO:0006930,GO:0005178,GO:0031589,GO:0016328,GO:0007608,GO:0016340,GO:0030718,GO:0016324,GO:0007601,GO:0031252,GO:0007629,GO:0008305,GO:0008360,GO:0045214,GO:0005887,GO:0005886,GO:0007155,GO:0008340,GO:0007157,GO:0050839,GO:0035099,GO:0007015,GO:0007427,GO:0007426,GO:0007377,GO:0007391,GO:0007229,GO:0007508,GO:0005515,GO:0046982,GO:0043034	CG1560-PA				SM00187		PF07974,PF08725,PF00362	PS50234	PR01186,PR01186,PR01186,PR01186,PR01186,PR01186		G3DSA:2.10.25.10,G3DSA:1.20.5.100,G3DSA:2.60.40.1510,G3DSA:2.10.25.10,G3DSA:3.40.50.410	SSF57196,SSF53300,SSF69179	27~47		REACT_13552							
aly349.2	Elongation factor G, mitochondrial	GO:0070125,GO:0005634,GO:0003924,GO:0005739,GO:0003746,GO:0006414,GO:0005525	CG4567-PA	MF_00054_B			SM00889,SM00838	TIGR00484,TIGR00231	PF14492,PF00009,PF03144,PF00679,PF03764	PS51722	PR00315,PR00315,PR00315,PR00315,PR00315	PS00301	G3DSA:3.40.50.300,G3DSA:2.40.30.10,G3DSA:3.30.230.10,G3DSA:3.30.70.870,G3DSA:3.30.70.240	SSF54211,SSF50447,SSF54980,SSF54980,SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly349.20	Integrin beta-7	GO:0016203,GO:0007494,GO:0034446,GO:0016339,GO:0035160,GO:0034113,GO:0007160,GO:0050900,GO:0035001,GO:0004872,GO:0007411,GO:0007298,GO:0005925,GO:0003344,GO:0007417,GO:0003366,GO:0007517,GO:0070062,GO:0007431,GO:0016020,GO:0051492,GO:0007475,GO:0048803,GO:0016477,GO:0006930,GO:0005178,GO:0031589,GO:0007608,GO:0016340,GO:0030718,GO:0009986,GO:0031252,GO:0008305,GO:0008360,GO:0005886,GO:0007155,GO:0008340,GO:0007157,GO:0050839,GO:0072678,GO:0043113,GO:0035099,GO:0007015,GO:0007427,GO:0007426,GO:0007377,GO:0007391,GO:0007229,GO:0007508,GO:0050901,GO:0005515,GO:0043235,GO:0034669,GO:0046982	CG1560-PA						PF08725,PF07974		PR01186,PR01186,PR01186,PR01186,PR01186,PR01186	PS00243,PS00243	G3DSA:2.10.25.10,G3DSA:1.20.5.100,G3DSA:2.10.25.10,G3DSA:2.60.40.1510				REACT_13552							
aly349.21	Integrin beta-5	GO:0016203,GO:0007494,GO:0016339,GO:0035160,GO:0007160,GO:0035001,GO:0004872,GO:0090136,GO:0007411,GO:0007298,GO:0005925,GO:0003344,GO:0007417,GO:0007517,GO:0070062,GO:0007431,GO:0051492,GO:0007475,GO:0048803,GO:0016477,GO:0043149,GO:0006930,GO:0005178,GO:0031589,GO:0007608,GO:0016340,GO:0030718,GO:0009986,GO:0031252,GO:0008305,GO:0008360,GO:0005886,GO:0007155,GO:0008340,GO:0007157,GO:0050839,GO:0007179,GO:0035099,GO:0007015,GO:0007427,GO:0007426,GO:0007377,GO:0007391,GO:0007229,GO:0007508,GO:0034684,GO:0005515,GO:0043235,GO:0046982	CG1560-PA						PF08725				G3DSA:1.20.5.630,G3DSA:2.10.25.10				REACT_13552							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly349.22	Serine/threonine-protein kinase 24	GO:0019991,GO:0060439,GO:0048679,GO:0032147,GO:0042981,GO:0046777,GO:0023014,GO:0005737,GO:0007346,GO:0070062,GO:0007430,GO:0004674,GO:0005634,GO:0016020,GO:0031098,GO:0097194,GO:0004672,GO:0046872,GO:0005524,GO:0030336,GO:0006468,GO:0007015,GO:0008631,GO:0042542,GO:0005730,GO:0004702	CG5169-PA				SM00220		PF00069	PS50011		PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112	130~157								
aly349.23	Tubulin glycylase 3A	GO:0005737,GO:0070737,GO:0070735,GO:0015630,GO:0018094,GO:0070736,GO:0005874,GO:0004835	CG11323-PA						PF03133	PS51221				SSF56059,SSF56059	303~323								
aly349.24	Tubulin glycylase 3A	GO:0005737,GO:0070737,GO:0070735,GO:0015630,GO:0018094,GO:0070736,GO:0006464,GO:0005874,GO:0004835	CG11323-PA						PF03133	PS51221				SSF56059,SSF56059									
aly349.25	UPF0430 protein CG31712	GO:0005575,GO:0008150,GO:0003674	CG31712-PA						PF15346						88~108,115~240								
aly349.26	Mannose-P-dolichol utilization defect 1 protein homolog	GO:0006488,GO:0016021,GO:0006810,GO:0005783,GO:0006486	CG3792-PA			PIRSF023381	SM00679,SM00679		PF04193,PF04193														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly349.27	Tetratricopeptide repeat protein 14 homolog	GO:0005575,GO:0008150,GO:0003674,GO:0005515	CG6621-PA				SM00028,SM00028,SM00028		PF13181,PF13414	PS50005,PS50293,PS50005,PS50126,PS50005			G3DSA:2.40.50.140,G3DSA:1.25.40.10	SSF48452	456~476								
aly349.28	Unknown		n/a																				
aly349.29	Unknown		n/a																				
aly349.3	Sodium-driven chloride bicarbonate exchanger	GO:0015701,GO:1902600,GO:0005452,GO:0009791,GO:0006820,GO:0006821,GO:0009416,GO:0035264,GO:0051453,GO:0015992,GO:0008509,GO:0035641,GO:0035725,GO:0015106,GO:0043025,GO:0006811,GO:0006814,GO:0098656,GO:0005887,GO:0005886,GO:0016323,GO:0055085,GO:0015301,GO:0048854,GO:0008510,GO:0021860,GO:0097442,GO:0097440,GO:0097441,GO:0016021	CG42253-PC					TIGR00834	PF07565,PF00955		PR01231,PR01231,PR01231,PR01231,PR01231,PR01231,PR01231,PR01232,PR01232,PR01232,PR01232,PR01232,PR01232		G3DSA:1.10.287.570,G3DSA:3.40.1100.10,G3DSA:3.40.1100.10	SSF55804,SSF55804	1109~1129		REACT_15518						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly349.30	Transcription factor SOX-2	GO:0043565,GO:0006351,GO:0007399,GO:0031490,GO:0003700,GO:0005634,GO:0003705,GO:0045665,GO:0006355,GO:0030111,GO:0045944,GO:0045893,GO:0005515,GO:0007411,GO:0007417	CG18024-PB				SM00398		PF12336,PF00505	PS50118			G3DSA:1.10.30.10	SSF47095										
aly349.31	Unknown		n/a																				
aly349.32	Protein l(2)37Cc	GO:0005737,GO:0005811,GO:0016020,GO:0005740,GO:0005739,GO:0007275,GO:0002165,GO:0071456,GO:0005875	CG10691-PB				SM00244		PF01145		PR00679,PR00679,PR00679,PR00679,PR00679,PR00679,PR00679			SSF117892	186~208								
aly349.33	Inactive peptidyl-prolyl cis-trans isomerase shutdown	GO:0005737,GO:0000413,GO:0006457,GO:0070725,GO:0051321,GO:0016020,GO:0005789,GO:0005528,GO:0031047,GO:0003755,GO:0043186,GO:0034587,GO:0048477,GO:0061077,GO:0018208	CG4735-PA				SM00028,SM00028,SM00028		PF00254	PS50059,PS50293,PS50005			G3DSA:1.25.40.10,G3DSA:3.10.50.40	SSF54534,SSF48452	327~347								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly349.34	Myosin-VIIa	GO:0032027,GO:0008586,GO:0005902,GO:0031477,GO:0035317,GO:0005737,GO:0042623,GO:0045179,GO:0008407,GO:0003779,GO:0048800,GO:0016459,GO:0003774,GO:0005524,GO:0007605,GO:0030898,GO:0030048,GO:0008152,GO:0035293,GO:0007469,GO:0007015,GO:0007423,GO:0016461	CG7595-PA				SM00295,SM00295,SM00015,SM00015,SM00015,SM00242,SM00139,SM00139		PF00373,PF00784,PF00784,PF00063,PF09379	PS50002,PS50057,PS50057,PS51016,PS51016,PS50096,PS51456	PR00193,PR00193,PR00193,PR00193,PR00193		G3DSA:2.30.30.40,G3DSA:3.40.50.300,G3DSA:3.10.20.90,G3DSA:1.20.80.10,G3DSA:1.20.80.10,G3DSA:2.30.29.30	SSF52540,SSF50729,SSF47031,SSF54236,SSF47031,SSF54236	845~865								
aly349.35	26S proteasome non-ATPase regulatory subunit 7	GO:0004175,GO:0005838,GO:0008283,GO:0043161,GO:0009987,GO:0030425,GO:0007052,GO:0006511,GO:0005515,GO:0000502,GO:0006508,GO:0000022,GO:0022008,GO:0008541	CG3416-PB				SM00232		PF01398,PF13012						279~325								
aly349.36	Inosine triphosphate pyrophosphatase	GO:0005737,GO:0009204,GO:0009143,GO:0000166,GO:0048812,GO:0009117,GO:0047429,GO:0046872	CG8891-PA	MF_03148				TIGR00042	PF01725				G3DSA:3.90.950.10	SSF52972		00230+3.6.1.19,00983+3.6.1.19,00240+3.6.1.19		PWY-7206					
aly349.37	Insulin-like growth factor-binding protein complex acid labile subunit	GO:0007155,GO:0042567,GO:0005654,GO:0070062,GO:0005515	CG5195-PA				SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00369		PF12799,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855,PF13855	PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52058,SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly349.38	L-threonine 3-dehydrogenase, mitochondrial	GO:0050662,GO:0019518,GO:0044237,GO:0005739,GO:0008743,GO:0003978	CG5955-PA						PF01370				G3DSA:3.40.50.720,G3DSA:3.40.50.720,G3DSA:3.90.25.10	SSF51735										
aly349.39	Golgi apparatus protein 1	GO:0000137,GO:0005797,GO:0016021,GO:0000138,GO:0000139,GO:0008150,GO:0003674	CG33214-PB						PF00839,PF00839,PF00839,PF00839,PF00839,PF00839,PF00839,PF00839,PF00839,PF00839,PF00839,PF00839	PS51289,PS51289,PS51289,PS51289,PS51289,PS51289,PS51289,PS51289,PS51289,PS51289,PS51289,PS51289,PS51289,PS51289													
aly349.4	Protein Wnt-4	GO:0035206,GO:0008045,GO:0008585,GO:0006928,GO:0004871,GO:0048041,GO:0009798,GO:0007275,GO:0007435,GO:0005615,GO:0000122,GO:0031290,GO:0016201,GO:0030182,GO:0042067,GO:0009986,GO:0060071,GO:0060070,GO:0045165,GO:0005886,GO:0001737,GO:0035567,GO:0016477,GO:0009952,GO:0016055,GO:0001664,GO:0005109,GO:0005576,GO:0003407,GO:0005515,GO:0005102,GO:0005578	CG4698-PA				SM00097		PF00110		PR01349,PR01349,PR01349,PR01349,PR01349						REACT_14797						
aly349.40	DNA primase large subunit	GO:0016779,GO:0046872,GO:0000278,GO:0005634,GO:1990077,GO:0003887,GO:0006260,GO:0006261,GO:0003896,GO:0003677,GO:0001745,GO:0005658,GO:0006269,GO:0071897,GO:0051539	CG5553-PA			PIRSF009449			PF04104														
aly349.41	Manganese-transporting ATPase 13A1	GO:0000166,GO:0006812,GO:0016021,GO:0016020,GO:0019829,GO:0005789,GO:0016887,GO:0015662,GO:0046872,GO:0005524	CG6230-PA					TIGR01657,TIGR01494,TIGR01494,TIGR01494	PF00122,PF12710		PR00119,PR00119,PR00119,PR00119	PS00154	G3DSA:3.40.50.1000,G3DSA:3.40.50.1000,G3DSA:2.70.150.10,G3DSA:3.40.1110.10	SSF81665,SSF81665,SSF81665,SSF56784,SSF56784,SSF81653,SSF81660	880~900								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly349.42	Adult-specific cuticular protein ACP-20	GO:0040003,GO:0005214,GO:0008010,GO:0008012,GO:0031012,GO:0042302	CG9290-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly349.43	Unknown		n/a																				
aly349.44	LIM domain transcription factor LMO4	GO:0021522,GO:0005667,GO:0021527,GO:0050865,GO:0021514,GO:0008134,GO:0031333,GO:0003281,GO:0001158,GO:0045944,GO:0008270,GO:0048538,GO:0006366,GO:0042659,GO:0001843	CG5708-PA				SM00132,SM00132		PF00412,PF00412	PS50023,PS50023		PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716,SSF57716									
aly349.45	Unknown		n/a																				
aly349.46	Unknown		n/a																				
aly349.47	Unknown	GO:0003677	CG8359-PA				SM00595		PF02944,PF10545	PS51029,PS51031													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly349.5	Protein Wnt-1	GO:0005783,GO:0050840,GO:0007616,GO:0035263,GO:0001745,GO:0061382,GO:0007367,GO:0060914,GO:0016023,GO:0005771,GO:0005770,GO:0030917,GO:0042127,GO:0048076,GO:0035170,GO:0035277,GO:0007523,GO:0007442,GO:0042326,GO:0007447,GO:0007446,GO:0007444,GO:0007448,GO:0042691,GO:0046847,GO:0061331,GO:0016055,GO:0035167,GO:0035311,GO:0002168,GO:0007346,GO:0014019,GO:0035217,GO:0035153,GO:0060070,GO:0035017,GO:0035019,GO:0007223,GO:0007423,GO:0005539,GO:0006355,GO:0035147,GO:0016318,GO:0007498,GO:0007450,GO:0035224,GO:0035225,GO:0035220,GO:0007418,GO:0046672,GO:0010002,GO:0009798,GO:0008544,GO:0000122,GO:0030707,GO:0072091,GO:0008284,GO:0048332,GO:0009986,GO:0051017,GO:0032876,GO:0045599,GO:0030139,GO:0035289,GO:0005109,GO:0045944,GO:0005515,GO:0016015,GO:0048542,GO:0005102,GO:0045611,GO:0030032,GO:0061320,GO:0007394,GO:0009996,GO:0061328,GO:0048754,GO:0035288,GO:0003136,GO:0007275,GO:0007479,GO:0005615,GO:0007476,GO:0043066,GO:0048728,GO:0005112,GO:0005110,GO:0048749,GO:0035215,GO:0061332,GO:0048190,GO:0008595,GO:0005886,GO:0035290,GO:0007507,GO:0007398,GO:0045121,GO:0007391,GO:0005578,GO:0005576,GO:0045892,GO:0007419,GO:0005769	CG4889-PA				SM00097		PF00110		PR01349,PR01349,PR01349,PR01349,PR01349	PS00246					REACT_14797							
aly349.6	Zinc metalloproteinase nas-14	GO:0004222,GO:0008586,GO:0007415,GO:0010629,GO:0005576,GO:0005509,GO:0008045,GO:0016485,GO:0007411,GO:0006508,GO:0008270	CG6863-PB				SM00235		PF01400				G3DSA:3.40.390.10	SSF55486	328~348								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly349.7	Protein Wnt-6	GO:0070172,GO:0005788,GO:0001658,GO:0010628,GO:0007165,GO:0072079,GO:0009798,GO:0005615,GO:0000122,GO:0072080,GO:0060684,GO:0009887,GO:0030182,GO:0009986,GO:0060070,GO:0045893,GO:0005886,GO:0007267,GO:0045165,GO:0042475,GO:0009952,GO:0016055,GO:0001664,GO:0005109,GO:0005576,GO:0005102,GO:0005578	CG4969-PB				SM00097		PF00110		PR01349,PR01349,PR01349,PR01349,PR01349	PS00246					REACT_14797						
aly349.8	Unknown		n/a																				
aly349.9	Protein Wnt-10a	GO:0007435,GO:0009952,GO:0005109,GO:0000122,GO:0042067,GO:0016055,GO:0001664,GO:0008585,GO:0005578,GO:0060070,GO:0005576,GO:0045165,GO:0005886,GO:0030182,GO:0009798,GO:0005102,GO:0001737,GO:0007275,GO:0005615	CG4971-PB				SM00097		PF00110		PR01349,PR01349,PR01349,PR01349,PR01349	PS00246					REACT_14797						
aly3495.1	Unknown		n/a																				
aly3495.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3495.3	Unknown		n/a																				
aly3495.4	Unknown		n/a																				
aly3496.1	Unknown		n/a																				
aly3496.2	Unknown		n/a				SM00595		PF10545	PS51029													
aly3496.3	Unknown		n/a																				
aly3496.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3496.5	Unknown		n/a																				
aly3496.6	Unknown		n/a																				
aly3496.7	Unknown	GO:0015074,GO:0006313,GO:0003677	n/a						PF01498														
aly3498.1	Protein takeout	GO:0007631,GO:0007623,GO:0005615,GO:0007617,GO:0005576,GO:0042594,GO:0042595,GO:0008343,GO:0008049,GO:0007622	CG2016-PE				SM00700		PF06585														
aly3498.2	Circadian clock-controlled protein	GO:0007623,GO:0005615,GO:0032504	CG10407-PA				SM00700		PF06585														
aly3498.3	Unknown	GO:0005615,GO:0032504	CG10407-PA				SM00700		PF06585														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3498.4	Circadian clock-controlled protein	GO:0007623,GO:0005615	CG1124-PA				SM00700		PF06585														
aly3498.5	Circadian clock-controlled protein	GO:0007623,GO:0005615	CG14661-PA				SM00700		PF06585														
aly3499.1	Palmitoyltransferase ZDHHC17	GO:0008021,GO:0018345,GO:0050714,GO:0016079,GO:0005794,GO:0042953,GO:0004871,GO:0007283,GO:0045202,GO:0005515,GO:0007268,GO:0019706,GO:0030660,GO:0043123,GO:0016409,GO:0016021,GO:0015095,GO:0008270	CG6017-PB				SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796,PF01529	PS50088,PS50088,PS50088,PS50216,PS50088,PS50297			G3DSA:1.25.40.20	SSF48403										
aly3499.10	Tyrosine-protein phosphatase 10D	GO:0007424,GO:0045177,GO:0004728,GO:0007616,GO:0006470,GO:0004725,GO:0008045,GO:0035335,GO:0004721,GO:0030424,GO:0005001,GO:0005515,GO:0005886,GO:0007411,GO:0016021,GO:0007417	CG1817-PF				SM00194,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00404		PF00041,PF00041,PF00102	PS50056,PS50853,PS50853,PS50055,PS50853	PR00700,PR00700,PR00700,PR00700,PR00700,PR00700	PS00383	G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.90.190.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF49265,SSF52799										
aly3499.11	Tyrosine-protein phosphatase 10D	GO:0007424,GO:0045177,GO:0004728,GO:0007616,GO:0006470,GO:0004725,GO:0008045,GO:0035335,GO:0004721,GO:0030424,GO:0005001,GO:0005886,GO:0007411,GO:0016021,GO:0007417	CG1817-PF				SM00060,SM00060		PF00041,PF00041	PS50853,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF49265										
aly3499.12	Double-strand break repair protein MRE11	GO:0000723,GO:0031572,GO:0006302,GO:0004519,GO:0004527,GO:0030145,GO:0006289,GO:0006974,GO:0016233,GO:0006259,GO:0051321,GO:0005634,GO:0051276	CG16928-PA			PIRSF000882		TIGR00583	PF00149,PF04152				G3DSA:3.60.21.10	SSF56300,SSF56300	479~499								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3499.13	Interleukin-1 receptor-associated kinase 4	GO:0019732,GO:0019221,GO:1990266,GO:0007165,GO:0008063,GO:0048262,GO:0035556,GO:0046777,GO:0005737,GO:0005634,GO:0000287,GO:0004674,GO:0004672,GO:0005524,GO:0043123,GO:0006468,GO:0006606,GO:0045087,GO:0035172,GO:0006952,GO:0030162,GO:0019904,GO:0005886,GO:0007352,GO:0002446,GO:0009950,GO:0009620,GO:0001816,GO:0005515,GO:0030097	CG5974-PA				SM00220		PF14786,PF00069,PF00069	PS50011		PS00108,PS00107	G3DSA:1.10.510.10,G3DSA:1.10.533.10,G3DSA:3.30.200.20	SSF56112,SSF47986										
aly3499.14	Transient receptor potential-gamma protein	GO:0015279,GO:0016028,GO:0005261,GO:0005887,GO:0005262,GO:0051480,GO:0006812,GO:0005829,GO:0016020,GO:0070588,GO:0006816,GO:0034704,GO:0009416,GO:0034703,GO:0005515,GO:0050908,GO:0006828	CG5996-PD				SM00248,SM00248	TIGR00870	PF12796,PF00520,PF08344	PS50297,PS50297,PS50088,PS50088	PR01097,PR01097,PR01097		G3DSA:1.25.40.20	SSF48403	751~771		REACT_18266						
aly3499.15	Caseinolytic peptidase B protein homolog	GO:0040011,GO:0006457,GO:0016887,GO:0048085,GO:0051085,GO:0034605,GO:0005788,GO:0005524,GO:0005739,GO:0051082,GO:0005515,GO:0042053,GO:0043104	CG3024-PA				SM00248,SM00248,SM00382		PF13637,PF10431,PF07724	PS50088,PS50297	PR00300,PR00300,PR00300,PR00300		G3DSA:1.10.8.60,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.25.40.20	SSF52540,SSF52540,SSF48403									
aly3499.16	Uncharacterized protein KIAA0930 homolog		CG9646-PA						PF09741														
aly3499.17	Spondin-1	GO:0007155,GO:0005576,GO:0005578,GO:0004867	CG6953-PA				SM00131,SM00209,SM00209,SM00209		PF02014,PF00090,PF00090,PF00090,PF00014,PF06468	PS50092,PS51019,PS50279,PS50092,PS51020,PS50092	PR00759,PR00759,PR00759	PS00280	G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:4.10.410.10,G3DSA:2.20.100.10	SSF82895,SSF82895,SSF57362,SSF82895									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3499.18	Probable phospholipid-transporting ATPase IA	GO:0000287,GO:0005783,GO:0006812,GO:0015914,GO:0004012,GO:0019829,GO:0042584,GO:0005886,GO:0015662,GO:0016021,GO:0005524	CG42321-PH					TIGR01652,TIGR01494	PF16212,PF12710				G3DSA:3.40.1110.10,G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF81665,SSF81660,SSF56784,SSF56784									
aly3499.19	Probable phospholipid-transporting ATPase IA	GO:0000287,GO:0005783,GO:0006812,GO:0015914,GO:0004012,GO:0019829,GO:0042584,GO:0005886,GO:0015662,GO:0016021,GO:0005524	CG42321-PH						PF00122			PS00154	G3DSA:2.70.150.10,G3DSA:3.40.1110.10	SSF81653,SSF56784,SSF81665,SSF81665									
aly3499.2	Unknown		n/a																				
aly3499.20	Choline/ethanolaminephosphotransferase 1	GO:0006646,GO:0016780,GO:0008654,GO:0016021,GO:0016020,GO:0031965,GO:0005789,GO:0004307,GO:0046872,GO:0004142	CG6016-PA						PF01066			PS00379											
aly3499.21	Unknown	GO:0005615	CG2016-PE				SM00700		PF06585														
aly3499.22	Unknown		CG5597-PA							PS50835			G3DSA:2.60.40.10	SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3499.23	Phosphatidylcholine:ceramide cholinephosphotransferase 1	GO:0030148,GO:0016020,GO:0007030,GO:0016301,GO:0016049,GO:0005783,GO:0006665,GO:0016021,GO:0006915,GO:0060305,GO:0000139,GO:0033188,GO:0003674,GO:0000138,GO:0030173,GO:0005886,GO:0006686,GO:0047493,GO:0005634,GO:0044281	CG32380-PA						PF14360														
aly3499.3	Unknown		n/a																				
aly3499.4	Unknown		n/a											SSF57903									
aly3499.5	Unknown	GO:0003676	n/a						PF03184														
aly3499.6	Unknown		n/a																				
aly3499.7	MOB kinase activator-like 2	GO:0005737,GO:0016028,GO:0000902,GO:0007616,GO:0005634,GO:0071944,GO:0007611,GO:0019901,GO:0046872,GO:0045886,GO:0008355,GO:0005515,GO:0005886,GO:0070451,GO:0042052	CG11711-PA						PF03637				G3DSA:1.20.140.30	SSF101152									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3499.8	Unknown		n/a																				
aly3499.9	Eukaryotic translation initiation factor 4 gamma 2	GO:0005845,GO:0005737,GO:0008135,GO:0006446,GO:0035071,GO:0016281,GO:0016020,GO:0048102,GO:0046331,GO:0005488,GO:0044822,GO:0003743	CG3845-PD				SM00543,SM00515		PF02854	PS51363			G3DSA:1.25.40.180,G3DSA:1.25.40.180	SSF48371,SSF48371									
aly35.1	Unknown	GO:0005634,GO:0008270,GO:0003676	CG10269-PA				SM00868		PF07776					SSF57716									
aly35002.1	Unknown		n/a																				
aly35002.2	Lactotransferrin	GO:0019732,GO:0019731,GO:0060349,GO:0001503,GO:0008236,GO:0005615,GO:0001817,GO:0043066,GO:0046872,GO:0045669,GO:1900229,GO:1900159,GO:2001205,GO:1902732,GO:0006811,GO:0042581,GO:0002227,GO:0033690,GO:0031665,GO:0032680,GO:0055072,GO:2000308	n/a						PF00405	PS51408	PR00422,PR00422,PR00422		G3DSA:3.40.190.10	SSF53850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly35002.3	Transferrin	GO:0006879,GO:0005615,GO:0006811,GO:0009617,GO:0055072,GO:0008199,GO:0005381,GO:0006826,GO:0046872,GO:0005576	CG3666-PA				SM00094		PF00405	PS51408			G3DSA:3.40.190.10,G3DSA:3.40.190.10	SSF53850									
aly35002.4	Transferrin	GO:0006879,GO:0006811,GO:0009617,GO:0055072,GO:0008199,GO:0005381,GO:0006826,GO:0046872,GO:0005576	CG3666-PA				SM00094		PF00405	PS51408			G3DSA:3.40.190.10,G3DSA:3.40.190.10	SSF53850									
aly35002.5	Unknown	GO:0016021,GO:0016020,GO:0005272,GO:0006814	CG30181-PA						PF00858														
aly35002.6	E3 ubiquitin-protein ligase ZNRF3	GO:0090090,GO:2000051,GO:0038018,GO:0004842,GO:0016055,GO:0016567,GO:0006511,GO:0008270,GO:0005887,GO:0072089,GO:0016874	CG11982-PA				SM00184		PF13639	PS50089			G3DSA:3.30.40.10	SSF57850									
aly35002.7	Programmed cell death protein 4	GO:0005737,GO:0007569,GO:2000738,GO:0030727,GO:0045892,GO:0005488,GO:0043508,GO:0005634,GO:0005829,GO:0003723	CG10990-PA				SM00544		PF02847	PS51366,PS51366			G3DSA:1.25.40.180	SSF48371,SSF48371									
aly35034.1	Chorion class A protein Ld2/Ld41	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723,PF01723														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3507.1	Unknown		CG14434-PA						PF01928	PS51707			G3DSA:2.40.320.10	SSF55154									
aly3507.10	Zinc finger protein 668	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG5245-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly3507.11	Zinc finger protein 1 homolog	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667									
aly3507.12	Zinc finger and BTB domain-containing protein 17 (Fragment)	GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG4282-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60	SSF57667,SSF57667	896~916,1470~1490,1841~1841,988~1008								
aly3507.13	Zinc finger protein 208	GO:0045931,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178,GO:0008270	CG14938-PA				SM00355,SM00355		PF12874,PF13912,PF13912,PF13912,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	1156~1156								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3507.14	GDNF-inducible zinc finger protein 1	GO:0005737,GO:0005794,GO:0005819,GO:0006351,GO:0005730,GO:0003700,GO:0005634,GO:0043565,GO:0005654,GO:0045892,GO:0008270,GO:0003676,GO:0001658,GO:0001206,GO:0000978,GO:0046872,GO:0001078,GO:0005876,GO:0000980	CG8474-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12874,PF12874,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667	23~43								
aly3507.15	Zinc finger protein 341	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly3507.16	PR domain zinc finger protein 4	GO:0005737,GO:0035075,GO:0046872,GO:0071363,GO:0005123,GO:0030308,GO:0003700,GO:0031670,GO:0005634,GO:0007552,GO:0005654,GO:0006355,GO:0010977,GO:0006351,GO:0003676,GO:0003677,GO:0008168,GO:0045316,GO:0005829	CG45074-PB				SM00355,SM00355,SM00355		PF12874	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly3507.17	Unknown	GO:0046872	n/a				SM00355,SM00355			PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60										
aly3507.2	Zinc finger protein 208	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0008270	CG14711-PA				SM00868,SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57716,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	148~168								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3507.3	Unknown	GO:0046872	n/a									PS00028											
aly3507.4	Zinc finger protein 91	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0070895,GO:0007476,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178,GO:0008270	CG14938-PA				SM00355,SM00355			PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	1520~1540								
aly3507.5	Zinc finger protein 182	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG1233-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly3507.6	Zinc finger protein ZFP69	GO:0003700,GO:0005634,GO:0006351,GO:0003677,GO:0046872,GO:0008270	CG15436-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667	36~56								
aly3507.7	Zinc finger protein 91	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0070895,GO:0007476,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178,GO:0008270	CG14938-PA				SM00355,SM00355		PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3507.8	Zinc finger protein Xfin	GO:0045931,GO:0005737,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0003723,GO:0003676,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355		PF13912,PF13912,PF13912,PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	402~422								
aly3507.9	Zinc finger protein 668	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG15436-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667									
aly35076.1	Unknown		n/a																				
aly3510.1	Intersectin-2	GO:0005737,GO:0008021,GO:0008104,GO:0006897,GO:0007269,GO:0042734,GO:0005813,GO:0045179,GO:0045746,GO:0002052,GO:0051124,GO:0005509,GO:0005515,GO:0005886,GO:0005089,GO:0045860,GO:1903861,GO:0048488,GO:0070062	CG1099-PD				SM00326		PF14604	PS50002			G3DSA:2.30.30.40	SSF50044	44~92,4~31								
aly3510.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3512.1	Chromatin modification-related protein YNG2	GO:1900404,GO:0051321,GO:2000873,GO:0032777,GO:0006281,GO:0005634,GO:0004402,GO:0046580,GO:0003676,GO:0071456,GO:2001020,GO:0005829,GO:0016568,GO:0008270	CG4903-PA									PS00028	G3DSA:3.30.40.10	SSF57903									
aly3512.10	Tiggy-winkle hedgehog protein	GO:0048066,GO:0048103,GO:0048100,GO:0007386,GO:0001746,GO:0001745,GO:0007458,GO:0007367,GO:0060914,GO:0016023,GO:0005615,GO:0042127,GO:0007280,GO:0035277,GO:0001751,GO:0042993,GO:0007442,GO:0007440,GO:0007447,GO:0007446,GO:0045464,GO:0007346,GO:0009880,GO:0048703,GO:0048702,GO:0048099,GO:0042063,GO:0042306,GO:0007424,GO:0007427,GO:0007224,GO:0016540,GO:0007228,GO:0006357,GO:0042078,GO:0007498,GO:0035224,GO:0007418,GO:0060956,GO:0008233,GO:0008544,GO:0005737,GO:0005634,GO:0030707,GO:0031397,GO:0007487,GO:0055002,GO:0035231,GO:0035232,GO:0035288,GO:0030713,GO:0021960,GO:0004197,GO:0005515,GO:0016015,GO:0045861,GO:0004175,GO:0016335,GO:0030139,GO:0035289,GO:0045880,GO:0008354,GO:0007478,GO:0040007,GO:0007473,GO:0007474,GO:0016539,GO:0005113,GO:0035217,GO:0035215,GO:0048663,GO:0030182,GO:0046620,GO:0048592,GO:0008595,GO:0005886,GO:0007267,GO:0008347,GO:0035290,GO:0007506,GO:0007507,GO:0007398,GO:0030908,GO:0005576,GO:0030900,GO:0005768	CG4637-PB				SM00306,SM00305		PF01079,PF01085	PS50817	PR00632,PR00632,PR00632,PR00632,PR00632,PR00632,PR00632,PR00632,PR00632		G3DSA:2.170.16.10,G3DSA:3.30.1380.10	SSF51294,SSF55166									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3512.11	Max-like protein X	GO:0000977,GO:0031325,GO:0048102,GO:0044281,GO:0003677,GO:0005737,GO:0007517,GO:0000122,GO:0005634,GO:0006112,GO:0042803,GO:0035071,GO:0008134,GO:0006913,GO:0045892,GO:0008343,GO:0001227,GO:0003700,GO:0006355,GO:0048813,GO:0006351,GO:0046983,GO:0046982	CG3350-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459	102~122								
aly3512.12	F-box only protein 28	GO:0005634,GO:0003713,GO:0045893,GO:0009952	CG11866-PA				SM00256		PF00646	PS50181			G3DSA:1.20.1280.50	SSF81383									
aly3512.13	Putative carbonic anhydrase 3	GO:0031233,GO:0004089,GO:0006730,GO:0008270	CG6906-PA				SM01057		PF00194	PS51144			G3DSA:3.10.200.10	SSF51069									
aly3512.14	Coiled-coil domain-containing protein 12		CG15525-PA						PF08315						65~85								
aly3512.15	Unknown		n/a												234~264								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3512.16	Unknown		CG15564-PA												25~52								
aly3512.17	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	GO:0047453,GO:0052855,GO:0046496,GO:0005524	CG10424-PA	MF_01965				TIGR00196	PF01256	PS51383		PS01049	G3DSA:3.40.1190.20	SSF53613									
aly3512.2	Unknown		n/a												219~239								
aly3512.3	Signal recognition particle 19 kDa protein	GO:0005786,GO:0008312,GO:0006614,GO:0048500	CG4457-PA						PF01922				G3DSA:3.30.56.30	SSF69695									
aly3512.4	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit wuho	GO:0030488,GO:0036265,GO:0005634,GO:0007275,GO:0007283,GO:0005515,GO:0001674,GO:0048477,GO:0001673	CG15897-PA	MF_03056			SM00320,SM00320,SM00320		PF00400	PS50082,PS50294			G3DSA:2.130.10.10	SSF50978					UPA00989				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3512.5	Mitotic checkpoint serine/threonine-protein kinase BUB1	GO:0007067,GO:0007063,GO:0071173,GO:0005737,GO:0000942,GO:0016020,GO:0005654,GO:0004674,GO:0051301,GO:0004672,GO:0000776,GO:2001244,GO:0005524,GO:0006468,GO:0000278,GO:0008283,GO:0006915,GO:0007059,GO:0007264,GO:0051983,GO:0000777,GO:0005829,GO:0016032,GO:0007094,GO:0007093	CG14030-PA				SM00220,SM00777		PF08311,PF00069	PS51489,PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112	1576~1596		REACT_152,REACT_383						
aly3512.6	Zinc finger protein 830	GO:0005737,GO:0016607,GO:0051276,GO:0005694,GO:0001832,GO:0005654,GO:0033260,GO:0044773,GO:0007067,GO:0046872,GO:0060729,GO:0005634,GO:0051301	CG11839-PB				SM00451		PF12171					SSF57667	219~246,9~29,249~269,146~166									
aly3512.7	26S proteasome non-ATPase regulatory subunit 5	GO:0043248,GO:0022624,GO:0044183,GO:0006974,GO:0005488,GO:0008540	CG12096-PA						PF10508				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371									
aly3512.8	J domain-containing protein CG6693	GO:0005575,GO:0008150,GO:0003674	CG6693-PA				SM00271		PF00226	PS50076	PR00625,PR00625,PR00625	PS00636	G3DSA:1.10.287.110	SSF46565	112~132								
aly3512.9	Unknown		n/a												10~30,133~167,61~88								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly35137.1	Unknown		n/a												21~41								
aly3516.1	Organic cation transporter protein	GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0008513,GO:0016021	CG8654-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly3516.10	CAAX prenyl protease 1 homolog	GO:0004222,GO:0070062,GO:0030327,GO:0005637,GO:0016021,GO:0016020,GO:0006998,GO:0005789,GO:0071586,GO:0006508,GO:0046872	CG9000-PA						PF16491,PF01435				G3DSA:3.30.2010.10										
aly3516.11	Lysine-specific histone demethylase 1A	GO:1902166,GO:0034720,GO:0007596,GO:0050681,GO:0019899,GO:0003700,GO:0003677,GO:0021983,GO:0043426,GO:0016491,GO:0032091,GO:0006482,GO:0050660,GO:0006355,GO:0006325,GO:0005634,GO:0070828,GO:0007474,GO:0005654,GO:0016458,GO:0030851,GO:0005667,GO:0033169,GO:0045944,GO:0048477,GO:2000179,GO:0055001,GO:2000648,GO:0017053,GO:0008283,GO:0008134,GO:0045648,GO:0007264,GO:0030374,GO:0000790,GO:0001701,GO:0045892,GO:0043392,GO:0046886,GO:0008593,GO:0051572,GO:0051573,GO:0043433,GO:0055114,GO:0044212,GO:0051091,GO:0034648,GO:0006357,GO:0000122,GO:0045654,GO:0032451,GO:0032452,GO:0032453,GO:0032454,GO:0006351,GO:0005515,GO:0010725,GO:0003682,GO:0002039,GO:0043518	CG17149-PA						PF04433,PF01593,PF03045	PS50934			G3DSA:1.10.10.10,G3DSA:1.10.287.80,G3DSA:3.50.50.60	SSF46689,SSF51905									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3516.12	Protein toll	GO:0009897,GO:0007416,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0007165,GO:0008063,GO:0060049,GO:0006955,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0002229,GO:0002227,GO:0042802,GO:0016201,GO:0009880,GO:0007507,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005886,GO:0007155,GO:0007352,GO:0043234,GO:0006952,GO:0009950,GO:0009620,GO:0004888,GO:0045944,GO:0005515,GO:0048935,GO:0030097,GO:0045610,GO:0005769,GO:0035007	CG6890-PA				SM00255,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00082,SM00082,SM00369		PF01582,PF13855,PF13855,PF13855,PF13855,PF13855	PS50104,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.40.50.10140,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52200,SSF52047,SSF52047,SSF52058,SSF52058									
aly3516.13	Unknown		n/a																				
aly3516.14	Unknown		n/a																				
aly3516.2	Organic cation transporter protein	GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0008513,GO:0016021	CG8654-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly3516.3	Lysocardiolipin acyltransferase 1	GO:0016021,GO:0005789,GO:0003841,GO:0008152,GO:0016024,GO:0007275	CG4753-PB				SM00563		PF16076,PF01553														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3516.4	Organic cation transporter-like protein	GO:0030307,GO:0016021,GO:0007390,GO:0022857,GO:0015101,GO:0040018,GO:0015695,GO:0008513,GO:0055085	CG8654-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly3516.5	Organic cation transporter protein	GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0008513,GO:0016021	CG8654-PA						PF00083	PS50850		PS00217	G3DSA:1.20.1250.20	SSF103473									
aly3516.6	Polycomb protein Scm	GO:0030708,GO:0005515,GO:0003700,GO:0035102,GO:0005634,GO:0005700,GO:0006355,GO:0016458,GO:0016568,GO:0045892,GO:0008270,GO:0007409,GO:0022008,GO:0030713,GO:0042802,GO:0006351	CG9495-PA				SM00454,SM00561,SM00561		PF00536,PF02820,PF02820	PS50105,PS51079,PS51079			G3DSA:1.10.150.50,G3DSA:2.30.30.160,G3DSA:2.30.30.160	SSF63748,SSF63748,SSF47769									
aly3516.7	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	GO:0005794,GO:0017101,GO:0000049,GO:0005783,GO:0005829,GO:0006915,GO:0033133,GO:0006412,GO:0006954,GO:0007155,GO:0006006,GO:0001525,GO:0005634,GO:0005615	CG8235-PA						PF01588	PS50886			G3DSA:2.40.50.140	SSF50249	33~93		REACT_71						
aly3516.8	Ribosomal protein S6 kinase alpha-3	GO:0035106,GO:0050941,GO:0031594,GO:0035556,GO:0032496,GO:0007049,GO:0005737,GO:0005634,GO:0000287,GO:0007474,GO:0004674,GO:0004711,GO:0002224,GO:0042683,GO:0043027,GO:0006468,GO:0007528,GO:0008306,GO:0046580,GO:0042308,GO:0008340,GO:0019901,GO:0005840,GO:0043154,GO:0046533,GO:0045944,GO:0005524,GO:0005515,GO:0006417,GO:0045475	CG17596-PA			PIRSF000606	SM00133,SM00220,SM00220		PF00069,PF00069,PF00433	PS50011,PS50011,PS51285		PS00107,PS00107,PS00108,PS00108	G3DSA:3.30.200.20,G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10	SSF56112,SSF56112			REACT_18266						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3516.9	Organic cation transporter protein	GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0008513,GO:0016021	CG8654-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly3527.1	Probable nuclear hormone receptor HR3	GO:0016319,GO:0043565,GO:0006351,GO:0005515,GO:0000122,GO:0003700,GO:0005634,GO:0007552,GO:0003707,GO:0006355,GO:0045944,GO:0008270,GO:0043401,GO:0040034,GO:0004887,GO:0004879,GO:0000977	CG33183-PE				SM00399		PF00105	PS51030	PR00047,PR00047,PR00047,PR00047,PR00398,PR00398,PR00398	PS00031	G3DSA:1.10.565.10,G3DSA:1.10.565.10,G3DSA:3.30.50.10	SSF57716,SSF48508	192~212		REACT_71						
aly353.1	Serine protease HTR4	GO:0004252,GO:0007528,GO:0001558,GO:0038056,GO:0005515,GO:0005520,GO:0030514,GO:0005576	CG13253-PC						PF00219	PS51323				SSF57184									
aly353.2	Pogo transposable element with KRAB domain	GO:0006355,GO:0005634,GO:0007275,GO:0003677	n/a				SM00674		PF05225,PF03221,PF03184	PS50835,PS51253			G3DSA:3.30.40.10,G3DSA:1.10.10.60	SSF57903,SSF46689									
aly3535.1	Fasciclin-2	GO:0016319,GO:0050808,GO:0048149,GO:0050803,GO:0008582,GO:0007614,GO:0061174,GO:0007612,GO:0042059,GO:0030424,GO:0031594,GO:0001746,GO:0007413,GO:0008355,GO:0005737,GO:0042995,GO:0036062,GO:0016021,GO:0048786,GO:0048803,GO:0043005,GO:0035159,GO:0031225,GO:0048667,GO:0035152,GO:0035158,GO:0072499,GO:0008038,GO:0007528,GO:0045211,GO:0008360,GO:0005886,GO:0007156,GO:0097482,GO:0042734,GO:0007611,GO:0072553,GO:0005515,GO:0005829	CG3665-PG				SM00409,SM00409,SM00409,SM00409,SM00409,SM00060,SM00060,SM00408,SM00408,SM00408,SM00408,SM00408		PF00041,PF00041,PF07679,PF07679,PF07679,PF07679,PF13895	PS50853,PS50835,PS50835,PS50835,PS50853,PS50835,PS50835	PR01838,PR01838,PR01838,PR01838		G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF49265,SSF48726,SSF48726,SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3535.2	Fasciclin-2	GO:0016319,GO:0050808,GO:0048149,GO:0050803,GO:0008582,GO:0007614,GO:0061174,GO:0007612,GO:0042059,GO:0030424,GO:0031594,GO:0001746,GO:0007413,GO:0008355,GO:0005737,GO:0042995,GO:0036062,GO:0016021,GO:0048786,GO:0048803,GO:0043005,GO:0035159,GO:0031225,GO:0048667,GO:0035152,GO:0035158,GO:0072499,GO:0008038,GO:0007528,GO:0045211,GO:0008360,GO:0005886,GO:0007156,GO:0097482,GO:0042734,GO:0007611,GO:0072553,GO:0005515,GO:0005829	CG3665-PG				SM00060,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408		PF00041,PF07679,PF07679,PF07679,PF07679	PS50835,PS50835,PS50853,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF48726,SSF48726,SSF48726,SSF48726									
aly3535.3	Unknown		n/a																				
aly3535.4	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase I	GO:0030206,GO:0046872,GO:0006486,GO:0016021,GO:0016020,GO:0000139,GO:0030166,GO:0015012,GO:0005886,GO:0015020,GO:0015018	CG32775-PA						PF03360				G3DSA:3.90.550.10	SSF53448									
aly3535.5	Unknown		n/a																				
aly35377.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly354.1	Transmembrane protease serine 4	GO:0004252,GO:0016021,GO:0005044,GO:0006508	CG4927-PC				SM00020		PF00089	PS50240		PS00135	G3DSA:2.40.10.10	SSF50494									
aly354.2	Acetylcholine receptor subunit alpha-like 2	GO:0006810,GO:0006812,GO:0005230,GO:0016020,GO:0015464,GO:0005892,GO:0045211,GO:0004889,GO:0005887,GO:0007271,GO:0098655,GO:0030054	CG6844-PA					TIGR00860	PF02932,PF02931		PR00254,PR00254,PR00254,PR00254,PR00252,PR00252,PR00252,PR00252	PS00236	G3DSA:2.70.170.10,G3DSA:1.20.120.370,G3DSA:1.20.120.370	SSF63712,SSF90112,SSF90112			REACT_13685						
aly354.3	Unknown		n/a																				
aly354.4	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly354.5	Unknown	GO:0006508,GO:0035007,GO:0004252	CG6361-PB						PF00089			PS00134	G3DSA:2.40.10.10	SSF50494									
aly354.6	Acetylcholine receptor subunit alpha-like 1	GO:0006810,GO:0006812,GO:0005230,GO:0016020,GO:0015464,GO:0005892,GO:0045211,GO:0004889,GO:0005887,GO:0017085,GO:0007271,GO:0098655,GO:0030054	CG5610-PB						PF02931				G3DSA:2.70.170.10	SSF63712									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3542.1	Histidine decarboxylase	GO:0004398,GO:0042051,GO:0043052,GO:0006520,GO:0016831,GO:0030170,GO:0042423	CG3454-PA						PF00282		PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800	PS00392	G3DSA:3.40.640.10,G3DSA:3.90.1150.10,G3DSA:1.20.1340.10	SSF53383									
aly3542.10	Decaprenyl-diphosphate synthase subunit 2	GO:0005737,GO:0050347,GO:0000010,GO:0050878,GO:0006744,GO:0051290,GO:0008299,GO:0044281,GO:1990234,GO:0005759,GO:0046982	CG10585-PA																				
aly3542.2	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005886,GO:0006508	CG8213-PC				SM00020		PF00089,PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly3542.3	Unknown	GO:0003674,GO:0005615,GO:0032504	CG42326-PE						PF00024	PS50948,PS50948				SSF57414									
aly3542.4	Unknown		n/a																				
aly3542.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3542.6	Peptidyl-prolyl cis-trans isomerase CWC27 homolog	GO:0000413,GO:0006457,GO:0071011,GO:0071013,GO:0000398,GO:0003755	CG10907-PA						PF06432,PF00160	PS50072	PR00153,PR00153,PR00153,PR00153,PR00153	PS00170	G3DSA:2.40.100.10	SSF50891	320~347	00563+2.4.1.198			UPA00196				
aly3542.7	Unknown	GO:0006030,GO:0005576,GO:0008061	CG13675-PD						PF01607				G3DSA:2.170.140.10	SSF57625									
aly3542.8	Probable chitinase 2	GO:0005975,GO:0000272,GO:0005575,GO:0005576,GO:0008061,GO:0004553,GO:0004568,GO:0006032,GO:0006036	CG2054-PA				SM00636		PF00704			PS01095	G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.10.50.10	SSF54556,SSF51445,SSF51445		00520+3.2.1.14		PWY-6902					
aly3542.9	Androgen-dependent TFPI-regulating protein	GO:0016021,GO:0005886	CG3625-PB						PF04750														
aly35444.1	Unknown		n/a						PF13358						87~107								
aly35526.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly35529.1	Putative uncharacterized transposon-derived protein F52C9.6		n/a																				
aly35529.2	Protein-lysine N-methyltransferase Mettl10	GO:0005737,GO:0008168	CG9643-PA										G3DSA:3.40.50.150	SSF53335									
aly35529.3	Protein-lysine N-methyltransferase mettl10	GO:0005737,GO:0008168	CG9643-PA																				
aly3553.1	Leishmanolysin-like peptidase	GO:0005737,GO:0007100,GO:0045842,GO:0004222,GO:0051298,GO:0006338,GO:0007444,GO:0016020,GO:0008406,GO:0031252,GO:0007155,GO:0007052,GO:0051301,GO:0007076,GO:0006508,GO:0008233,GO:0046872,GO:0051225,GO:0008354,GO:0007420	CG3953-PA						PF01457				G3DSA:2.30.34.10	SSF55486									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3555.1	Fatty acid-binding protein, heart	GO:0006631,GO:0007616,GO:0046320,GO:0044281,GO:0032868,GO:0005875,GO:0055091,GO:0070062,GO:0070538,GO:0019433,GO:0005324,GO:0044539,GO:0036041,GO:0005504,GO:0071073,GO:0008285,GO:0005215,GO:0006810,GO:0008289,GO:0042632,GO:0005615,GO:0050543,GO:0008092,GO:0005829,GO:0042493,GO:0016528,GO:0070542	CG6783-PC								PR00178,PR00178	PS00214	G3DSA:2.40.128.20	SSF50814									
aly3555.2	Cell growth-regulating nucleolar protein	GO:0005634,GO:0046872,GO:0044822,GO:0005730	CG12909-PA						PF08790					SSF57667,SSF57667	222~242								
aly3555.3	Inhibitor of carbonic anhydrase	GO:0006879,GO:0005615,GO:0008199,GO:0055037,GO:0019991,GO:0046658,GO:0005381,GO:0006826,GO:0004857,GO:0005576,GO:0005506,GO:0005769,GO:0005918	CG10620-PA				SM00094,SM00094		PF00405,PF00405	PS51408,PS51408	PR00422,PR00422,PR00422,PR00422,PR00422,PR00422,PR00422	PS00205	G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.190.10	SSF53850,SSF53850,SSF53850									
aly3555.4	Telomerase reverse transcriptase	GO:0005634,GO:0003721,GO:0030529,GO:0000781,GO:0003723,GO:0003677,GO:0046872	n/a				SM00975		PF12009,PF00078	PS50878				SSF56672									
aly3555.5	Glycerate kinase	GO:0005737,GO:0008887,GO:0006468,GO:0005739,GO:0005524	CG9886-PA						PF05161,PF13660				G3DSA:3.40.50.10180,G3DSA:3.40.1480.10,G3DSA:3.40.1480.10	SSF82544,SSF82544									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3555.6	DNA replication licensing factor Mcm6	GO:0003682,GO:0042555,GO:0046872,GO:0007307,GO:0005634,GO:0006270,GO:0006267,GO:0005656,GO:0046331,GO:0006260,GO:0051301,GO:0003677,GO:0003678,GO:0007067,GO:0043138,GO:0048477,GO:0005524	CG4039-PA				SM00350		PF00493,PF14551	PS50051	PR01657,PR01657,PR01657,PR01657,PR01657,PR01662,PR01662,PR01662,PR01662	PS00847	G3DSA:3.40.50.300,G3DSA:3.30.1640.10,G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:2.20.28.10	SSF52540,SSF50249			REACT_152,REACT_383,REACT_1538							
aly3555.7	DNA mismatch repair protein Mlh1	GO:0032389,GO:0045190,GO:0006298,GO:0030983,GO:0016887,GO:0007060,GO:0006303,GO:0000289,GO:0005634,GO:0016020,GO:0007129,GO:0005712,GO:0005654,GO:0043060,GO:0045950,GO:0032407,GO:0003697,GO:0005524,GO:0032390,GO:0006281,GO:0016321,GO:0007283,GO:0000795,GO:0007131,GO:0001673,GO:0008630,GO:0000712,GO:0048477,GO:0051257,GO:0032300,GO:0016446	CG11482-PA					TIGR00585	PF01119,PF16413,PF13589			PS00058	G3DSA:3.30.565.10,G3DSA:3.30.230.10	SSF54211,SSF55874	494~514								
aly3555.8	Unknown		n/a												60~84,171~191,193~213								
aly3560.1	UBX domain-containing protein 4	GO:0005635,GO:0006986,GO:0005789,GO:0030433	CG8042-PA										G3DSA:3.40.30.10	SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3560.2	Homeobox protein unplugged	GO:0007424,GO:0007426,GO:0007420,GO:0043565,GO:0003700,GO:0005634,GO:0006355,GO:0051960,GO:0006351	CG1650-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly3561.1	4-hydroxybutyrate coenzyme A transferase	GO:0008411,GO:0006084,GO:0022008,GO:0005811,GO:0016740	CG7920-PA						PF13336,PF13336,PF02550				G3DSA:3.30.750.70,G3DSA:3.40.1080.10	SSF100950,SSF100950									
aly3561.10	Unknown		n/a																				
aly3561.11	Unknown		n/a																				
aly3561.2	Casein kinase I isoform alpha	GO:0006909,GO:0030111,GO:0032436,GO:0002121,GO:0007067,GO:0051301,GO:0005737,GO:0000902,GO:0005634,GO:0005815,GO:0004674,GO:0004672,GO:0005524,GO:0016607,GO:0006468,GO:0006281,GO:0045879,GO:0030162,GO:0030163,GO:0022008,GO:0000777,GO:0007224,GO:0016055,GO:0045732,GO:0005515	CG2028-PB				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3561.3	Probable sodium/potassium/calcium exchanger CG1090	GO:0015293,GO:0016021,GO:0006816,GO:0006814,GO:0035725,GO:0008273,GO:0055085	CG1090-PG					TIGR00367	PF01699,PF01699								REACT_15518						
aly3561.4	Zinc finger protein 398	GO:0007492,GO:0010001,GO:0007499,GO:0061024,GO:0003676,GO:0003677,GO:0008354,GO:0007417,GO:0007362,GO:0043565,GO:0007435,GO:0001706,GO:0000122,GO:0009948,GO:0005634,GO:0007369,GO:0046872,GO:0035239,GO:0008134,GO:0046331,GO:0045893,GO:0007400,GO:0007375,GO:0007374,GO:0007419,GO:0003700,GO:0007431,GO:0006355,GO:0006351,GO:0008293,GO:0001708	CG9768-PA				SM00355,SM00355,SM00355		PF00096,PF00096,PF12874	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly3561.5	Unknown	GO:0005488	n/a											SSF48371	29~49								
aly3561.6	Negative elongation factor A	GO:0006351,GO:0034244,GO:0032021,GO:0017053,GO:0005634,GO:0003723,GO:0005694,GO:0007275,GO:0007070,GO:0003729	CG5874-PB																				
aly3561.7	Leucine-rich repeat-containing protein 27	GO:0007265,GO:0005938,GO:0005515,GO:0032154	CG6860-PB				SM00369,SM00369,SM00369		PF13855	PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3561.8	Protein O-GlcNAcase	GO:0032024,GO:0016231,GO:0046060,GO:0046326,GO:0031343,GO:0043243,GO:0005634,GO:0016020,GO:0004402,GO:0005739,GO:0016573,GO:0010524,GO:0070265,GO:0051054,GO:0006612,GO:0060051,GO:0045475,GO:0060124,GO:0010616,GO:0007568,GO:0006491,GO:0051928,GO:0004415,GO:0005829,GO:0006044,GO:0051901,GO:0006517,GO:0045862,GO:0048545	CG5871-PA						PF07555				G3DSA:3.40.630.30	SSF51445				PWY-7437					
aly3561.9	Protein glass	GO:0009649,GO:0042051,GO:0003700,GO:0005634,GO:0007601,GO:0003705,GO:0035271,GO:0006355,GO:0045944,GO:0006351,GO:0043153,GO:0003677,GO:0007605,GO:0010114,GO:0046872,GO:0050896,GO:0001752	CG7672-PC				SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF00096,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										
aly35699.1	RNA 3'-terminal phosphate cyclase	GO:0006396,GO:0005634,GO:0005654,GO:0003824,GO:0003723,GO:0044822,GO:0005524,GO:0003963	CG4061-PA	MF_00200		PIRSF005378		TIGR03399	PF01137,PF05189			PS01287	G3DSA:3.65.10.20,G3DSA:3.65.10.20	SSF55205,SSF52913	206~226								
aly35699.2	Minor histocompatibility antigen H13	GO:0007424,GO:0031625,GO:0005791,GO:0005783,GO:0042500,GO:0016021,GO:0016020,GO:0033619,GO:0006465,GO:0071556,GO:0004190,GO:0034620,GO:0005886,GO:0071458,GO:0008233,GO:0009986,GO:0042803	CG11840-PA				SM00730		PF04258														
aly35699.3	WD repeat-containing protein CG11141	GO:0005575,GO:0008150,GO:0003674,GO:0005515	CG11141-PB										G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly357.1	Tyrosine-protein phosphatase 99A	GO:0016021,GO:0006470,GO:0004725,GO:0005886,GO:0030424,GO:0005001,GO:0008045,GO:0035335,GO:0007414,GO:0007415	CG2005-PB				SM00404,SM00194		PF00102,PF00102	PS50055,PS50055,PS50056	PR00700,PR00700,PR00700,PR00700,PR00700	PS00383	G3DSA:3.90.190.10,G3DSA:3.90.190.10,G3DSA:3.90.190.10,G3DSA:3.90.190.10	SSF52799,SSF52799,SSF52799	579~606								
aly357.2	Unknown	GO:0005575,GO:0008150,GO:0003674	CG32017-PB																				
aly3570.1	Unknown		n/a																				
aly3570.2	Fatty acid synthase	GO:0006633,GO:0047451,GO:0004320,GO:0008144,GO:0008270,GO:0001649,GO:0016491,GO:0005737,GO:0070062,GO:0016295,GO:0005835,GO:0016020,GO:0071353,GO:0005739,GO:0030879,GO:0005794,GO:0044822,GO:0004315,GO:0016788,GO:0047117,GO:0042587,GO:0005886,GO:0055114,GO:0006084,GO:0042470,GO:0004312,GO:0004313,GO:0016296,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319	CG17374-PC				SM00829,SM00822		PF08659,PF14765,PF00550,PF00107	PS50075			G3DSA:3.40.50.720,G3DSA:1.10.1200.10,G3DSA:3.40.50.720	SSF51735,SSF51735,SSF50129,SSF47336										
aly3570.3	Fatty acid synthase	GO:0006633,GO:0047451,GO:0016295,GO:0005835,GO:0004320,GO:0016296,GO:0016788,GO:0004317,GO:0004312,GO:0004313,GO:0047117,GO:0004316,GO:0008270,GO:0004314,GO:0004315,GO:0004319,GO:0055114,GO:0016491	CG17374-PC				SM00825		PF00109,PF16197,PF02801			PS00606	G3DSA:3.40.47.10,G3DSA:3.40.47.10	SSF53901,SSF53901										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3570.4	Unknown	GO:0022008,GO:0032934,GO:0015918	CG3934-PA						PF02221				G3DSA:2.60.40.770	SSF81296									
aly3570.5	Fatty acid synthase	GO:0006633,GO:0047451,GO:0006631,GO:0004320,GO:0042587,GO:0015939,GO:0031325,GO:0008144,GO:0035338,GO:0008270,GO:0001649,GO:0016491,GO:0005737,GO:0070062,GO:0016295,GO:0005835,GO:0016020,GO:0071353,GO:0005739,GO:0006112,GO:0030879,GO:0005794,GO:0006767,GO:0006766,GO:0044822,GO:0004315,GO:0016788,GO:0003824,GO:0047117,GO:0008152,GO:0005886,GO:0044255,GO:0055114,GO:0006084,GO:0042470,GO:0005829,GO:0004312,GO:0004313,GO:0016296,GO:0019432,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319,GO:0044281	CG17374-PC						PF00109				G3DSA:3.40.47.10	SSF53901									
aly3570.6	Fatty acid synthase	GO:0006633,GO:0047451,GO:0004320,GO:0008144,GO:0008270,GO:0001649,GO:0016491,GO:0005737,GO:0070062,GO:0016295,GO:0005835,GO:0016020,GO:0071353,GO:0005739,GO:0030879,GO:0005794,GO:0044822,GO:0004315,GO:0016788,GO:0047117,GO:0042587,GO:0005886,GO:0055114,GO:0006084,GO:0042470,GO:0004312,GO:0004313,GO:0016296,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319	CG17374-PC				SM00829,SM00827		PF00107,PF14765,PF02801,PF00698,PF16197				G3DSA:3.40.366.10,G3DSA:3.40.366.10,G3DSA:3.40.47.10,G3DSA:3.90.180.10,G3DSA:3.40.50.720	SSF51735,SSF53901,SSF50129,SSF52151,SSF52151,SSF55048									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3570.7	Fatty acid synthase	GO:0006633,GO:0047451,GO:0016295,GO:0005835,GO:0004320,GO:0016296,GO:0016788,GO:0004317,GO:0004312,GO:0004313,GO:0047117,GO:0004316,GO:0008270,GO:0004314,GO:0004315,GO:0004319,GO:0055114,GO:0016491	CG17374-PC				SM00827,SM00823,SM00825,SM00822,SM00829		PF00698,PF16197,PF00107,PF00550,PF08659,PF02801,PF00109,PF14765	PS50075		PS00606	G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.720,G3DSA:1.10.1200.10,G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.50.720,G3DSA:3.40.366.10,G3DSA:3.40.366.10,G3DSA:3.90.180.10	SSF47336,SSF53901,SSF53901,SSF53474,SSF52151,SSF52151,SSF51735,SSF55048,SSF51735,SSF50129	2016~2036,2156~2165								
aly3570.8	Unknown		n/a										G3DSA:3.40.50.1820										
aly35864.1	Methionine--tRNA ligase, cytoplasmic	GO:0005737,GO:0004825,GO:0000049,GO:0006431,GO:0005829,GO:0046686,GO:0022008,GO:0005875,GO:0005524	CG15100-PA						PF09334		PR01041,PR01041		G3DSA:3.40.50.620	SSF52374		00450+6.1.1.10,00970+6.1.1.10	REACT_71						
aly3594.1	Unknown		n/a																				
aly3594.2	Unknown	GO:0007415,GO:0005515,GO:0016198,GO:0005576,GO:0003674,GO:0005887,GO:0007155,GO:0007157,GO:0007275	CG14334-PA							PS50835			G3DSA:2.60.40.10	SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3594.3	Unknown		n/a																				
aly3595.1	Antichymotrypsin-1	GO:0005615,GO:0004867	n/a										G3DSA:3.30.497.10,G3DSA:2.30.39.10	SSF56574									
aly3595.2	Zinc finger SWIM domain containing protein 5	GO:0008270,GO:0005615	CG32542-PA							PS50966					328~348								
aly3595.3	Zinc finger SWIM domain containing protein 4	GO:0008270	CG32542-PA																				
aly3595.4	Collagen alpha 5(VI) chain	GO:0016201,GO:0005581,GO:0030574,GO:0030198,GO:0008045,GO:0007155,GO:0022617,GO:0005578,GO:0005576	CG6867-PA				SM00284,SM00409,SM00409,SM00408,SM00408		PF01391,PF01391,PF01391,PF07679,PF07679,PF02191	PS50835,PS51132,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly3595.5	Unknown		n/a										G3DSA:1.10.437.10	SSF56854									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3595.6	Sodium/potassium/calcium exchanger Nckx30C	GO:0048749,GO:0015293,GO:0016021,GO:0006816,GO:0006814,GO:0035725,GO:0048812,GO:0008273,GO:0055085	CG18660-PD						PF01699								REACT_15518						
aly3598.1	Probable cationic amino acid transporter	GO:0015297,GO:0015326,GO:1902475,GO:0016020,GO:0015171,GO:0005765,GO:0015807,GO:0015179,GO:0005887,GO:0010923,GO:0003333	CG12531-PA						PF13906,PF13520														
aly3598.10	Pancreas transcription factor 1 subunit alpha	GO:0005737,GO:0043565,GO:0048699,GO:0031016,GO:0005667,GO:0006351,GO:0009790,GO:0003700,GO:0005634,GO:0030154,GO:0009887,GO:0048384,GO:0006355,GO:0045893,GO:0030902,GO:0003677,GO:0046983,GO:0031017,GO:0009888	CG33323-PB				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459										
aly3598.11	Enolase	GO:0000015,GO:0000287,GO:0005811,GO:0004634,GO:0006096	CG17654-PD	MF_00318		PIRSF001400			PF03952,PF00113		PR00148,PR00148,PR00148,PR00148,PR00148,PR00148		G3DSA:3.30.390.10,G3DSA:3.20.20.120	SSF51604,SSF54826		00680+4.2.1.11,00010+4.2.1.11	REACT_474	PWY-1042,PWY-2221,PWY-1622,PWY-6901,PWY-7218,PWY-6886,PWY-5723,PWY-6142,PWY-5484,PWY-7124,PWY-	UPA00109				
aly3598.12	Lysophospholipid acyltransferase 5	GO:0008654,GO:0016021,GO:0016020,GO:0007009,GO:0007291,GO:0071617,GO:0005886,GO:0047184,GO:0030258,GO:0008354	CG9655-PA						PF03062														
aly3598.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3598.14	Ubiquitin carboxyl-terminal hydrolase isozyme L5	GO:0004175,GO:0031011,GO:0005737,GO:0005838,GO:0070628,GO:0043161,GO:0005634,GO:0006281,GO:0006508,GO:0016579,GO:0044822,GO:0006351,GO:0004221,GO:0061136,GO:0008242,GO:0004866,GO:0010951,GO:0000502,GO:0022008,GO:0021670,GO:0004843,GO:0006310,GO:0005829,GO:0048853,GO:0005622,GO:0006355,GO:0006511,GO:0030901	CG3431-PA			PIRSF038120			PF01088		PR00707,PR00707,PR00707,PR00707,PR00707		G3DSA:3.40.532.10	SSF54001									
aly3598.15	Techylectin-5B	GO:0046872,GO:0005576,GO:0016337,GO:0030246	CG41520-PA				SM00186		PF00147	PS51406			G3DSA:4.10.530.10,G3DSA:3.90.215.10	SSF56496	35~62,324~344,119~139								
aly3598.16	Peroxiredoxin-6	GO:0016787,GO:0016209,GO:0016023,GO:0005829,GO:0016042,GO:0005764,GO:0004602,GO:0042744,GO:0008379,GO:0045454,GO:0051920,GO:0004601,GO:0055114	CG3083-PA			PIRSF000239			PF00578	PS51352			G3DSA:3.40.30.10	SSF52833		00480+1.11.1.15							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3598.17	Cdc42 homolog	GO:0006909,GO:0007264,GO:0030031,GO:0032794,GO:0030426,GO:0030036,GO:0030707,GO:0046664,GO:0035318,GO:0007165,GO:0031175,GO:0007411,GO:0007274,GO:0007275,GO:0005737,GO:0007254,GO:0030833,GO:0005634,GO:0016020,GO:0007349,GO:0051491,GO:0060446,GO:0008582,GO:0048477,GO:0005525,GO:0035099,GO:0050975,GO:0005912,GO:0003924,GO:0045177,GO:0042060,GO:0035011,GO:0035010,GO:0016028,GO:0045200,GO:0005938,GO:0007409,GO:0007286,GO:0030041,GO:0008045,GO:0005886,GO:0030424,GO:0007179,GO:0007266,GO:0030011,GO:0007015,GO:0010592,GO:0007010,GO:0050770,GO:0007396,GO:0030866,GO:0007391,GO:0005622,GO:0048813,GO:0008360,GO:0005515,GO:0046843	CG12530-PA				SM00173,SM00175,SM00174	TIGR00231	PF00071	PS51420	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly3598.18	Unknown		n/a																				
aly3598.19	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3598.2	5'-AMP-activated protein kinase subunit gamma-2	GO:0006633,GO:0009267,GO:0010800,GO:0006469,GO:0042595,GO:0035556,GO:0008603,GO:0071901,GO:0006629,GO:0005737,GO:0045787,GO:0005634,GO:0005654,GO:0004674,GO:0006110,GO:0008607,GO:0004679,GO:0005524,GO:0006468,GO:0031588,GO:0042632,GO:0019217,GO:0006914,GO:0016208,GO:0019901,GO:0004862,GO:0043531,GO:2001020,GO:0030295,GO:0005615,GO:0030730,GO:0005977,GO:0030554,GO:0005829,GO:0045860	CG17299-PR				SM00116,SM00116,SM00116,SM00116		PF00571,PF00571,PF00571	PS51371,PS51371,PS51371,PS51371			G3DSA:3.10.580.10,G3DSA:3.10.580.10	SSF54631,SSF54631									
aly3598.20	Unknown		n/a																				
aly3598.3	Unknown		n/a																				
aly3598.4	Prostatic acid phosphatase	GO:0052642,GO:0051930,GO:0016791,GO:0005615,GO:0060168,GO:0016311,GO:0042131,GO:0016021,GO:0008253,GO:0006144,GO:0030175,GO:0005765,GO:0009117,GO:0012506,GO:0005886,GO:0006772,GO:0005634,GO:0046085,GO:0003993,GO:0070062	CG7899-PB						PF00328			PS00616	G3DSA:3.40.50.1240	SSF53254										
aly3598.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3598.6	D-3-phosphoglycerate dehydrogenase	GO:0019530,GO:0006566,GO:0006564,GO:0021915,GO:0070062,GO:0021782,GO:0043209,GO:0051287,GO:0031175,GO:0006541,GO:0070314,GO:0021510,GO:0004617,GO:0006544,GO:0009070,GO:0010468,GO:0055114,GO:0009448	CG6287-PA						PF00389,PF02826			PS00065	G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF52283,SSF51735									
aly3598.7	Unknown		CG3777-PB																				
aly3598.8	Autophagy-related protein 9A	GO:0055037,GO:0000421,GO:0000422,GO:0034067,GO:0031410,GO:0016021,GO:0005802,GO:0005776,GO:0000045,GO:0034497,GO:0010508,GO:0044805,GO:0003674,GO:0032688,GO:0015031,GO:0031902,GO:0034727,GO:0045087,GO:0000407	CG3615-PB						PF04109														
aly3598.9	Dephospho-CoA kinase domain-containing protein	GO:0016310,GO:0004140,GO:0005524,GO:0015937	CG1939-PA	MF_00376				TIGR00152	PF01121	PS51219			G3DSA:3.40.50.300	SSF52540		00770+2.7.1.24			UPA00241				
aly35996.1	Unknown		n/a												93~113								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly36.1	Delta-1-pyrroline-5-carboxylate synthase	GO:0019240,GO:0008652,GO:0004349,GO:0006561,GO:0006592,GO:0044822,GO:0005811,GO:0005737,GO:0004350,GO:0005524,GO:0005743,GO:0006536,GO:0005739,GO:0017084,GO:0055129,GO:0055114	CG7470-PA	MF_00412		PIRSF036429		TIGR00407,TIGR01092	PF00696,PF00171		PR00474,PR00474,PR00474,PR00474	PS01223,PS00902	G3DSA:3.40.309.10,G3DSA:3.40.1160.10,G3DSA:3.40.605.10,G3DSA:3.40.605.10	SSF53633,SSF53720		00330+1.2.1.41,00332+1.2.1.41+2.7.2.11,00332+2.7.2.11,00330+2.7.2.11,00332+1.2.1.41,00330+1.2.1.41+2.7.2.11	REACT_13		UPA00098				
aly36.2	Unknown		CG13315-PA																				
aly36.3	Unknown		n/a																				
aly36008.1	Acetyl-CoA carboxylase	GO:0006633,GO:0005737,GO:0000902,GO:0005811,GO:0005623,GO:0003989,GO:0004075,GO:0046872,GO:0005524,GO:2001295	CG11198-PA						PF08326							00253+6.4.1.2,00620+6.4.1.2,00640+6.4.1.2,00061+6.4.1.2,00254+6.4.1.2,00720+6.4.1.2	REACT_1505,REACT_22258	PWY-7388,PWY-5789,PWY-5743,PWY-5744,PWY-6722,PWY-6679,PWY-4381	UPA00655				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly36035.1	Unknown		n/a						PF05380														
aly36049.1	11-beta-hydroxysteroid dehydrogenase like 4B	GO:0016021,GO:0006694,GO:0008152,GO:0016491	CG31548-PA						PF00106				G3DSA:3.40.50.720	SSF51735									
aly3607.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG4797-PB						PF00083					SSF103473									
aly3607.2	Facilitated trehalose transporter Tret1	GO:0022891,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG4607-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly3607.3	Unknown		CG42644-PB									PS00290	G3DSA:2.60.40.10										
aly36088.1	Copper-transporting ATPase 2	GO:0005737,GO:0005794,GO:0004008,GO:0005507,GO:0006878,GO:0048085,GO:0006825,GO:0016021,GO:0055065,GO:0048066,GO:0000166,GO:0002164,GO:0030001,GO:0005886,GO:0019829,GO:0005375,GO:0046872,GO:0005524	CG1886-PB						PF00403,PF00403	PS50846,PS50846	PR00942,PR00942		G3DSA:3.30.70.100,G3DSA:3.30.70.100	SSF55008,SSF55008									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly361.1	Tripartite motif-containing protein 45	GO:0005737,GO:0045171,GO:0060348,GO:0005654,GO:0008270,GO:0005622	CG8419-PA				SM00336,SM00336,SM00184		PF00643,PF00097	PS50119,PS50119		PS00518	G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:4.10.45.10	SSF57850,SSF57845										
aly361.10	SUN domain-containing ossification factor	GO:0046331,GO:0005791,GO:0046850,GO:0016021,GO:0016020,GO:0030867,GO:0001503,GO:0032967,GO:0045669,GO:0007275	CG31678-PB						PF07738	PS51469,PS51257			G3DSA:2.60.120.260	SSF49785	800~820								
aly361.11	Methyltransferase-like protein 13	GO:0005575,GO:0008168,GO:0008152	CG2614-PA						PF01564,PF08241				G3DSA:3.40.50.150,G3DSA:3.40.50.150	SSF53335,SSF53335									
aly361.12	Eukaryotic translation initiation factor 2-alpha kinase 1	GO:0005737,GO:0004686,GO:0045793,GO:0071011,GO:0005829,GO:0017148,GO:0006468,GO:0000398,GO:0004674,GO:0004672,GO:0006417,GO:0071013,GO:0005524	CG1609-PC				SM00220		PF00069,PF00069	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:3.30.200.20	SSF56112,SSF56112,SSF56112	539~577								
aly361.13	Uncharacterized protein sll1483	GO:0005575,GO:0008150,GO:0003674,GO:0005615,GO:0030288	CG43333-PA				SM00554,SM00554		PF02469,PF02469	PS50213			G3DSA:2.30.180.10,G3DSA:2.30.180.10	SSF82153,SSF82153	130~150								
aly361.14	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly361.15	Dual specificity tyrosine-phosphorylation-regulated kinase 2	GO:0006468,GO:0007608,GO:0042048,GO:0005829,GO:0004674,GO:0016740,GO:0009416,GO:0004713,GO:0004672,GO:0004712,GO:0005524	CG4551-PG				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly361.16	Dedicator of cytokinesis protein 7	GO:0005089,GO:0006909,GO:0031175,GO:0005085,GO:0030426,GO:0030424,GO:0000226,GO:0045200,GO:0033138,GO:0005925,GO:0050767,GO:0045178,GO:0002244,GO:0043005,GO:0035011,GO:0035010,GO:0022027,GO:0007409,GO:0007264,GO:0035023,GO:0043473,GO:0090630,GO:0005622,GO:0005575,GO:0048365	CG11376-PA						PF14429,PF06920,PF11878	PS51650,PS51651													
aly361.17	Chromobox protein homolog 5	GO:0035064,GO:0007596,GO:0031618,GO:0070491,GO:0005719,GO:0031452,GO:0005634,GO:0005635,GO:0005654,GO:0005730,GO:0017053,GO:0000118,GO:0045892,GO:0000776,GO:0005720,GO:0000792,GO:0030674,GO:0000122,GO:0035097,GO:0010369,GO:0045944,GO:0016032,GO:0003682	CG7041-PA				SM00300,SM00298,SM00298		PF00385,PF01393	PS50013,PS50013	PR00504,PR00504,PR00504	PS00598	G3DSA:2.40.50.40,G3DSA:2.40.50.40	SSF54160,SSF54160	104~124								
aly361.18	Nuclear factor of activated T-cells 5	GO:0005737,GO:0007165,GO:0070884,GO:0007588,GO:0003700,GO:0006970,GO:0005634,GO:0006366,GO:0007476,GO:0001816,GO:0006355,GO:0001077,GO:0045944,GO:0006351,GO:0009651,GO:2001020,GO:0000978,GO:2000301,GO:0046580	CG11172-PB				SM00429		PF16179,PF00554	PS50254	PR01789,PR01789,PR01789		G3DSA:2.60.40.340,G3DSA:2.60.40.10	SSF49417,SSF81296									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly361.19	Unknown		n/a												149~176,217~240								
aly361.2	Heparin sulfate O-sulfotransferase	GO:0007424,GO:0016021,GO:0008146,GO:0004394,GO:0000139,GO:0007165,GO:0008152	CG10234-PA						PF03567				G3DSA:3.40.50.300	SSF52540	27~47								
aly361.20	Prolactin regulatory element-binding protein	GO:0048208,GO:0044267,GO:0006888,GO:0000902,GO:0030968,GO:0006355,GO:0009306,GO:0018279,GO:0005634,GO:0016020,GO:0000139,GO:0036498,GO:0061024,GO:0006351,GO:0005515,GO:0003677,GO:0015031,GO:0005789,GO:0043687,GO:0016021,GO:0005783	CG9175-PA				SM00320,SM00320			PS50082,PS50294,PS50082			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978										
aly361.21	BTB/POZ domain-containing protein 3	GO:0048813,GO:0005829,GO:0005634,GO:0021987,GO:0005515	CG17068-PA				SM00875,SM00225		PF07707,PF00651	PS50097			G3DSA:3.30.710.10	SSF54695										
aly361.22	Type II inositol 1,4,5-trisphosphate 5-phosphatase	GO:0016020,GO:0051056,GO:0055037,GO:0007165,GO:0043087,GO:0005737,GO:0001701,GO:0052658,GO:0016021,GO:0005770,GO:0046856,GO:0004445,GO:0046872,GO:0031901,GO:0005794,GO:0005793,GO:0030317,GO:0034593,GO:0007283,GO:0070613,GO:0005886,GO:0007264,GO:0000910,GO:0030675,GO:0006897,GO:0030670,GO:0032187,GO:0005829,GO:0043647,GO:0004439,GO:0005100,GO:2000431,GO:0005769,GO:0044281	CG3573-PA				SM00324,SM00128		PF03372,PF16776,PF00620	PS50238			G3DSA:2.60.40.360,G3DSA:1.10.555.10,G3DSA:3.60.10.10	SSF48350,SSF48350,SSF56219	497~517		REACT_11044							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly361.23	Unknown	GO:0003677	n/a							PS51031													
aly361.24	Stathmin-4	GO:0031110,GO:0005794,GO:0015631,GO:0007017,GO:0007399,GO:0008017,GO:0007019,GO:0051493,GO:0005737,GO:0008088,GO:0030424,GO:0043005,GO:0031175,GO:0007298,GO:0030426,GO:0005875,GO:0008354	CG31641-PD						PF00836	PS51663	PR00345,PR00345,PR00345			SSF101494	33~60,84~104,142~169,106~126,178~205									
aly361.25	Pre-mRNA-splicing factor CWC22 homolog	GO:0016607,GO:0005730,GO:0003723,GO:0022008,GO:0008380,GO:0005681,GO:0006397	CG9004-PA				SM00544,SM00543		PF02847	PS51366			G3DSA:1.25.40.180	SSF48371									
aly361.26	Unknown		n/a						PF14769														
aly361.27	rRNA-processing protein UTP23 homolog	GO:0070181,GO:0032040,GO:0006909,GO:0005730,GO:0044822,GO:0006364	CG17652-PB						PF04900				G3DSA:3.40.50.1010										
aly361.28	Anaphase-promoting complex subunit 13	GO:0070979,GO:0005575,GO:0003674,GO:0008150,GO:0007067,GO:0051301,GO:0005680	CG33981-PC						PF05839										UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly361.29	Ras-related protein Rab-5B	GO:0050803,GO:0035220,GO:0030139,GO:0048227,GO:0045202,GO:0007298,GO:0007067,GO:0048488,GO:0035088,GO:0031982,GO:0006325,GO:0016189,GO:0005811,GO:0007349,GO:0048803,GO:0048477,GO:0031901,GO:0005525,GO:0008285,GO:0019882,GO:0003924,GO:0016321,GO:0016348,GO:0032482,GO:0007409,GO:0005886,GO:0046664,GO:0007264,GO:0030100,GO:0034058,GO:0070062,GO:0007032,GO:0042470,GO:0007220,GO:0006897,GO:0016192,GO:0043025,GO:0048813,GO:0019003,GO:0005515,GO:0015031,GO:0005769	CG3664-PI				SM00173,SM00174,SM00175,SM00176	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly361.3	Probable UMP/CMP kinase 1	GO:0005737,GO:0006139,GO:0019205,GO:0006207,GO:0005634,GO:0004127,GO:0004017,GO:0009041,GO:0006221,GO:0005524	CG9541-PD						PF00406,PF00406		PR00094,PR00094,PR00094	PS00113	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540		00230+2.7.4.3		PWY-7219	UPA00588				
aly361.30	Reticulocalbin 2	GO:0007030,GO:0005576,GO:0005509,GO:0005788,GO:0005783	CG31650-PA				SM00054,SM00054,SM00054,SM00054,SM00054		PF13202,PF13202,PF13833	PS50222,PS50222,PS50222,PS50222,PS50222		PS00018,PS00018,PS00018,PS00018,PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473,SSF47473,SSF47473									
aly361.31	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly361.32	Enhancer of mRNA-decapping protein 4	GO:0033962,GO:0035195,GO:0005634,GO:0000932,GO:0050832,GO:0005515,GO:0045451	CG6181-PA						PF16529,PF16529	PS50294,PS50082			G3DSA:2.130.10.10	SSF50978									
aly361.33	Calcium channel flower	GO:0030672,GO:0005262,GO:0016021,GO:0044214,GO:0046530,GO:0030054,GO:0030285,GO:0042981,GO:0048488	CG6151-PA				SM01077		PF10233														
aly361.34	Ragulator complex protein LAMTOR5	GO:0005737,GO:0071230,GO:0019079,GO:0061462,GO:0005764,GO:0043154,GO:0008361,GO:0043066,GO:0071986,GO:0032008,GO:0043547	CG14812-PA						PF16672		PR02092,PR02092			SSF103196									
aly361.35	Unknown		n/a												91~125,158~185								
aly361.4	Adenylate kinase isoenzyme 1	GO:0005737,GO:0006139,GO:0070062,GO:0001520,GO:0019205,GO:0046034,GO:0009142,GO:0005886,GO:0004017,GO:0007050,GO:0004550,GO:0006172,GO:0006165,GO:0004849,GO:0046033,GO:0036126,GO:0005524	CG17146-PA	MF_00235					PF00406		PR00094,PR00094,PR00094,PR00094	PS00113	G3DSA:3.40.50.300	SSF52540		00230+2.7.4.3		PWY-7219	UPA00588				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly361.5	Homeobox protein TGIF2	GO:0043565,GO:0006351,GO:0038092,GO:0006367,GO:0045666,GO:0000122,GO:0003700,GO:0005813,GO:0005634,GO:0003714,GO:0010467,GO:0005654,GO:0006355,GO:0007283,GO:0001077,GO:0045893,GO:0010470,GO:0003677,GO:0007179,GO:0060041	CG8819-PC				SM00389		PF05920,PF00406	PS50071	PR00094,PR00094,PR00094		G3DSA:1.10.10.60,G3DSA:3.40.50.300	SSF52540,SSF46689		00230+2.7.4.3		PWY-7219	UPA00588				
aly361.6	Unknown		n/a																				
aly361.7	Collectin-11	GO:0032502,GO:0005581,GO:0030246,GO:0005576,GO:0007275,GO:0005537	CG13587-PA				SM00034		PF00059	PS50041		PS00615	G3DSA:3.10.100.10	SSF56436									
aly361.8	Calcium and integrin-binding protein 1	GO:0032433,GO:0030154,GO:0042383,GO:0005815,GO:0032587,GO:0016324,GO:0007229,GO:0006915,GO:0030426,GO:0007602,GO:0030027,GO:0007283,GO:0008597,GO:0055074,GO:0051301,GO:0007155,GO:0048471,GO:0001525,GO:0005634,GO:0007049,GO:0005509	CG9236-PB				SM00054,SM00054,SM00054		PF13499	PS50222,PS50222		PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									
aly361.9	Oligosaccharyl transferase complex subunit ostc-B	GO:0005575,GO:0008150,GO:0016021,GO:0003674	CG9662-PA						PF04756														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3613.1	Acyl-CoA:lysophosphatidylglycerol acyltransferase 1	GO:0005737,GO:0008654,GO:0016021,GO:0016020,GO:0005789,GO:0016746	n/a											SSF69593									
aly36138.1	Rho-related BTB domain-containing protein 1	GO:0005575,GO:0003924,GO:0005622,GO:0035011,GO:0007264,GO:0005525	CG5701-PB						PF00651				G3DSA:3.40.50.300,G3DSA:3.30.710.10	SSF54695,SSF52540									
aly3614.1	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098	PS50292	PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									
aly3614.2	Unknown		n/a																				
aly36155.1	Leishmanolysin-like peptidase	GO:0045842,GO:0007076,GO:0019915,GO:0008233,GO:0051225,GO:0051301,GO:0005737,GO:0007100,GO:0016020,GO:0008406,GO:0022900,GO:0008354,GO:0006508,GO:0046872,GO:0004222,GO:0051298,GO:0031252,GO:0007052,GO:0007155,GO:0007420,GO:0006338,GO:0007444,GO:1902769	CG3953-PA						PF01457				G3DSA:3.10.170.20	SSF55486									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3616.1	Ras-related protein Rap-2c	GO:0055038,GO:0031954,GO:0055037,GO:0090557,GO:0005923,GO:0005737,GO:0070062,GO:0016020,GO:0003713,GO:0061097,GO:0005525,GO:0030336,GO:0044291,GO:0003924,GO:1903506,GO:0032486,GO:0005886,GO:0006184,GO:0022008,GO:0007264,GO:0030718,GO:0005829,GO:0019003	CG3204-PA				SM00173,SM00175,SM00174	TIGR00231	PF00071	PS51257,PS51421	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly3616.10	Unknown		n/a																				
aly3616.11	Unknown		n/a								PR00021,PR00021,PR00021,PR00021												
aly3616.12	Unknown		n/a				SM00032,SM00032		PF00084	PS50923,PS50923			G3DSA:2.10.70.10,G3DSA:2.10.70.10	SSF57535									
aly3616.13	Unknown		n/a												280~300								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3616.14	Guanylate kinase	GO:0006163,GO:0004385,GO:0046939,GO:0005524	CG11811-PA				SM00072	TIGR03263	PF00625	PS50052		PS00856	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.30.63.10	SSF52540	129~149	00230+2.7.4.8		PWY-7221					
aly3616.15	G2/mitotic-specific cyclin-B	GO:0000086,GO:0008608,GO:0007067,GO:0051301,GO:0005737,GO:0001700,GO:0005819,GO:0035186,GO:0005634,GO:0000281,GO:0016538,GO:0009987,GO:0000092,GO:0006974,GO:0007079,GO:0035561,GO:0019908,GO:0051233,GO:0000775,GO:0000910,GO:0019901,GO:0000079,GO:0045495	CG3510-PA			PIRSF001771	SM00385,SM00385		PF00134,PF02984			PS00292	G3DSA:1.10.472.10,G3DSA:1.10.472.10	SSF47954,SSF47954	122~149								
aly3616.16	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246	n/a				SM00034		PF00059	PS50041,PS50041			G3DSA:3.10.100.10,G3DSA:3.10.100.10	SSF56436,SSF56436									
aly3616.17	Lachesin	GO:0007424,GO:0016331,GO:0035151,GO:0050767,GO:0009986,GO:0019991,GO:0035160,GO:0005575,GO:0042803,GO:0005918,GO:0061343,GO:0008150,GO:0043005,GO:0005886,GO:0003674,GO:0016337,GO:0007156,GO:0043025,GO:0031225	CG42343-PC				SM00408,SM00408,SM00408,SM00409,SM00409,SM00409		PF07679,PF07679,PF07679	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly3616.2	Phospholipid scramblase 2	GO:0017128,GO:0017121,GO:0016021,GO:0005886,GO:0048812,GO:0007268,GO:0046872	CG32056-PA						PF03803					SSF54518									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3616.3	Phospholipid scramblase 2	GO:0017128,GO:0017121,GO:0016021,GO:0005886,GO:0048812,GO:0007268,GO:0046872	CG32056-PA						PF03803					SSF54518									
aly3616.4	Regulator of microtubule dynamics protein 1	GO:0005737,GO:0005874,GO:0000922	n/a										G3DSA:1.25.40.10	SSF48452									
aly3616.5	Protein peanut	GO:0042051,GO:0000281,GO:0070938,GO:0006184,GO:0005875,GO:0043065,GO:0045171,GO:0045172,GO:0007349,GO:0005739,GO:0003779,GO:0005525,GO:0031105,GO:0016324,GO:0008017,GO:0006915,GO:0003924,GO:0032154,GO:0008152,GO:0005886,GO:0005940,GO:0000910,GO:0031625,GO:0000915,GO:0042803	CG8705-PB						PF00735	PS51719			G3DSA:3.40.50.300	SSF52540	532~573,495~518								
aly3616.6	Alpha-catulin	GO:0005856,GO:0015629,GO:0005829,GO:0005198,GO:0003779,GO:0005915,GO:0005886,GO:0007155,GO:0007266	CG2987-PC						PF01044,PF01044				G3DSA:1.20.120.230,G3DSA:1.20.120.230,G3DSA:1.20.120.230	SSF47220,SSF47220,SSF47220									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3616.7	Myosin-IIIa	GO:0032433,GO:0060002,GO:0008104,GO:0018107,GO:0042385,GO:0030175,GO:1990146,GO:0033227,GO:0009416,GO:0005875,GO:0005737,GO:0016028,GO:0016062,GO:0042623,GO:0006886,GO:0016027,GO:0051491,GO:0046777,GO:0004674,GO:0016459,GO:0004713,GO:0004672,GO:0003774,GO:0005524,GO:0005856,GO:0006468,GO:0032426,GO:0007605,GO:0007604,GO:0007601,GO:0007603,GO:0030898,GO:0043531,GO:0031941,GO:0000146,GO:0048839,GO:0007010,GO:0016059,GO:0035091,GO:0050896,GO:0018105,GO:0016461,GO:0001917,GO:0005516,GO:0004702,GO:0045494	CG5125-PB				SM00242,SM00015,SM00015,SM00015,SM00220		PF00069,PF00063,PF00612,PF00612,PF00612	PS51456,PS50096,PS50011,PS50096,PS50096	PR00193,PR00193,PR00193,PR00193,PR00193	PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10,G3DSA:3.40.50.300	SSF56112,SSF52540,SSF52540	50~77									
aly3616.8	DNA-directed RNA polymerase II subunit RPB1	GO:0005634,GO:0006366,GO:0005703,GO:0005700,GO:0005665,GO:0003677,GO:0007095,GO:0046872,GO:0003899	CG1554-PA				SM00663		PF04998,PF05000,PF04992,PF00623,PF04983,PF04990,PF05001,PF05001,PF05001,PF05001,PF05001,PF05001,PF05001,PF05001,PF05001,PF04997		PR01217,PR01217,PR01217,PR01217,PR01217,PR01217	PS00115,PS00115,PS00115,PS00115,PS00115,PS00115,PS00115,PS00115,PS00115,PS00115,PS00115,PS00115,PS00115,PS00115	G3DSA:3.30.1490.180,G3DSA:2.40.40.20,G3DSA:2.40.40.20	SSF64484		00240+2.7.7.6,00230+2.7.7.6	REACT_1788							
aly3616.9	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly362.1	Dystonin	GO:0005635,GO:0015629,GO:0035371,GO:0009898,GO:0030424,GO:0014704,GO:0005925,GO:0030056,GO:0030018,GO:0005737,GO:0001725,GO:0016023,GO:0031673,GO:0016020,GO:0005509,GO:0048471,GO:0042803,GO:0015630,GO:0042383,GO:0051010,GO:0005634,GO:0007050,GO:0005882,GO:0005938,GO:0007409,GO:0007155,GO:0005789,GO:0097481,GO:0097038,GO:0008090,GO:0046907,GO:0045104,GO:0005515,GO:0016021	n/a									PS00019	G3DSA:1.10.418.10	SSF47576									
aly362.2	Unknown		n/a																				
aly362.3	Unknown		n/a																				
aly3625.1	Unknown		n/a						PF00078														
aly3625.2	Unknown	GO:0003676	n/a							PS50879			G3DSA:3.30.420.10	SSF53098									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3625.3	Unknown		n/a																				
aly3625.4	Unknown	GO:0005575,GO:0007606,GO:0003674,GO:0005515	CG14948-PA				SM00409,SM00409			PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly36269.1	Src substrate protein p85	GO:0005783,GO:0007301,GO:0005905,GO:0048041,GO:0007298,GO:0005925,GO:0048260,GO:0030054,GO:0005856,GO:0001726,GO:0070064,GO:0070864,GO:0031532,GO:0006886,GO:0030027,GO:0002102,GO:0008360,GO:0097581,GO:0005886,GO:0030041,GO:0030516,GO:0043234,GO:0007010,GO:0043197,GO:0048870,GO:0030863,GO:0006898,GO:0030838,GO:0048812	CG3637-PA						PF02218,PF02218,PF02218	PS51090,PS51090,PS51090					1~21								
aly36280.1	Unknown		n/a																				
aly363.1	Unknown	GO:0016021,GO:0005886	CG11303-PC						PF00335					SSF48652,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly363.10	Bardet-Biedl syndrome 1 protein	GO:0006996,GO:0036064,GO:0050896,GO:0042384,GO:0035058,GO:0060170,GO:0005813,GO:0005829,GO:0001103,GO:0007601,GO:0043001,GO:0061512,GO:0003674,GO:0005119,GO:0005929,GO:0001895,GO:0005113,GO:0005930,GO:0045494,GO:0034464	CG14825-PA						PF14779				G3DSA:2.130.10.10	SSF50978									
aly363.11	Ephexin-1	GO:0005089,GO:0031594,GO:0016020,GO:0043547,GO:0042734,GO:0007480,GO:0043087,GO:0005829,GO:0009987,GO:0005085,GO:0030426,GO:0061002,GO:0035011,GO:0035025,GO:0046928,GO:0035023,GO:0048013,GO:0046875	CG42665-PD						PF00621	PS50010			G3DSA:1.20.900.10	SSF48065									
aly363.12	Ephexin-1	GO:0005089,GO:0031594,GO:0042734,GO:0007480,GO:0016020,GO:0030426,GO:0005737,GO:0035011,GO:0035025,GO:0046928,GO:0005515,GO:0048013,GO:0043087,GO:0061002	CG3799-PB				SM00326,SM00233		PF14604	PS50002			G3DSA:2.30.30.40,G3DSA:2.30.29.30	SSF50044,SSF50729									
aly363.13	Transmembrane emp24 domain-containing protein 5	GO:0070971,GO:0005794,GO:0018991,GO:0000003,GO:0005793,GO:0048193,GO:0005801,GO:0005215,GO:0016021,GO:0006810,GO:0033116,GO:0090161,GO:0005789,GO:0048042,GO:0015031	CG10733-PD						PF01105	PS50866				SSF101576	148~168								
aly363.14	tRNA pseudouridine synthase-like 1	GO:0008033,GO:0008138,GO:0006470,GO:0009982,GO:0005575,GO:0008150,GO:0003723,GO:0003674,GO:0001522	CG34140-PA	MF_00171			SM00195		PF00782,PF01416,PF01416	PS50054,PS50056		PS00383	G3DSA:3.90.190.10,G3DSA:3.30.70.660,G3DSA:3.30.70.580	SSF55120,SSF52799									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly363.15	Protein melted	GO:0008286,GO:0030730,GO:0006629,GO:0007398,GO:0035091,GO:0001708,GO:0010314,GO:0045464,GO:0008152,GO:0005886,GO:2001020,GO:0007422	CG8624-PC				SM00233			PS50003			G3DSA:1.25.10.10,G3DSA:2.30.29.30	SSF50729,SSF48371									
aly363.16	Cytoplasmic tRNA 2-thiolation protein 1	GO:0016779,GO:0000049,GO:0005829,GO:0032447,GO:0034227,GO:0002098	CG8078-PA	MF_03053					PF16503,PF01171			PS01263	G3DSA:3.40.50.620	SSF52402					UPA00988				
aly363.17	Mitochondrial ubiquitin ligase activator of nfkb 1-A	GO:0007165,GO:0030308,GO:0006919,GO:0000266,GO:0016874,GO:0005777,GO:0016567,GO:0031307,GO:0008270,GO:0004871,GO:0051646,GO:0007005,GO:0004842,GO:0042802,GO:0043123	CG1134-PA				SM00184		PF12483,PF13920	PS50089			G3DSA:3.30.40.10	SSF57850	249~276				UPA00143				
aly363.18	ATP-dependent RNA helicase DHX8	GO:0005737,GO:0000381,GO:0008380,GO:0071011,GO:0006396,GO:0005634,GO:0044822,GO:0000398,GO:0005524,GO:0005654,GO:0042802,GO:0004004,GO:0007286,GO:0022008,GO:0071013,GO:0005681,GO:0003723	CG8241-PA				SM00490,SM00316,SM00487,SM00847		PF00270,PF04408,PF00575,PF00271,PF07717	PS51192,PS50126,PS51194		PS00690	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:2.40.50.140	SSF52540,SSF50249									
aly363.19	Mediator of RNA polymerase II transcription subunit 9	GO:0001104,GO:0016592,GO:0006357,GO:0006366	CG42517-PC						PF07544					SSF140718,SSF140718									
aly363.2	Tetraspanin-6	GO:0039532,GO:0070062,GO:0016021,GO:0008150,GO:0003674,GO:0004871,GO:1901223,GO:0043123	CG9033-PB						PF00335	PS51257	PR00259,PR00259,PR00259			SSF48652									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly363.20	Uncharacterized protein NCBP2-AS2 homolog	GO:0016592	CG42518-PA												63~79								
aly363.21	GTP-binding protein 1	GO:0061014,GO:0005829,GO:0016020,GO:0003924,GO:0000177,GO:0005575,GO:0008152,GO:0044822,GO:0005525	CG5729-PA						PF00009	PS51722			G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:3.40.50.300	SSF50447,SSF50465,SSF52540									
aly363.22	Unknown		CG14442-PA																				
aly363.23	Unknown		n/a																				
aly363.24	RING finger protein 157	GO:0008270,GO:0005515	CG9941-PA				SM00184		PF13920	PS50089			G3DSA:3.30.40.10	SSF57850									
aly363.25	60S ribosomal protein L10	GO:0005737,GO:0005840,GO:0022625,GO:0051297,GO:0005622,GO:0003735,GO:0007052,GO:0000022,GO:0043025,GO:0006412,GO:0051298	CG17521-PE			PIRSF005590		TIGR00279	PF00252			PS01257	G3DSA:3.90.1170.10	SSF54686									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly363.26	DNA polymerase eta	GO:0005737,GO:0071494,GO:0006282,GO:0006290,GO:0000724,GO:0006281,GO:0019985,GO:0000731,GO:0070987,GO:0003887,GO:0006260,GO:0010225,GO:0046872,GO:0005654,GO:0003684	CG7143-PA						PF00817,PF11799	PS50173			G3DSA:3.30.1490.100,G3DSA:3.30.70.270	SSF100879,SSF56672	623~648	00240+2.7.7.7,00230+2.7.7.7							
aly363.27	Fidgetin-like protein 1	GO:0016787,GO:0000070,GO:0010569,GO:0051013,GO:0005813,GO:0000287,GO:0000091,GO:0008568,GO:0036078,GO:0031122,GO:0016887,GO:0046034,GO:0000228,GO:0005694,GO:0005524	CG3326-PA				SM00382		PF00004,PF09336			PS00674	G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540									
aly363.28	Josephin-1	GO:0005737,GO:0008242,GO:0005575,GO:0008150,GO:0005886,GO:0003674	CG3781-PA						PF02099	PS50957													
aly363.29	Apolipoprotein D	GO:0022626,GO:0005783,GO:0042246,GO:0048678,GO:0030425,GO:0000302,GO:0051895,GO:0010642,GO:0005615,GO:0014012,GO:2000405,GO:0048471,GO:0043025,GO:0007420,GO:0048662,GO:0006629,GO:0005215,GO:2000098,GO:0009267,GO:0042308,GO:0008340,GO:0034599,GO:0060588,GO:0070062,GO:1900016,GO:0007568,GO:0015485,GO:0042493,GO:0071638,GO:0006006	CG4604-PA						PF00061				G3DSA:2.40.128.20	SSF50814									
aly363.3	Tetraspanin-14	GO:0051604,GO:0016021,GO:0097197,GO:0019899,GO:0090002,GO:0045747,GO:0003674,GO:0005886,GO:0008150,GO:0009986	CG9033-PB			PIRSF002419			PF00335		PR00259,PR00259,PR00259			SSF48652									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly363.30	Probable cytosolic Fe-S cluster assembly factor GA29080	GO:0022008,GO:0046872,GO:0051539,GO:0016226	CG17683-PA				SM00902		PF02906,PF02256				G3DSA:3.40.50.1780,G3DSA:3.40.50.1780,G3DSA:4.10.260.20	SSF53920,SSF53920									
aly363.31	Dynein light chain 4, axonemal	GO:0005737,GO:0007017,GO:0042623,GO:0007018,GO:0003774,GO:0005929,GO:0030286,GO:0005874,GO:0005875	CG8407-PA						PF01221				G3DSA:3.30.740.10	SSF54648									
aly363.32	ARF GTPase-activating protein GIT2	GO:0005737,GO:0046872,GO:0032312,GO:0005096,GO:0031252,GO:0005654,GO:0008277,GO:0008060,GO:0008270,GO:0005925,GO:0048266,GO:0007525	CG16728-PA				SM00105,SM00555,SM00555		PF12205,PF01412,PF13637,PF08518,PF08518	PS50297,PS50088,PS50115	PR00405,PR00405,PR00405		G3DSA:1.25.40.20	SSF48403,SSF57863	454~495								
aly363.33	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	GO:0007030,GO:0034389,GO:0006487,GO:0016021,GO:0005811,GO:0005789,GO:0012505,GO:0022008,GO:0004579,GO:0018279	CG9022-PA						PF03345							00513+2.4.99.18,00510+2.4.99.18			UPA00378				
aly363.34	Unknown		n/a																				
aly363.35	Leucine-rich repeat flightless-interacting protein 2	GO:0009950,GO:0030275,GO:0016055,GO:0007527	CG8578-PA						PF09738						23~103								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly363.36	Mediator of RNA polymerase II transcription subunit 19	GO:0001104,GO:0016592,GO:0006357,GO:0006351	CG5546-PA						PF10278														
aly363.37	Chromatin modification-related protein png2	GO:0006351,GO:0016573,GO:0033698,GO:0032221,GO:0070210,GO:0005634,GO:0035267,GO:0035064,GO:0006355,GO:0046580,GO:0003676,GO:0071456,GO:2001020,GO:0006338,GO:0005829,GO:0016568,GO:0008270	CG4903-PA				SM00249,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50016,PS50157		PS00028,PS00028,PS00028,PS01359,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.40.10	SSF57903,SSF57667										
aly363.38	C-factor	GO:0004090,GO:0030435,GO:0005576,GO:0008152,GO:0016491	CG10964-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735	34~54								
aly363.39	Thioredoxin reductase 1, mitochondrial	GO:0005737,GO:0050661,GO:0050660,GO:0004362,GO:0016209,GO:0005739,GO:0005875,GO:0006974,GO:0042803,GO:0005829,GO:0008340,GO:0022008,GO:0001666,GO:0045454,GO:0055114,GO:0004791	CG2151-PB			PIRSF000350		TIGR01438	PF02852,PF07992		PR00368,PR00368,PR00368,PR00368,PR00411,PR00411,PR00411,PR00411,PR00411,PR00411,PR00411,PR00411,PR00411,PR00411,PR00411	PS00076	G3DSA:3.50.50.60,G3DSA:3.30.390.30,G3DSA:3.50.50.60	SSF55424,SSF51905,SSF51905,SSF51905		00450+1.8.1.9,00240+1.8.1.9								
aly363.4	Leukocyte antigen CD37	GO:0008285,GO:0030886,GO:0070062,GO:0016021,GO:0016020,GO:0002920,GO:0003674,GO:0001772,GO:0008150,GO:0042832,GO:0002639,GO:0050688	CG9033-PB						PF00335					SSF48652									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly363.40	Matrix metalloproteinase-25	GO:0007591,GO:0030425,GO:0031012,GO:0048102,GO:0035001,GO:0008270,GO:0008237,GO:0031225,GO:0016021,GO:0005509,GO:0006508,GO:0060022,GO:0002168,GO:0004222,GO:0035071,GO:0035159,GO:0009986,GO:0042060,GO:0006954,GO:0005886,GO:0007155,GO:0010952,GO:0007424,GO:0042246,GO:0007561,G	CG4859-PC			PIRSF001191	SM00120,SM00120,SM00120,SM00120,SM00235		PF00045,PF00413,PF01471	PS51642,PS51642,PS51642	PR00138,PR00138,PR00138,PR00138,PR00138		G3DSA:3.40.390.10,G3DSA:2.110.10.10	SSF50923,SSF47090,SSF55486									
aly363.41	WD repeat-containing protein 66	GO:0005515	n/a				SM00320,SM00320,SM00320,SM00320,SM00320						G3DSA:2.130.10.10,G3DSA:1.10.238.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978,SSF50978,SSF50978,SSF47473									
aly363.42	B-cell CLL/lymphoma 7 protein family member B	GO:0005575,GO:0008150,GO:0003674	CG17252-PA						PF04714														
aly363.43	Transmembrane GTPase Marf	GO:0070584,GO:0019896,GO:0010636,GO:0034389,GO:0007029,GO:0016021,GO:0003924,GO:0005740,GO:0090140,GO:0008053,GO:0005741,GO:0006697,GO:0005886,GO:0006184,GO:0005525,GO:0008344,GO:0007005,GO:0034976	CG3869-PD						PF04799,PF00350	PS51718			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	406~426								
aly363.44	Germinal-center associated nuclear protein	GO:0005737,GO:0005643,GO:0005829,GO:0031965,GO:0002376,GO:0015031,GO:0051028,GO:0005634	CG3437-PB						PF03399														
aly363.45	2-oxoglutarate dehydrogenase, mitochondrial	GO:0030976,GO:0006099,GO:0006096,GO:0009353,GO:0031966,GO:0005759,GO:0004591,GO:0006091,GO:0046872,GO:0005875	CG11661-PA				SM00861	TIGR00239	PF00676,PF16870,PF16078,PF02779				G3DSA:3.40.50.970,G3DSA:3.40.50.970	SSF52518,SSF52518		00380+1.2.4.2,00020+1.2.4.2,00310+1.2.4.2		PWY-5084					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly363.46	Sugar transporter SWEET1	GO:0006310,GO:0005794,GO:0051119,GO:0016021,GO:0000139,GO:0005886,GO:0034219	CG7272-PA						PF03083														
aly363.47	DnaJ homolog subfamily C member 16	GO:0045454,GO:0016021,GO:0005623	CG40178-PB				SM00271		PF00226,PF00085	PS51352,PS50076	PR00625,PR00625,PR00625,PR00625	PS00636	G3DSA:1.10.287.110,G3DSA:3.40.30.10	SSF46565,SSF52833	487~507								
aly363.48	DnaJ homolog subfamily C member 16	GO:0045454,GO:0016021,GO:0005623	CG40178-PB												5~25								
aly363.49	MICOS complex subunit Mic10	GO:0003674,GO:0016021,GO:0008150,GO:0005739,GO:0005743	CG41128-PB						PF04418														
aly363.5	Superoxide dismutase [Cu-Zn] 2	GO:0005507,GO:0005615,GO:0005634,GO:0005739,GO:0006979,GO:0019430,GO:0006801,GO:0009650,GO:0004784,GO:0046872,GO:0005783,GO:0005829,GO:0055114,GO:0008270	CG9027-PE						PF00080		PR00068,PR00068,PR00068,PR00068	PS00087,PS00332	G3DSA:2.60.40.200	SSF49329				PWY-6854					
aly363.50	APOPT family protein CG14806, mitochondrial	GO:0005575,GO:0008150,GO:0003674,GO:0005739	CG14806-PA						PF10231						63~83								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly363.51	Unknown		n/a																				
aly363.52	Alpha-ketoglutarate-dependent dioxygenase alkB homolog 2	GO:0006307,GO:0008198,GO:0015630,GO:0016706,GO:0035511,GO:0005634,GO:0005654,GO:0043734,GO:0051747	n/a											SSF51197									
aly363.53	Tetratricopeptide repeat protein 30A	GO:0030992,GO:0042384,GO:0018095,GO:0005215,GO:0042073,GO:0005879,GO:0005929	CG5142-PC				SM00028,SM00028,SM00028,SM00028		PF07719,PF13414	PS50293,PS50293,PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452,SSF48452	495~515								
aly363.54	Rab5 GDP/GTP exchange factor	GO:0060368,GO:0055037,GO:0006612,GO:0005085,GO:0030139,GO:0008270,GO:0003677,GO:0048261,GO:0045177,GO:0043547,GO:0043305,GO:0007474,GO:0002686,GO:0031398,GO:0035214,GO:0017137,GO:0017112,GO:0032483,GO:0050728,GO:0046580,GO:0006897,GO:0061630,GO:0031982,GO:0040015,GO:1900165,GO:1900235,GO:0016567,GO:0033004,GO:0001933,GO:0005769	CG9139-PA				SM00259,SM00167		PF02204,PF01754	PS51205,PS51036				SSF109993,SSF57716									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly363.55	E3 ubiquitin-protein ligase SIAH1	GO:0008022,GO:0007465,GO:0030154,GO:0008270,GO:0007283,GO:0061630,GO:0007275,GO:0007049,GO:0005737,GO:0004842,GO:0005634,GO:0030877,GO:0042787,GO:0006508,GO:2001244,GO:0051402,GO:0005886,GO:0016874,GO:0043621,GO:0031648,GO:0007423,GO:0005829,GO:0010498,GO:0000151,GO:0045676,GO:0016567,GO:0006511,GO:0005515,GO:0043161,GO:0005769	CG9949-PA						PF03145	PS51081,PS50089			G3DSA:3.90.890.10,G3DSA:3.30.40.10,G3DSA:2.60.210.10	SSF49599,SSF57850					UPA00143				
aly363.56	Adhesion G-protein coupled receptor G4	GO:0016021,GO:0007186,GO:0007218,GO:0004930	CG11318-PA				SM00303		PF01825,PF00002	PS50261,PS50221				SSF81321									
aly363.57	Dynein assembly factor 3, axonemal homolog	GO:0005575,GO:0008150,GO:0030030,GO:0003674,GO:0005737	CG17669-PA						PF14740,PF14737														
aly363.58	Unknown		n/a																				
aly363.59	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly363.6	Unknown		n/a																				
aly363.60	Disintegrin and metalloproteinase domain-containing protein 22	GO:0005178,GO:0004222,GO:0016021,GO:0030424,GO:0022011,GO:0007155,GO:0007162,GO:0008270,GO:0006509,GO:0008344,GO:0007417	CG42252-PJ				SM00050,SM00608		PF00200,PF07974,PF01421,PF01562,PF08516	PS50215,PS50026,PS50214	PR00289,PR00289	PS01186,PS00022,PS00427	G3DSA:3.40.390.10,G3DSA:4.10.70.10	SSF55486,SSF57552									
aly363.61	Unknown		n/a												197~228								
aly363.62	Carbonyl reductase [NADPH] 1	GO:0005737,GO:0042373,GO:0004090,GO:0047021,GO:0050221,GO:0017144	n/a						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly363.63	Unknown		n/a																				
aly363.64	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly363.65	Exonuclease	GO:0004518,GO:0004527,GO:0046872,GO:0003677	CG8366-PA						PF09588				G3DSA:3.90.320.10	SSF52980									
aly363.7	Superoxide dismutase [Cu-Zn]	GO:0000187,GO:0008270,GO:0009408,GO:0000303,GO:0032287,GO:0046716,GO:0031012,GO:0060088,GO:0060047,GO:0043524,GO:0005739,GO:0008340,GO:0043085,GO:0060087,GO:0005737,GO:0006302,GO:0050665,GO:0031410,GO:0005634,GO:0051087,GO:0005777,GO:0006309,GO:0010033,GO:0006749,GO:0008217,GO:0005507,GO:0043025,GO:0045541,GO:0042803,GO:0007626,GO:0002262,GO:0006879,GO:0032839,GO:0007605,GO:0060052,GO:0016209,GO:0045859,GO:0072593,GO:0048678,GO:0045471,GO:0007283,GO:0001541,GO:0004784,GO:0051881,GO:0001895,GO:0006979,GO:0055114,GO:0005615,GO:0043234,GO:0019226,GO:0046872,GO:0007568,GO:0007569,GO:0042542,GO:0005829,GO:0040014,GO:0042493,GO:0019430,GO:0030346,GO:0001819,GO:0007566,GO:0006801	CG11793-PA						PF00080		PR00068,PR00068,PR00068,PR00068		G3DSA:2.60.40.200	SSF49329				PWY-6854					
aly363.8	Acyl-CoA-binding protein homolog	GO:0042049,GO:0006810,GO:0008289,GO:0000062	CG8498-PA						PF00887	PS51228	PR00689,PR00689,PR00689,PR00689	PS00880	G3DSA:1.20.80.10	SSF47027									
aly363.9	Putative acyl-CoA-binding protein	GO:0050809,GO:0042049,GO:0006810,GO:0008289,GO:0000062,GO:0004857	CG8629-PA						PF00887	PS51228	PR00689,PR00689,PR00689		G3DSA:1.20.80.10	SSF47027									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly36308.1	Unknown		n/a																				
aly36374.1	Unknown		n/a																				
aly36374.2	PiggyBac transposable element-derived protein 2		n/a						PF13843,PF13843														
aly36444.1	Ubiquitin carboxyl-terminal hydrolase 30 homolog	GO:1901562,GO:0044313,GO:0016021,GO:0005741,GO:0035871,GO:0006511,GO:0016579,GO:0004843	CG3016-PA						PF00443	PS50235				SSF54001									
aly36454.1	Probable cytochrome P450 9f2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0035220,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG11466-PA										G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly3653.1	General transcription factor 3C polypeptide 2	GO:0005634,GO:0006351,GO:0005515	n/a										G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3653.2	Unknown		n/a																				
aly3653.3	Alpha-tocopherol transfer protein-like	GO:0008431,GO:0006810,GO:0005215,GO:0016020,GO:0005622,GO:0022008	CG15017-PA						PF00650				G3DSA:3.40.525.10,G3DSA:3.40.525.10	SSF52087,SSF46938									
aly3653.4	Alpha-tocopherol transfer protein-like	GO:0008431,GO:0006810,GO:0005215,GO:0016020,GO:0005622,GO:0022008	CG15017-PA				SM00516		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF46938,SSF52087									
aly3653.5	Alpha-tocopherol transfer protein-like	GO:0016020,GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG33966-PA				SM00516		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF46938,SSF52087									
aly3653.6	Alpha-tocopherol transfer protein-like	GO:0016020,GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG33966-PA				SM00516		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087,SSF46938									
aly3653.7	Puratrophin-1	GO:0005089,GO:0007480,GO:0005085,GO:0090630,GO:0005575,GO:0035025	CG33275-PA				SM00325,SM00233		PF00621	PS50003,PS50010			G3DSA:1.20.900.10,G3DSA:2.30.29.30	SSF50729,SSF48065									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3653.8	Unknown		n/a																				
aly3653.9	Unknown		n/a																				
aly36556.1	Kinesin-like protein KIF23	GO:0007018,GO:0007596,GO:0030111,GO:0070938,GO:0016887,GO:0005871,GO:0000022,GO:0051533,GO:0005874,GO:0032507,GO:0005819,GO:0045171,GO:0005813,GO:0005634,GO:0001709,GO:0000281,GO:0097149,GO:0007525,GO:0005654,GO:0032467,GO:0000278,GO:0003777,GO:0005925,GO:0051298,GO:0019886,GO:0008017,GO:0032154,GO:0016321,GO:0035323,GO:0007052,GO:0072686,GO:0008152,GO:0035324,GO:0022008,GO:0005930,GO:0098549,GO:0000910,GO:0000915,GO:0000916,GO:0007422,GO:0005829,GO:0005828,GO:0030496,GO:0007224,GO:0051256,GO:0005524,GO:0070507	CG1258-PA				SM00129		PF00225,PF16540	PS50067	PR00380,PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10,G3DSA:3.40.850.10	SSF52540,SSF52540	594~614,625~659,547~574								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly36556.2	Serine/threonine-protein kinase BRSK2	GO:0006887,GO:0005783,GO:0000086,GO:0018105,GO:0030010,GO:0035556,GO:0007067,GO:0051301,GO:0005737,GO:0006487,GO:0031532,GO:0005813,GO:0000287,GO:0004674,GO:0048471,GO:0005524,GO:0006468,GO:0030182,GO:0007528,GO:0007409,GO:0061178,GO:0019901,GO:0070059,GO:0048812,GO:0050321	CG6114-PA				SM00220		PF00069	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112										
aly366.1	Alanine--tRNA ligase, mitochondrial	GO:0004813,GO:0000049,GO:0006419,GO:0005739,GO:0000166,GO:0008270,GO:0003676,GO:0005524	CG4633-PA	MF_00036_B			SM00863		PF01411,PF01411,PF07973	PS50860	PR00980,PR00980,PR00980,PR00980		G3DSA:3.30.930.10	SSF50447,SSF101353,SSF55186,SSF55681		00970+6.1.1.7	REACT_71						
aly366.10	Unknown		n/a																				
aly366.11	Unknown		n/a												330~350,290~310								
aly366.12	Sodium/calcium exchanger 3	GO:0021537,GO:0016021,GO:0002244,GO:0043197,GO:0060402,GO:0043025,GO:0005432,GO:0007596,GO:0006816,GO:0005739,GO:0007602,GO:0007154,GO:0071320,GO:0006811,GO:0005509,GO:0042383,GO:0005886,GO:1990034,GO:1990035,GO:0005874,GO:0055085	CG5685-PG				SM00237,SM00237	TIGR00845	PF16494,PF01699,PF03160,PF03160					SSF141072,SSF141072			REACT_15518							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly366.2	Protein sel-1 homolog 1	GO:0007219,GO:0016021,GO:0030970,GO:0005789,GO:0005886,GO:0034976	CG10221-PA				SM00671,SM00671,SM00671,SM00671,SM00671,SM00671,SM00671,SM00671		PF08238,PF08238,PF08238,PF08238,PF08238,PF08238,PF08238,PF08238				G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF81901,SSF81901,SSF81901	120~140,185~205,85~105								
aly366.3	Molybdopterin synthase catalytic subunit	GO:0006777,GO:0006338,GO:0005829,GO:0004402,GO:0005700,GO:0030366,GO:0005671,GO:0016573,GO:0019008	CG10238-PA	MF_03052					PF02391				G3DSA:3.90.1170.40	SSF54690		00790+2.8.1.12		PWY-6823	UPA00344				
aly366.4	Transforming acidic coiled-coil-containing protein 3	GO:0000242,GO:0008104,GO:0035046,GO:0007279,GO:0000226,GO:0032886,GO:0007067,GO:0001666,GO:0007143,GO:0005876,GO:0007344,GO:0030953,GO:0007026,GO:0005813,GO:0000922,GO:0022008,GO:0005875,GO:0005737,GO:0015630,GO:0008283,GO:0008017,GO:0007052,GO:0022027,GO:0000235,GO:0019904,GO:0021987,GO:0042994,GO:0051726,GO:0005515,GO:0030097,GO:0007097	CG9765-PK						PF05010						1631~1686,1775~1824,1701~1733								
aly366.5	Intraflagellar transport protein 46 homolog	GO:0005737,GO:0030992,GO:0042384,GO:0007224,GO:0005813,GO:0042073,GO:0031512,GO:0005929	CG15161-PA						PF12317														
aly366.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly366.7	Cyclin-dependent kinase-like 1	GO:0005737,GO:0007507,GO:0006468,GO:0070062,GO:0051726,GO:0005634,GO:0000281,GO:0004674,GO:0004693,GO:0005524	CG7236-PC				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly366.8	Tat-linked quality control protein TatD	GO:0004536,GO:0016888,GO:0046872,GO:0006515,GO:0005737	CG3308-PA			PIRSF005902			PF01026				G3DSA:3.20.20.140	SSF51556									
aly366.9	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	GO:0004654,GO:0045926,GO:0051260,GO:0035458,GO:0071042,GO:0043631,GO:0034599,GO:0005737,GO:0006396,GO:0016020,GO:0097222,GO:0005739,GO:0034046,GO:0000962,GO:0000965,GO:0000964,GO:0005758,GO:0006402,GO:2000627,GO:0070207,GO:0044822,GO:0061014,GO:0008266,GO:0006401,GO:0045025,GO:0071850,GO:0070584,GO:0090503,GO:0043457,GO:0035198,GO:2000772,GO:0000175,GO:0035928,GO:0000957,GO:0003723,GO:0000958,GO:0035927	CG11337-PB						PF01138,PF01138,PF03726,PF03725,PF03725				G3DSA:1.10.10.400,G3DSA:3.30.230.70,G3DSA:3.30.230.70,G3DSA:3.30.230.70	SSF54791,SSF54211,SSF55666,SSF54211,SSF55666		00230+2.7.7.8,00240+2.7.7.8	REACT_21257						
aly36674.1	Fatty acid synthase	GO:0006633,GO:0047451,GO:0042587,GO:0008144,GO:0008270,GO:0001649,GO:0016491,GO:0070062,GO:0016295,GO:0005835,GO:0004320,GO:0071353,GO:0005739,GO:0030879,GO:0042802,GO:0042803,GO:0005794,GO:0044822,GO:0004315,GO:0016788,GO:0047117,GO:0008152,GO:0005886,GO:0055114,GO:0008610,GO:0006084,GO:0042470,GO:0005829,GO:0004312,GO:0004313,GO:0016296,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319	CG17374-PC						PF00698				G3DSA:3.40.366.10	SSF52151									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly36689.1	Unknown		n/a																				
aly368.1	Sugar transporter ERD6-like 14	GO:0005355,GO:0004252,GO:0022891,GO:0004175,GO:0016021,GO:0008643,GO:0006508,GO:0055085	CG6484-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly368.2	Unknown		n/a																				
aly368.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly36809.1	Dystonin	GO:0016319,GO:0035147,GO:0008022,GO:0015629,GO:0005178,GO:0035371,GO:0030426,GO:0035149,GO:0030424,GO:0030175,GO:0000226,GO:0030011,GO:0030716,GO:0005874,GO:0030018,GO:0005856,GO:0007517,GO:0005925,GO:0070062,GO:0007026,GO:0016023,GO:0030056,GO:0031673,GO:0005635,GO:0009611,GO:0051491,GO:0007475,GO:0003779,GO:0005509,GO:0009925,GO:0031581,GO:0005882,GO:0042803,GO:0016203,GO:0005737,GO:0015630,GO:0005938,GO:0016204,GO:0007229,GO:0008017,GO:0051010,GO:0031252,GO:0044295,GO:0007050,GO:0005604,GO:0000235,GO:0030036,GO:0007409,GO:0007155,GO:0030516,GO:0005789,GO:0045111,GO:0007424,GO:0005634,GO:0007017,GO:0007010,GO:0007423,GO:0008092,GO:0045104,GO:0001578,GO:0005829,GO:0048870,GO:0045773,GO:0016199,GO:0045169,GO:0048813,GO:0030198,GO:0005515,GO:0016021,GO:0005912	CG18076-PH				SM00150		PF00435				G3DSA:1.20.58.60,G3DSA:1.20.58.60	SSF46966,SSF46966	9~43								
aly3686.1	Unknown		n/a																				
aly3686.10	DNA replication licensing factor Mcm7	GO:0003682,GO:0042555,GO:0005634,GO:0006270,GO:0005656,GO:0006267,GO:0003677,GO:0003678,GO:0007095,GO:0043138,GO:0032508,GO:0005875,GO:0005524	CG4978-PA				SM00350,SM00382		PF00493,PF00493,PF14551	PS50051	PR01663,PR01663,PR01663,PR01663,PR01663,PR01657,PR01657,PR01657,PR01657,PR01657	PS00847	G3DSA:3.30.1640.10,G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:3.40.50.300	SSF50249,SSF50249,SSF52540	52~72		REACT_152,REACT_383,REACT_1538						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3686.11	Synaptogyrin-2	GO:0031594,GO:0030672,GO:0070062,GO:0016079,GO:0016021,GO:0016020,GO:0017158,GO:0022008,GO:0048489	CG10808-PA						PF01284	PS51225													
aly3686.12	Caskin-2	GO:0005737,GO:0005515,GO:0030424,GO:0035591,GO:0019903,GO:0007409,GO:0007411,GO:0005925,GO:0007185	CG12424-PC				SM00454,SM00454		PF00536,PF00536	PS50105,PS50105			G3DSA:1.10.150.50,G3DSA:1.10.150.50	SSF47769,SSF47769	655~675								
aly3686.2	Unknown		n/a																				
aly3686.3	Maternal protein pumilio	GO:0005635,GO:0042078,GO:0048149,GO:0008258,GO:0007616,GO:0008582,GO:0042059,GO:0050804,GO:0031594,GO:0007067,GO:0005737,GO:0045786,GO:0000900,GO:0001709,GO:0003730,GO:0016477,GO:0048477,GO:0007281,GO:0008595,GO:0060213,GO:0045892,GO:0061176,GO:0007268,GO:0000288,GO:0097482,GO:0045727,GO:0007280,GO:0048813,GO:0003723,GO:0017148,GO:0016441,GO:0061177	CG9755-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3686.4	Protein mago nashi	GO:0035145,GO:0008104,GO:0008103,GO:0046579,GO:0046594,GO:0000226,GO:0007309,GO:0005737,GO:0005634,GO:0045451,GO:0048477,GO:0008380,GO:0006406,GO:0000335,GO:0071011,GO:0016325,GO:0071013,GO:0044822,GO:0007317,GO:0007315,GO:0007173,GO:0007267,GO:0007318,GO:0000398,GO:0005515,GO:0070374,GO:0045495	CG9401-PA						PF02792				G3DSA:3.30.1560.10	SSF89817									
aly3686.5	40S ribosomal protein S8	GO:0005840,GO:0005622,GO:0003735,GO:0000462,GO:0022008,GO:0006414,GO:0006412,GO:0022627	CG7808-PE					TIGR00307	PF01201			PS01193											
aly3686.6	Serpin B12	GO:0005737,GO:0005615,GO:0002244,GO:0030162,GO:0004867,GO:0010951,GO:0070062	CG12807-PA				SM00093		PF00079,PF00079				G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:2.30.39.10,G3DSA:2.30.39.10	SSF56574,SSF56574									
aly3686.7	Uncharacterized protein CG7065	GO:0005575,GO:0003674,GO:0008150	CG7065-PA						PF12171					SSF57667									
aly3686.8	Uncharacterized protein CG7065	GO:0005575,GO:0003674,GO:0008150	CG7065-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3686.9	DNA polymerase alpha catalytic subunit	GO:0003677,GO:0001882,GO:0005654,GO:0008408,GO:0006303,GO:0005730,GO:0005634,GO:0005635,GO:0000166,GO:0003887,GO:0006260,GO:0046872,GO:0005658,GO:0006269,GO:0008283,GO:0022008,GO:0016363,GO:0051539,GO:0006273,GO:0006272,GO:0006271,GO:0006270,GO:0003682,GO:0008296,GO:0071897	CG6349-PA				SM00486	TIGR00592	PF00136,PF08996,PF03104,PF12254		PR00106,PR00106,PR00106	PS00116	G3DSA:3.90.1600.10,G3DSA:3.90.1600.10,G3DSA:3.30.420.10,G3DSA:1.10.287.690	SSF90234,SSF53098,SSF53098,SSF56672,SSF56672	1111~1131	00240+2.7.7.7,00230+2.7.7.7							
aly36927.1	Ras-related protein Rab-33B	GO:1903434,GO:1903358,GO:0005796,GO:0006888,GO:0031982,GO:0000042,GO:0005811,GO:2000156,GO:0043025,GO:0005525,GO:0048705,GO:0005794,GO:0030334,GO:0050774,GO:0009306,GO:0006914,GO:0003924,GO:0032482,GO:0008360,GO:2000785,GO:0007155,GO:0070062,GO:0007015,GO:0006891,GO:0016192,GO:0000139	CG3320-PA				SM00175	TIGR00231	PF00071	PS51419			G3DSA:3.40.50.300	SSF52540									
aly3694.1	Protein slit	GO:0031012,GO:0001764,GO:0007411,GO:0050929,GO:0022409,GO:0003151,GO:0007432,GO:0008406,GO:0071666,GO:0005509,GO:0008078,GO:0035385,GO:0030182,GO:2000274,GO:0035050,GO:0048495,GO:0046331,GO:0005886,GO:0050919,GO:0008201,GO:0008347,GO:0007427,GO:0007502,GO:0010632,GO:0016199,GO:0007509,GO:0048813,GO:0005576,GO:0005515,GO:0005578	CG43758-PF				SM00013,SM00369,SM00369,SM00369,SM00369,SM00082,SM00082		PF01463,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3694.2	Protein slit	GO:0031012,GO:0001764,GO:0007411,GO:0050929,GO:0022409,GO:0003151,GO:0007432,GO:0008406,GO:0071666,GO:0005509,GO:0008078,GO:0035385,GO:0030182,GO:0002074,GO:0035050,GO:0048495,GO:0046331,GO:0005886,GO:0050919,GO:0008201,GO:0008347,GO:0007427,GO:0007502,GO:0010632,GO:0016199,GO:0007509,GO:0048813,GO:0005576,GO:0005515,GO:0005578	CG43758-PF				SM00365,SM00365,SM00365,SM00365,SM00365,SM00082,SM00082,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00013,SM00181,SM00181,SM00181,SM00282,SM00041,SM00179,SM00179,SM00179		PF13855,PF13855,PF00008,PF00008,PF00054,PF12661,PF12661	PS51450,PS51450,PS50026,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS01225,PS50026,PS50026,PS50025,PS50026		PS00010,PS00022,PS01186,PS01187,PS01186,PS00022,PS01186,PS00010,PS00022,PS01185	G3DSA:2.60.120.200,G3DSA:2.10.25.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57184,SSF49899,SSF52058,SSF52058										
aly3694.3	Suppressor of cytokine signaling 5	GO:0032436,GO:0019221,GO:0007616,GO:0043697,GO:0008586,GO:0042059,GO:0007298,GO:0005737,GO:0048802,GO:0016049,GO:0009968,GO:0016567,GO:0040008,GO:0045873,GO:0030971,GO:0007259,GO:0045629,GO:0005154,GO:0045627,GO:0019210,GO:0006469,GO:0046426,GO:0007482,GO:0046425,GO:0048072,GO:0004860,GO:0007175,GO:0007173,GO:0030718,GO:0045677	CG15154-PD						PF07525	PS50225				SSF158235					UPA00143				
aly3694.4	Suppressor of cytokine signaling 5	GO:0032436,GO:0019221,GO:0007616,GO:0043697,GO:0008586,GO:0042059,GO:0007298,GO:0005737,GO:0048802,GO:0016049,GO:0009968,GO:0016567,GO:0040008,GO:0045873,GO:0030971,GO:0007259,GO:0045629,GO:0005154,GO:0045627,GO:0019210,GO:0006469,GO:0046426,GO:0007482,GO:0046425,GO:0048072,GO:0004860,GO:0007175,GO:0007173,GO:0030718,GO:0045677	CG15154-PD										G3DSA:3.30.505.10	SSF55550									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37.1	ADAMTS-like protein 3	GO:0006508,GO:0004222,GO:0008270,GO:0008237,GO:0005578	CG31619-PC				SM00209		PF00090	PS50092	PR01857,PR01857,PR01705,PR01705,PR01705		G3DSA:2.20.100.10	SSF82895									
aly37.2	UPF0769 protein C21orf59 homolog	GO:0005575,GO:0005829,GO:0048812,GO:0003674,GO:0005634	CG18675-PA						PF11069														
aly37.3	Unknown		n/a																				
aly37.4	Unknown		n/a																				
aly3701.1	Eukaryotic translation initiation factor 4E-binding protein 3-like	GO:0005737,GO:0019731,GO:0045792,GO:0014743,GO:0006641,GO:0009617,GO:0070129,GO:0006952,GO:0001558,GO:0042594,GO:0045947,GO:0008190,GO:0008340,GO:0006979,GO:0006955	CG8846-PA						PF05456														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3701.2	Cyclin-dependent kinase 5 activator 1	GO:0018107,GO:0033136,GO:0031175,GO:0030426,GO:0030425,GO:0030424,GO:0021766,GO:0009790,GO:0021722,GO:0001764,GO:0043525,GO:0008045,GO:0004693,GO:0007411,GO:0007413,GO:0005737,GO:0071158,GO:0007213,GO:0005634,GO:0016020,GO:0005654,GO:0048511,GO:0005509,GO:0071902,GO:0016533,GO:0043025,GO:0016534,GO:0061001,GO:0006468,GO:0030182,GO:0048471,GO:0035235,GO:0016301,GO:0021819,GO:0090314,GO:0035011,GO:0045892,GO:0007158,GO:0007409,GO:0005886,GO:0030517,GO:0008340,GO:0048013,GO:0021549,GO:0008344,GO:0043539,GO:0031594,GO:0007420,GO:0043197,GO:0070059,GO:0045296,GO:0043292,GO:0014069,GO:0070507,GO:0032956	CG5387-PA						PF03261,PF03261				G3DSA:1.10.472.10	SSF47954										
aly3705.1	Unknown	GO:0006030,GO:0005576,GO:0008061	n/a				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly3705.2	Unknown	GO:0006030,GO:0005576,GO:0008061	n/a						PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly37074.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37097.1	Unknown	GO:0022008,GO:0003676	CG9422-PA																				
aly371.1	Potassium voltage-gated channel protein Shaw	GO:0071805,GO:0006813,GO:0016021,GO:0051260,GO:0008076,GO:0022843,GO:0005249,GO:0005886,GO:0005251,GO:0055085,GO:0030431	CG2822-PC						PF00520		PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR01491,PR01491,PR01491		G3DSA:1.20.120.350,G3DSA:1.10.287.70	SSF81324									
aly371.2	Unknown		n/a																				
aly3712.1	Putative adenosylhomocysteinase 3	GO:0016787,GO:0005783,GO:0006730,GO:0004013,GO:0033353,GO:0043005,GO:0005829,GO:0043231	CG9977-PA				SM00997,SM00996		PF05221,PF00670			PS00739,PS00738	G3DSA:3.40.50.1480,G3DSA:3.40.50.720	SSF52283,SSF51735		00270+3.3.1.1		PWY-5041	UPA00314				
aly3712.10	Unknown	GO:0005179,GO:0005576	n/a						PF00159	PS50276,PS51257			G3DSA:1.20.5.570										
aly3712.11	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3712.2	Unknown		n/a																				
aly3712.3	Differentially expressed in FDCP 8 homolog	GO:0005622,GO:0005575,GO:0003674,GO:0008270,GO:0008150,GO:0035556	CG11534-PA				SM00109		PF13901	PS50081			G3DSA:3.30.60.20	SSF57889,SSF48695,SSF48695	56~76								
aly3712.4	Unknown		n/a						PF16060														
aly3712.5	Unknown		n/a																				
aly3712.6	Unknown		n/a				SM00355,SM00355		PF13909,PF13909														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3712.7	Actin-like protein 6A	GO:0035060,GO:0031011,GO:0021510,GO:0035267,GO:0007067,GO:0007517,GO:0043967,GO:0043044,GO:0003713,GO:0000281,GO:0016514,GO:0000980,GO:0043234,GO:0006281,GO:0043968,GO:0000790,GO:0045893,GO:0005886,GO:0090544,GO:0006310,GO:0006351,GO:0007399,GO:0006338,GO:0070983,GO:1903955,GO:0040008,GO:0006355,GO:0048813,GO:0003407,GO:0071564,GO:0000978,GO:0003682,GO:2000637,GO:0005634,GO:1903146	CG6546-PA				SM00268		PF00022,PF00022		PR00190,PR00190,PR00190		G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.90.640.10	SSF53067,SSF53067									
aly3712.8	Unknown		n/a																				
aly3712.9	Unknown		n/a																				
aly3716.1	Cytoplasmic aconitate hydratase	GO:0005783,GO:0009791,GO:0006099,GO:0010040,GO:0005737,GO:0070062,GO:0005739,GO:0005506,GO:0046872,GO:0005794,GO:0006879,GO:0006447,GO:0030350,GO:0007370,GO:0051539,GO:0005829,GO:0050892,GO:0006101,GO:0003723,GO:0006417,GO:0003994,GO:0003729	CG4900-PA						PF00330		PR00415,PR00415,PR00415,PR00415,PR00415,PR00415,PR00415,PR00415,PR00415	PS00450,PS01244	G3DSA:3.30.499.10,G3DSA:3.30.499.10,G3DSA:3.40.1060.10,G3DSA:3.30.499.10,G3DSA:3.30.499.10	SSF53732		00290+4.2.1.33			UPA00048				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3717.1	Unknown		n/a																				
aly3717.2	Segmentation protein even-skipped	GO:0009997,GO:0035289,GO:0008045,GO:0007417,GO:0043565,GO:0007517,GO:0007366,GO:0000122,GO:0005634,GO:0001709,GO:0000980,GO:0003007,GO:0008595,GO:1901739,GO:0007350,GO:0035290,GO:0007507,GO:0045165,GO:0050770,GO:0007377,GO:0007376,GO:0003700,GO:0007512,GO:0003705,GO:0006355,GO:0045944,GO:0006351,GO:0007399	CG2328-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly3720.1	Unknown		CG34386-PC																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3721.1	Low-density lipoprotein receptor-related protein 2	GO:0048082,GO:0006898,GO:0042493,GO:0020028,GO:0005903,GO:0005905,GO:0033280,GO:0005737,GO:0040003,GO:0005615,GO:0016021,GO:0016020,GO:0045056,GO:0046879,GO:0005509,GO:0032403,GO:0043234,GO:0032526,GO:0006766,GO:0031100,GO:0016324,GO:0060070,GO:0030165,GO:0010951,GO:0044332,GO:0030100,GO:0010165,GO:0050750,GO:0016197,GO:0007568,GO:0030492,GO:0045121,GO:0005041,GO:0031526,GO:0042813,GO:0005515,GO:0017147,GO:0042953,GO:0005768,GO:0004872	CG42611-PA				SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00181,SM00135,SM00192		PF12662,PF07645,PF07645,PF14670,PF00057,PF16472,PF00058,PF00058,PF00058,PF00058,PF00058,PF00058,PF00058	PS51120,PS50068,PS50026,PS51120,PS50068,PS50068,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS50026,PS51120,PS51120,PS50068,PS51120,PS51120,PS50068,PS50068,PS50068,PS50068,PS50068,PS51120,PS51120,PS51120,PS50068,PS50068,PS51120,PS50026,PS50068,PS51120,PS50068,PS51120,PS51120,PS51120,PS50068,PS50068,PS51120,PS50068,PS50068,PS50068,PS50068,PS51120,PS50026,PS51120,PS50068,PS51120,PS50068,PS50068,PS51120,PS50068,PS51120,PS50068,PS51120,PS50068,PS51120,PS50068,PS50068,PS51120,PS50068,PS51120,PS50068,PS51120,PS50068,PS51120,PS51120,PS51120,PS50068,PS50068,PS50068,PS50068	PR00261,PR00261,PR00261,PR00261,PR00261	PS01187,PS01209,PS01209,PS01187,PS01209,PS00010,PS01209,PS01187,PS01187,PS01209,PS01209,PS01209,PS01209,PS00010,PS01209,PS01209,PS01186,PS01209,PS01186,PS01209,PS01186,PS01209,PS01209,PS01186,PS01209,PS01209,PS01209,PS01209,PS01209,PS01209,PS01209,PS01209,PS01209,PS01209,PS01186,PS01209,PS00010,PS01209,PS01209,PS01209,PS00010,PS01209	G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.120.10.30,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.1220.10,G3DSA:4.10.1220.10,G3DSA:4.10.1220.10,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:4.10.400.10,G3DSA:4.10.400.10	SSF57424,SSF57424,SSF57424,SSF57424,SSF57184,SSF57184,SSF57424,SSF57424,SSF57196,SSF57184,SSF57184,SSF63825,SSF57196,SSF63825,SSF63825,SSF63825,SSF57424,SSF57196,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF63825,SSF57424,SSF57424,SSF57196,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57196,SSF63825,SSF63825,SSF57424,SSF57196,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF63825,SSF57196,SSF57424									
aly3721.2	Alanine aminotransferase 2	GO:0042853,GO:0004021,GO:0042851,GO:0009058,GO:0030170,GO:0006103	CG1640-PB						PF00155				G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383									
aly3721.3	Alanine aminotransferase 2	GO:0042853,GO:0004021,GO:0042851,GO:0003824,GO:0009058,GO:0005739,GO:0030170,GO:0006103	CG1640-PB						PF00155				G3DSA:3.40.640.10	SSF53383									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3721.4	Unknown	GO:0042813,GO:0060070,GO:0046331,GO:0005515,GO:0017147,GO:0044332	CG32206-PE				SM00192,SM00192,SM00042		PF00057,PF00431	PS01180,PS50068	PR00261,PR00261	PS01209	G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290	SSF49854,SSF49854,SSF57424									
aly37212.1	Unknown		n/a																				
aly37304.1	BTB/POZ domain-containing protein 10	GO:0004370,GO:0005737,GO:0050975,GO:0035071,GO:0005730,GO:0005634,GO:0051260,GO:0042327,GO:0005654,GO:0048102,GO:0046331,GO:1901215	CG1216-PB						PF16017				G3DSA:3.30.710.10	SSF54695									
aly3731.1	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly3731.10	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131		G3DSA:3.20.20.80	SSF51445									
aly3731.2	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00572	G3DSA:3.20.20.80	SSF51445									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3731.3	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131		G3DSA:3.20.20.80	SSF51445									
aly3731.4	Protein SYS1 homolog	GO:0015031,GO:0016021,GO:0000139	CG11753-PA			PIRSF031402			PF09801														
aly3731.5	Trifunctional nucleotide phosphoesterase protein YfkN	GO:0016787,GO:0005618,GO:0008663,GO:0008254,GO:0008253,GO:0000166,GO:0009166,GO:0005576,GO:0046872	CG11883-PC						PF00149,PF02872		PR01607,PR01607,PR01607,PR01607,PR01607		G3DSA:3.60.21.10,G3DSA:3.90.780.10	SSF55816,SSF56300									
aly3731.6	Carbonyl reductase [NADPH] 1	GO:0005737,GO:0042373,GO:0004090,GO:0047021,GO:0008152,GO:0050221,GO:0017144,GO:0016491	CG31549-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly3731.7	Lipase member H-B	GO:0008970,GO:0016020,GO:0052689,GO:0016042,GO:0005575,GO:0005576,GO:0016298	CG6296-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly3731.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3731.9	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly37338.1	Protein serrate	GO:0016330,GO:0005887,GO:0035167,GO:0007436,GO:0007219,GO:0007431,GO:0016021,GO:0007476,GO:0007451,GO:0045746,GO:0042688,GO:0042689,GO:0005509,GO:0005112,GO:0048749,GO:0035214,GO:0005154,GO:0016324,GO:0009986,GO:0035170,GO:0014009,GO:0046331,GO:0035017,GO:0005886,GO:0030718,GO:0030673,GO:0007423,GO:0036011,GO:0007435,GO:0005515,GO:0005102	CG6127-PA				SM00215,SM00051,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181		PF12661,PF07645,PF00008,PF00008,PF00008,PF00008,PF00008,PF00008,PF00008,PF07657,PF01414	PS50026,PS50026,PS50026,PS50026,PS50026,PS51257,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS51051	PR00010,PR00010,PR00010,PR00010	PS00022,PS00010,PS01186,PS01186,PS00022,PS01187,PS00022,PS00022,PS00022,PS01187,PS01186,PS00010,PS01186,PS00022,PS00022,PS00022,PS01186,PS01187,PS00010,PS01186,PS01187,PS00010,PS00022,PS01186,PS01186,PS00022,PS01186,PS01187,PS01186,PS00010,PS00022	G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57184,SSF57196,SSF57184,SSF57196,SSF57184,SSF57196	1061~1061,972~992		REACT_299						
aly37338.10	Unknown		n/a																				
aly37338.11	Esterase FE4	GO:0005575,GO:0007476,GO:0052689	CG1131-PC						PF00135				G3DSA:3.40.50.1820	SSF53474	288~308								
aly37338.12	Acetylcholinesterase	GO:0042135,GO:0052689,GO:0005575,GO:0005576,GO:0008150,GO:0045202,GO:0008152,GO:0005886,GO:0003990,GO:0030054	CG10175-PD						PF00135				G3DSA:3.40.50.1820	SSF53474	514~515								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.13	Juvenile hormone esterase	GO:0004453,GO:0052689	CG6414-PA						PF00135			PS00122,PS00271	G3DSA:3.40.50.1820	SSF53474									
aly37338.14	Serine/threonine-protein kinase D3	GO:0005737,GO:0006468,GO:0016020,GO:0019992,GO:0016301,GO:0005654,GO:0004674,GO:0035556,GO:0046872,GO:0004697,GO:0005524	CG7125-PG				SM00220,SM00109,SM00109,SM00233		PF00130,PF00130,PF00069,PF00169	PS50081,PS50081,PS50003,PS50011		PS00107,PS00479,PS00108	G3DSA:2.30.29.30,G3DSA:3.30.60.20,G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:3.30.60.20	SSF56112,SSF50729,SSF57889,SSF57889										
aly37338.15	Zinc finger protein 26	GO:0003700,GO:0005634,GO:0006355,GO:0003676,GO:0003677,GO:0046872	CG7987-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly37338.16	Zinc finger protein 497	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG6654-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										
aly37338.17	Zinc finger protein 570	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG5245-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	403~423										
aly37338.18	Transmembrane protein 179	GO:0016021	CG13603-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.19	Protein YIF1B B	GO:0009306,GO:0016021,GO:0048812,GO:0000902	CG5484-PC						PF03878														
aly37338.2	Protein kinase C	GO:0008285,GO:0006468,GO:0034389,GO:0007252,GO:0009950,GO:0007616,GO:0007030,GO:0005622,GO:0004674,GO:0048812,GO:0046872,GO:0019992,GO:0045471,GO:0004697,GO:0004698,GO:0005524	CG1954-PA				SM00133		PF00433	PS51285													
aly37338.20	RNA-binding protein Nova-1	GO:0005634,GO:0003723,GO:0000398,GO:0003729	CG42670-PR				SM00322,SM00322,SM00322		PF00013,PF00013,PF00013	PS50084,PS50084,PS50084			G3DSA:3.30.1370.10,G3DSA:3.30.1370.10,G3DSA:3.30.1370.10	SSF54791,SSF54791,SSF54791									
aly37338.21	Putative tyrosine-protein kinase Wsck	GO:0042127,GO:0006468,GO:0016021,GO:0038083,GO:0045087,GO:0030154,GO:0004715,GO:0004713,GO:0005886,GO:0007169,GO:0004672,GO:0031234,GO:0005524	CG31127-PA				SM00321,SM00060		PF00041,PF01822,PF07714	PS51212,PS50853,PS50011	PR00109,PR00109,PR00109		G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:2.60.40.10	SSF56112,SSF49265									
aly37338.22	Unknown	GO:0005634,GO:0072686,GO:0008017	CG11120-PA												378~398								
aly37338.23	Hippocampus abundant transcript 1 protein	GO:0005215,GO:0016021,GO:0005886,GO:0055085,GO:0015144	CG11537-PD						PF07690	PS50850	PR01035,PR01035,PR01035,PR01035,PR01035,PR01035	PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.24	AP-2 complex subunit sigma	GO:0008565,GO:0008021,GO:0016183,GO:0006897,GO:0005794,GO:0006886,GO:0006901,GO:0007269,GO:0005886,GO:0030122,GO:0022008,GO:0030121,GO:0030135	CG6056-PA			PIRSF015588			PF01217			PS00989	G3DSA:3.30.450.60	SSF64356									
aly37338.25	Putative phospholipase B-like 2	GO:0016787,GO:0043202,GO:0070062,GO:0007444,GO:0016042,GO:0005576,GO:0003674,GO:0002121,GO:0046843	CG10645-PC						PF04916														
aly37338.26	Unknown		n/a																				
aly37338.27	Peptidyl-prolyl cis-trans isomerase FKBP62	GO:0005737,GO:0006457,GO:0005515,GO:0007422,GO:0005634,GO:0051924,GO:0016027,GO:0005528,GO:0003755,GO:0050908,GO:0070370,GO:0018208	CG4535-PA				SM00028,SM00028		PF13414,PF00515	PS50293,PS50005,PS50005			G3DSA:1.25.40.10	SSF48452									
aly37338.28	Atlastin	GO:0051124,GO:0031114,GO:0005783,GO:0008582,GO:0061025,GO:0031227,GO:0005737,GO:0007517,GO:0007029,GO:0016021,GO:0016020,GO:0051260,GO:0032561,GO:0042802,GO:0042803,GO:0005794,GO:0016320,GO:0003924,GO:0007528,GO:0012505,GO:0008152,GO:0007030,GO:0007019,GO:0000139,GO:0005525	CG6668-PA						PF02841,PF02263	PS51715			G3DSA:1.20.1000.10,G3DSA:3.40.50.300	SSF48340,SSF52540	408~428								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.29	Atlastin	GO:0051124,GO:0031114,GO:0005783,GO:0008582,GO:0061025,GO:0031227,GO:0005737,GO:0007517,GO:0007029,GO:0016021,GO:0016020,GO:0051260,GO:0032561,GO:0042802,GO:0005525,GO:0005794,GO:0016320,GO:0003924,GO:0007528,GO:0012505,GO:0008152,GO:0007030,GO:0007019,GO:0000139,GO:0042803	CG6668-PA						PF02263	PS51715			G3DSA:1.20.1000.10,G3DSA:3.40.50.300	SSF48340,SSF52540										
aly37338.3	Calcium-independent protein kinase C	GO:0008285,GO:0006468,GO:0034389,GO:0007252,GO:0009950,GO:0007616,GO:0016020,GO:0007030,GO:0005622,GO:0019992,GO:0048812,GO:0046872,GO:0004674,GO:0035556,GO:0045471,GO:0004697,GO:0004698,GO:0005524	CG1954-PA				SM00239,SM00109,SM00109		PF00168,PF00130,PF00130	PS50004,PS50081,PS50081	PR00008,PR00008,PR00008,PR00008	PS00479,PS00479	G3DSA:2.60.40.150,G3DSA:3.30.60.20,G3DSA:3.30.60.20,G3DSA:3.30.200.20	SSF57889,SSF57889,SSF49562										
aly37338.30	Viral IAP-associated factor homolog	GO:0005737,GO:0043281,GO:0003674	CG18593-PA						PF02114				G3DSA:3.40.30.10	SSF52833	33~53								
aly37338.31	Unknown		n/a																				
aly37338.32	Integrator complex subunit 1	GO:0016180,GO:0034472,GO:0016021,GO:0016020,GO:0031965,GO:0032039,GO:0003674	CG3173-PA						PF12432														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.33	Unknown		n/a												486~520,373~393,12~39,206~226,171~191,237~257,289~323,331~351,44~71,447~478,261~281								
aly37338.34	ATP synthase-coupling factor 6, mitochondrial	GO:0015986,GO:0015992,GO:0000276,GO:0005739,GO:0046331,GO:0005756,GO:0008553,GO:0015078	CG4412-PA						PF05511					SSF111357									
aly37338.35	AMP deaminase 2	GO:0097009,GO:0046039,GO:0046034,GO:0005829,GO:0043101,GO:0046033,GO:0032264,GO:0046872,GO:0006188,GO:0005515,GO:0052652,GO:0003876,GO:0006144,GO:0055086,GO:0044281	CG32626-PK			PIRSF001251		TIGR01429	PF00962				G3DSA:3.20.20.140,G3DSA:3.20.20.140	SSF51556		00230+3.5.4.6	REACT_1698	PWY-6596	UPA00591				
aly37338.36	AMP deaminase 2	GO:0097009,GO:0046039,GO:0046034,GO:0046033,GO:0032264,GO:0046872,GO:0009117,GO:0006188,GO:0005515,GO:0052652,GO:0003876	CG32626-PK			PIRSF001251		TIGR01429	PF00962				G3DSA:3.20.20.140,G3DSA:3.20.20.140	SSF51556		00230+3.5.4.6	REACT_1698	PWY-6596	UPA00591				
aly37338.37	Ribosome-releasing factor 2, mitochondrial	GO:0003924,GO:0005739,GO:0032790,GO:0003746,GO:0006414,GO:0032543,GO:0005525	CG31159-PA				SM00838	TIGR00231	PF00679,PF14492,PF00009	PS51722		PS00301	G3DSA:3.30.70.870,G3DSA:2.40.30.10,G3DSA:3.30.230.10,G3DSA:3.30.70.240,G3DSA:3.40.50.300	SSF54980,SSF52540,SSF54980,SSF50447,SSF54211									
aly37338.38	5'-3' exoribonuclease 2 homolog	GO:0008409,GO:0000738,GO:0005730,GO:0004527,GO:0005634,GO:0006355,GO:0003676,GO:0006353,GO:0022008,GO:0046872,GO:0004534,GO:0006397	CG10354-PB			PIRSF037239			PF03159						122~142								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.39	Thyroid transcription factor 1	GO:0043565,GO:0003700,GO:0005634,GO:0005654,GO:0006355,GO:0048813,GO:0045893,GO:0003677,GO:0006351	CG17594-PA						PF00046	PS50071			G3DSA:1.10.10.60	SSF46689									
aly37338.4	ADP-ribosylation factor-like protein 2	GO:0031113,GO:0031116,GO:0006471,GO:0051457,GO:0007049,GO:0005737,GO:0070062,GO:0005813,GO:0005634,GO:0048488,GO:0005758,GO:0005525,GO:0016328,GO:0010811,GO:0051297,GO:0003924,GO:0034260,GO:0007269,GO:0022008,GO:0007264,GO:0016197,GO:0070830,GO:0005622,GO:0005575,GO:0019003	CG7435-PA				SM00178,SM00177,SM00175	TIGR00231	PF00025	PS51417	PR00328,PR00328,PR00328,PR00328		G3DSA:3.40.50.300	SSF52540									
aly37338.40	Multiple PDZ domain protein	GO:0016333,GO:0016332,GO:0008022,GO:0016334,GO:0005080,GO:0045196,GO:0030425,GO:0034334,GO:0035003,GO:0007163,GO:0007043,GO:0043220,GO:0005875,GO:0005737,GO:0002009,GO:0035088,GO:0045176,GO:0031410,GO:0005635,GO:0045179,GO:0005923,GO:0034332,GO:0032033,GO:0035509,GO:0016324,GO:0016327,GO:0008594,GO:0045211,GO:0045186,GO:0014069,GO:0005912,GO:0005886,GO:0007155,GO:0016032,GO:0001736,GO:0005918,GO:0035209,GO:0005515,GO:0045494	CG12021-PC				SM00228,SM00228,SM00228,SM00228		PF00595,PF00595,PF00595,PF00595	PS50106,PS50106,PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156,SSF50156,SSF50156,SSF50156									
aly37338.41	Retinol dehydrogenase 13	GO:0042462,GO:0010842,GO:0005743,GO:0008152,GO:0009644,GO:0016491	CG30491-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.42	DNA-directed RNA polymerase III subunit RPC1	GO:0006383,GO:0005634,GO:0005666,GO:0008270,GO:0032549,GO:0003899,GO:0003677,GO:0006351	CG17209-PC				SM00663		PF04997,PF00623,PF04983,PF05000,PF04998				G3DSA:2.40.40.20,G3DSA:2.40.40.20	SSF64484,SSF64484		00240+2.7.7.6,00230+2.7.7.6	REACT_1788						
aly37338.43	Bromodomain adjacent to zinc finger domain protein 1A	GO:0006333,GO:0008270,GO:0031497,GO:0003677,GO:0008544,GO:0000228,GO:0042766,GO:0007517,GO:0016590,GO:0008623,GO:0005634,GO:0004402,GO:0006261,GO:0048666,GO:0043462,GO:0045892,GO:0016584,GO:0031445,GO:0006338,GO:0007399,GO:0006334,GO:0016589,GO:0006355,GO:0048813,GO:0006351,GO:0005515	CG1966-PA				SM00249,SM00571		PF10537,PF00628,PF02791,PF15614	PS51136,PS50016,PS50827		PS01359	G3DSA:3.30.40.10	SSF57903	309~353,651~685								
aly37338.44	Histone acetyltransferase GCN5	GO:0003713,GO:0016590,GO:0006333,GO:0008270,GO:0031497,GO:0003677,GO:0042766,GO:0032968,GO:0010484,GO:0000124,GO:0007517,GO:0008544,GO:0008623,GO:0005634,GO:0004402,GO:0070577,GO:0005671,GO:0016573,GO:0048666,GO:0043966,GO:0043462,GO:0045892,GO:0000775,GO:0016584,GO:0031445,GO:0006338,GO:0007399,GO:0006334,GO:0016589,GO:0006355,GO:0048813,GO:0006351,GO:0005515,GO:0046695,GO:0005829,GO:0016568	CG1966-PA				SM00297		PF00439	PS50014	PR00503,PR00503,PR00503,PR00503	PS00633	G3DSA:1.20.920.10	SSF47370									
aly37338.45	Unknown		CG30415-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.46	Kinesin-like protein KIF16B	GO:0007492,GO:0032801,GO:0005871,GO:0008543,GO:0080025,GO:0001704,GO:0005874,GO:0005547,GO:0043325,GO:0031901,GO:0008017,GO:0003777,GO:0007173,GO:0045022,GO:0008574,GO:0006895,GO:0035091,GO:0007018,GO:0032266,GO:0005524,GO:0001919,GO:0005768,GO:0005769	CG5658-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10,G3DSA:2.60.200.20	SSF52540,SSF49879	604~659,720~775,944~971								
aly37338.47	Protein-lysine N-methyltransferase N6amt2	GO:0005737,GO:0070062,GO:0005575,GO:0003676,GO:0008168,GO:0032259	CG9154-PA						PF10237			PS00092											
aly37338.48	N-acetyltransferase 6	GO:0005737,GO:0004252,GO:0008080	CG8481-PB						PF13508	PS51186			G3DSA:3.40.630.30	SSF55729									
aly37338.49	Protein RRP5 homolog	GO:0032040,GO:0000381,GO:0005730,GO:0008134,GO:0005634,GO:0044822,GO:0005622,GO:0006364,GO:0006397,GO:0005829,GO:0006396,GO:0003729	CG5728-PA				SM00386,SM00386,SM00386,SM00386,SM00386,SM00316,SM00316,SM00316		PF05843	PS50126,PS50126,PS50126			G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:1.25.40.10	SSF50249,SSF50249,SSF50249,SSF48452,SSF48452	844~864,1135~1155,939~966,690~710,804~831								
aly37338.5	Pinin	GO:0016607,GO:0006351,GO:0071011,GO:0071013,GO:0000398,GO:0008380,GO:0006355,GO:0005681,GO:0003677,GO:0030057,GO:0006396,GO:0006397	CG8383-PB						PF04697,PF04696						153~197,261~281								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.50	Flavin reductase (NADPH)	GO:0042602,GO:0005654,GO:0070062,GO:0032504,GO:0005829,GO:0042167,GO:0003959,GO:0005886,GO:0004074	CG9471-PA						PF13460				G3DSA:3.40.50.720	SSF51735									
aly37338.51	Mitochondrial GTPase 1	GO:0003924,GO:0042254,GO:0005739,GO:0005525	CG17141-PA			PIRSF006230			PF01926	PS51721			G3DSA:3.40.50.300,G3DSA:1.10.1580.10	SSF52540									
aly37338.52	Radial spoke head protein 4 homolog A	GO:0005856,GO:0007017,GO:0005730,GO:0035082,GO:0008017,GO:0005930,GO:0005654,GO:0031514,GO:0001534,GO:0003341,GO:0005634,GO:0005875	CG3121-PA						PF04712						554~562,109~129								
aly37338.53	Nuclear export mediator factor NEMF homolog	GO:0006611,GO:0005634	CG11847-PB						PF05833,PF11923,PF05670				G3DSA:2.30.310.10		303~340,686~706,457~484								
aly37338.54	Exosome complex component RRP46	GO:0005737,GO:0034475,GO:0000178,GO:0045006,GO:0071028,GO:0051607,GO:0005730,GO:0031125,GO:0005634,GO:0071051,GO:0000176,GO:0000177,GO:0000175,GO:0034427,GO:0035327,GO:0003723,GO:0016075,GO:0006401,GO:0043928,GO:0010468,GO:0006397	CG4043-PA						PF01138				G3DSA:3.30.230.70	SSF55666,SSF54211			REACT_21257						
aly37338.55	Decaprenyl-diphosphate synthase subunit 2	GO:0005737,GO:0006744,GO:0000010,GO:0050878,GO:0051290,GO:0005739,GO:0008299,GO:1990234,GO:0046982	CG10585-PA						PF00348				G3DSA:1.10.600.10,G3DSA:1.10.600.10	SSF48576,SSF48576									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.56	Decaprenyl-diphosphate synthase subunit 2	GO:0005737,GO:0050347,GO:0000010,GO:0050878,GO:0006744,GO:0051290,GO:0008299,GO:0044281,GO:1990234,GO:0005759,GO:0046982	CG10585-PA						PF00348				G3DSA:1.10.600.10	SSF48576,SSF48576									
aly37338.57	Homeobox protein homothorax	GO:0034504,GO:0005829,GO:0000060,GO:0003677,GO:0035282,GO:0005737,GO:0043565,GO:0007479,GO:0007432,GO:0007380,GO:0005634,GO:0007383,GO:0007476,GO:0045664,GO:0048749,GO:0005515,GO:0007480,GO:0008134,GO:0001654,GO:0007525,GO:0001752,GO:0009954,GO:0007420,GO:0007422,GO:0003700,GO:0010092,GO:0003705,GO:0006357,GO:0045944,GO:0005667,GO:0042659,GO:0048735	CG17117-PC				SM00389		PF05920	PS50071			G3DSA:1.10.10.60	SSF46689									
aly37338.58	Homeobox protein homothorax	GO:0034504,GO:0005829,GO:0000060,GO:0003677,GO:0035282,GO:0005737,GO:0043565,GO:0007479,GO:0007432,GO:0007380,GO:0005634,GO:0007383,GO:0007476,GO:0045664,GO:0048749,GO:0005515,GO:0007480,GO:0008134,GO:0001654,GO:0007525,GO:0001752,GO:0009954,GO:0007420,GO:0007422,GO:0003700,GO:0010092,GO:0003705,GO:0006357,GO:0045944,GO:0005667,GO:0042659,GO:0048735	CG17117-PC						PF16493														
aly37338.59	Unknown	GO:0005575,GO:0008150,GO:0003674	CG33299-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.6	Paired box protein Pax-1	GO:0060017,GO:0007389,GO:0009887,GO:0001501,GO:0005667,GO:0008283,GO:0003700,GO:0005634,GO:0060349,GO:0043374,GO:0006355,GO:0048813,GO:0045944,GO:0006351,GO:0048538,GO:0003677,GO:0061056,GO:0001756,GO:0043367,GO:0007526	CG9610-PC				SM00351		PF00292	PS51057	PR00027,PR00027,PR00027,PR00027	PS00034	G3DSA:1.10.10.10,G3DSA:1.10.10.10	SSF46689									
aly37338.60	Phosphatidylglycerophosphatase and protein tyrosine phosphatase 1	GO:0006655,GO:0008138,GO:0006470,GO:0004725,GO:0008962,GO:0006200,GO:0005743,GO:0004439,GO:0046855,GO:0022008	CG10371-PB				SM00195		PF00782	PS50056		PS00383	G3DSA:3.90.190.10	SSF52799									
aly37338.61	Succinate dehydrogenase [ubiqui] cytochrome b small subunit, mitochondrial	GO:0000104,GO:0020037,GO:0046872,GO:0016021,GO:0005740,GO:0005743,GO:0006099,GO:0008177,GO:0048039,GO:0005749	CG10219-PA						PF05328				G3DSA:1.20.1300.10	SSF81343	182~187								
aly37338.62	26S protease regulatory subunit 6A	GO:0004175,GO:0036402,GO:0022624,GO:0017025,GO:0031595,GO:0031597,GO:0008540,GO:0005737,GO:0005838,GO:0043161,GO:0005634,GO:0016020,GO:0001824,GO:1901800,GO:0006508,GO:0005524,GO:0009987,GO:0017111,GO:0030163,GO:0030433,GO:0000502,GO:0045899,GO:0000932	CG10370-PA				SM00382	TIGR01242	PF00004			PS00674	G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540	52~72		REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045							
aly37338.63	Tubulin polyglutamylase TTLL5	GO:0005737,GO:0018095,GO:0005813,GO:0005634,GO:0009566,GO:0006464,GO:0006351,GO:0005929,GO:0007288,GO:0016874,GO:0030317,GO:0004835	CG31108-PA						PF03133	PS51221				SSF56059,SSF56059									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.64	RNA-binding protein lark	GO:0005737,GO:0008270,GO:0045475,GO:0007623,GO:0007562,GO:0071011,GO:0071013,GO:0045995,GO:0000398,GO:0030036,GO:0000166,GO:0008104,GO:0009790,GO:0007303,GO:0003723,GO:0003676,GO:0045804,GO:0008062,GO:0005634,GO:0007067,GO:0003729	CG7903-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928										
aly37338.65	Unknown		n/a																				
aly37338.66	Transcription termination factor 2	GO:0005737,GO:0008094,GO:0034454,GO:0005634,GO:0006353,GO:0004386,GO:0006355,GO:0007283,GO:0003677,GO:0006369,GO:0007143,GO:0005524	CG2684-PA				SM00490		PF00176,PF00271	PS51194			G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	343~363									
aly37338.67	Unknown		n/a												350~370								
aly37338.68	Protein CLP1 homolog	GO:0031124,GO:0005849,GO:0000214,GO:0003674,GO:0006388,GO:0022008,GO:0005524	CG5970-PA						PF16575,PF16573				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540										
aly37338.69	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37338.7	High affinity copper uptake protein 1	GO:0006878,GO:0006825,GO:0016021,GO:0035434,GO:0015088,GO:0002027,GO:0015679,GO:0005886,GO:0005375	CG3977-PC						PF04145														
aly37338.70	Unknown		n/a																				
aly37338.8	Unknown		n/a																				
aly37338.9	Juvenile hormone esterase	GO:0060179,GO:0006719,GO:0048149,GO:0005739,GO:0004453,GO:0052689,GO:0005515	CG8425-PA						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly3738.1	Lachesin	GO:0004714,GO:0005515,GO:0005886,GO:0007155,GO:0007169,GO:0031225	CG32791-PA				SM00408,SM00408,SM00408,SM00406,SM00406,SM00409,SM00409,SM00409		PF07679,PF07679,PF07679	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly3738.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3738.3	TWiK family of potassium channels protein 18	GO:0040011,GO:0005267,GO:0006936,GO:0071805,GO:0006813,GO:0016021,GO:0016020,GO:0015271	CG1688-PA						PF07885,PF07885		PR01333,PR01333		G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324									
aly374.1	Nipped-B-like protein B	GO:0007507,GO:0048565,GO:0005634,GO:0071733,GO:0003146,GO:0005576,GO:0008061,GO:0006030,GO:0060828,GO:0035118,GO:0007049,GO:0007417	CG13676-PA				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly374.10	Protein daughterless	GO:0016330,GO:0061101,GO:0001012,GO:0030707,GO:0045464,GO:0003677,GO:0061382,GO:0007530,GO:0043565,GO:0005634,GO:0008407,GO:0006366,GO:0048477,GO:0000981,GO:0042803,GO:0048663,GO:0008134,GO:0006974,GO:0045893,GO:0035019,GO:0022008,GO:0007399,GO:0007423,GO:0007422,GO:0003700,GO:0007541,GO:0006355,GO:0001077,GO:0045944,GO:0000977,GO:0005667,GO:0046983,GO:0046982	CG5102-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459									
aly374.11	Nucleolar GTP-binding protein 1	GO:0005634,GO:0005730,GO:0090307,GO:0042254,GO:0005525	CG8801-PA			PIRSF038919			PF08155,PF06858	PS51710	PR00326,PR00326,PR00326		G3DSA:3.40.50.300	SSF52540	485~512,395~422								
aly374.12	Presequence protease, mitochondrial	GO:0005759,GO:0006508,GO:0046872,GO:0004222	CG3107-PB						PF08367,PF05193				G3DSA:3.30.830.10,G3DSA:3.30.830.10,G3DSA:3.30.830.10	SSF63411,SSF63411,SSF63411,SSF63411									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly374.13	Protein RRNAD1	GO:0016021	CG2906-PD						PF13679				G3DSA:3.40.50.150	SSF53335									
aly374.14	Zinc finger protein 485	GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG10366-PA				SM00868,SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57716										
aly374.15	Histone-lysine N-methyltransferase PRDM9	GO:0006311,GO:0060903,GO:0010845,GO:0043565,GO:0042800,GO:0010844,GO:0007283,GO:0005654,GO:0034968,GO:0016571,GO:0006351,GO:0003676,GO:0051568,GO:0045944,GO:0046872,GO:0005694	CG7372-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF12874,PF12874,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667,SSF57667,SSF57667										
aly374.16	Zinc finger protein 99	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG5245-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly374.17	Unknown		n/a																				
aly374.18	Glutamate decarboxylase	GO:0009449,GO:0042136,GO:0008345,GO:0005829,GO:0016831,GO:0019752,GO:0004351,GO:0007528,GO:0045213,GO:0030170,GO:0009612,GO:0006538,GO:0007416,GO:0008355	CG14994-PB						PF00282,PF00282			PS00392	G3DSA:3.90.1150.10,G3DSA:1.20.1340.10,G3DSA:3.40.640.10,G3DSA:3.40.640.10	SSF53383										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly374.19	Unknown		n/a																				
aly374.2	Unknown		CG12017-PA																				
aly374.20	Mediator of RNA polymerase II transcription subunit 16	GO:0005634,GO:0003712,GO:0001104,GO:0006355,GO:0006351,GO:0006367,GO:0006366,GO:0016592	CG5465-PA						PF11635				G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978									
aly374.21	PiggyBac transposable element-derived protein 4		CG9839-PA						PF13843														
aly374.22	Serine protease easter	GO:0004252,GO:0009950,GO:0045087,GO:0008063,GO:0031638,GO:0006952,GO:0050830,GO:0005576,GO:0007311,GO:0045752,GO:0006508,GO:0008233,GO:0008236	CG5896-PB				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly374.23	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly374.3	Protein FAM214A		CG9005-PA						PF13889,PF13915														
aly374.4	Unknown		n/a												318~352,6~37,258~306,174~229								
aly374.5	Unknown		n/a						PF15868														
aly374.6	Unknown		n/a																				
aly374.7	BTB/POZ domain-containing protein KCTD20	GO:0004370,GO:0005737,GO:0050975,GO:0035071,GO:0051260,GO:0042327,GO:0048102,GO:0046331	CG1216-PB						PF16017														
aly374.8	YEATS domain-containing protein 2	GO:0072686,GO:0043966,GO:0006338,GO:0000122,GO:0017025,GO:0005634,GO:0004402,GO:0005700,GO:0006355,GO:0005671,GO:0045892,GO:0016573	CG13400-PA						PF03366	PS51037													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly374.9	ATP-dependent zinc metalloprotease YME1 homolog	GO:0004176,GO:0004222,GO:0016021,GO:0005743,GO:0006508,GO:0046872,GO:0005524	CG3499-PB	MF_01458			SM00382	TIGR01241	PF00004,PF01434,PF01434			PS00674	G3DSA:3.40.50.300,G3DSA:1.10.8.60	SSF52540,SSF140990										
aly3744.1	Zinc finger protein ZPR1	GO:0001833,GO:0045927,GO:0032797,GO:1990261,GO:0030426,GO:0035149,GO:0030424,GO:0010628,GO:0000226,GO:0008270,GO:0005737,GO:0043204,GO:0007430,GO:0005730,GO:0005634,GO:0005654,GO:0006360,GO:0048471,GO:0043025,GO:0008380,GO:0033120,GO:0061564,GO:0021510,GO:0042023,GO:0071931,GO:0042307,GO:0071364,GO:0097504,GO:0001834,GO:0031641,GO:0030576,GO:2000672,GO:0015030,GO:1902742,GO:0006397	CG9060-PA				SM00709,SM00709	TIGR00310	PF03367,PF03367														
aly3744.2	Unknown	GO:0032296,GO:0035074,GO:0006308,GO:0003723,GO:0003677,GO:0004844	CG18410-PB												61~97								
aly3744.3	Unknown		n/a												29~49								
aly3746.1	Unknown	GO:0005319,GO:0017129,GO:0006641,GO:0005811,GO:0008525,GO:0035149,GO:0006869,GO:0048813,GO:0008039,GO:0042157	CG9342-PA										G3DSA:1.25.10.20				REACT_22258						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3746.2	Microsomal triglyceride transfer protein large subunit	GO:0017129,GO:0005783,GO:0006869,GO:0035149,GO:0042157,GO:0005791,GO:0005811,GO:0008525,GO:0031988,GO:0005319,GO:0005794,GO:0007623,GO:0006629,GO:0006641,GO:0008289,GO:0008039,GO:0016323,GO:0051592,GO:0042632,GO:0008203,GO:0006497,GO:0031528,GO:0031526,GO:0048813,GO:0043235,GO:0042953	CG9342-PA						PF01347				G3DSA:2.30.230.10	SSF56968			REACT_22258						
aly3746.3	Calpain-11	GO:0005737,GO:0042335,GO:0009953,GO:0015629,GO:0016540,GO:0004198,GO:0030036,GO:0005622,GO:0050832,GO:0021919,GO:0001669,GO:0005509,GO:0008340,GO:0006909,GO:0008233,GO:0043025,GO:0006508	CG7563-PD						PF01067				G3DSA:2.60.120.380	SSF49758									
aly3746.4	Ring canal kelch homolog	GO:0035183,GO:0007300,GO:0045172,GO:0030036,GO:0005856,GO:0007349,GO:0030717,GO:0030723,GO:0003779,GO:0007301,GO:0007303,GO:0007297,GO:0005515,GO:0035324,GO:0048477,GO:0005737,GO:0005938	CG7210-PB				SM00875,SM00225		PF00651,PF07707	PS50097			G3DSA:3.30.710.10	SSF54695									
aly3746.5	Unknown		n/a				SM00595		PF10545,PF10545	PS51029													
aly3746.6	Unknown		CG12155-PA				SM00595		PF10545	PS51029													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3746.7	Calpain	GO:0005737,GO:0042335,GO:0009953,GO:0015629,GO:0016540,GO:0004198,GO:0030036,GO:0005622,GO:0050832,GO:0021919,GO:0005509,GO:0008340,GO:0006909,GO:0043025,GO:0006508	CG7563-PD						PF01067,PF00648	PS50203			G3DSA:3.90.70.10,G3DSA:2.60.120.380	SSF54001,SSF49758									
aly3758.1	Cuticle protein CP14.6	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG6956-PA						PF00379	PS51155		PS00233											
aly3758.10	Transmembrane protein 138	GO:0005774,GO:0016021,GO:0042384,GO:0005929	CG13999-PA						PF14935														
aly3758.11	GA-binding protein subunit beta-1	GO:0044212,GO:0016573,GO:0006338,GO:0003700,GO:0005634,GO:0004402,GO:0006355,GO:0005671,GO:0045944,GO:0006351,GO:0005515,GO:0046982	CG32343-PD				SM00248,SM00248,SM00248,SM00248		PF13606,PF12796	PS50088,PS50297,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403									
aly3758.12	NF-kappa-B-activating protein	GO:0005737,GO:0019827,GO:0007219,GO:0071425,GO:0033077,GO:0000122,GO:0044822,GO:0046638,GO:0005654,GO:0031490,GO:1903955,GO:0030851,GO:0045892,GO:0006351,GO:0030097,GO:0003682	n/a						PF06047						255~292								
aly3758.13	Serine protease 52	GO:0004252,GO:0016021,GO:0006508	CG30289-PA						PF00089			PS00135	G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3758.14	Unknown		n/a																				
aly3758.2	Unknown	GO:0005515	n/a										G3DSA:2.60.40.10	SSF49265									
aly3758.3	Unknown	GO:0016021,GO:0016020,GO:0005272,GO:0006814	CG34369-PB						PF00858														
aly3758.4	Unknown		n/a																				
aly3758.5	Zinc finger protein 1	GO:0007507,GO:0007517,GO:0061321,GO:0019730,GO:0007399,GO:0000122,GO:0007498,GO:0005634,GO:0003677,GO:0008406,GO:0003705,GO:0048103,GO:0007280,GO:0007516,GO:0000977,GO:0008045,GO:0048542,GO:0046872,GO:0008354,GO:0007417	CG1322-PE				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00389		PF00046	PS50157,PS50157,PS50157,PS50157,PS50157,PS50071,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00027,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:1.10.10.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF46689,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3758.6	E3 ubiquitin-protein ligase listerin	GO:0061630,GO:0051865,GO:0016874,GO:0005488,GO:0008270	CG32210-PA										G3DSA:1.25.10.10	SSF48371,SSF48371									
aly3758.7	Unknown		n/a																				
aly3758.8	E3 ubiquitin-protein ligase listerin	GO:0016567,GO:0016874,GO:0008270	CG32210-PA				SM00744		PF13639	PS50089			G3DSA:3.30.40.10	SSF57850					UPA00143				
aly3758.9	Unknown		n/a																				
aly3762.1	Transmembrane protein 8A	GO:0007155,GO:0005765,GO:0070062,GO:0005887,GO:0005886	CG13654-PA						PF12036	PS50026		PS01186,PS00022	G3DSA:2.10.25.10										
aly3762.10	Unknown	GO:0009269,GO:0042169,GO:0030165,GO:0016021	CG14686-PA						PF07841														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3762.11	Serine/threonine-protein phosphatase 5	GO:2000324,GO:0006470,GO:0071944,GO:0007165,GO:0004871,GO:0007067,GO:0010288,GO:0005737,GO:0043204,GO:0005634,GO:0016020,GO:0005654,GO:0016576,GO:0046872,GO:0042802,GO:0043123,GO:0000278,GO:0006281,GO:0070301,GO:0051291,GO:0008289,GO:0071276,GO:0043278,GO:1901215,GO:0006351,GO:0043231,GO:0005829,GO:0004722,GO:0004721,GO:1990635,GO:0003723,GO:0001933	CG8402-PC			PIRSF033096	SM00156,SM00028,SM00028,SM00028		PF08321,PF13414,PF00515,PF00149	PS50005,PS50293,PS50005,PS50005	PR00114,PR00114,PR00114,PR00114,PR00114,PR00114,PR00114		G3DSA:1.25.40.10,G3DSA:3.60.21.10	SSF48452,SSF56300									
aly3762.12	Apolipoprotein D	GO:0022626,GO:0005783,GO:0006869,GO:0042246,GO:0048678,GO:0030425,GO:0000302,GO:0048662,GO:0001525,GO:0051895,GO:0010642,GO:0005615,GO:0014012,GO:0033500,GO:0060588,GO:2000405,GO:0048471,GO:0043025,GO:0005319,GO:0007420,GO:0070328,GO:0006629,GO:0032504,GO:2000098,GO:0008289,GO:0042308,GO:0008340,GO:0006979,GO:0070062,GO:1900016,GO:0031409,GO:0007568,GO:0015485,GO:0042493,GO:0071638,GO:0005576,GO:0006006	CG33126-PB						PF00061,PF00061,PF00061,PF00061,PF00061,PF00061,PF00061,PF08212,PF08212,PF08212,PF08212,PF08212		PR01273,PR01273,PR01273,PR01273	PS00213,PS00213,PS00213,PS00213,PS00213,PS00213,PS00213	G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20,G3DSA:2.40.128.20	SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814,SSF50814									
aly3762.13	Bilin-binding protein	GO:0031409,GO:0070328,GO:0005615,GO:0032504,GO:0008289,GO:0018298,GO:0033500,GO:0005576,GO:0008340,GO:0006979	CG33126-PB			PIRSF036893			PF00061		PR00179,PR00179,PR00179,PR01273,PR01273,PR01273,PR01273,PR01273,PR01273	PS00213	G3DSA:2.40.128.20	SSF50814									
aly3762.14	Lopap	GO:0016504,GO:0031409,GO:0008236,GO:0005576	n/a						PF00061		PR01273,PR01273,PR01273	PS00213	G3DSA:2.40.128.20	SSF50814									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3762.15	Insecticyanin-B	GO:0005576,GO:0031409	n/a						PF00061		PR01273,PR01273,PR01273		G3DSA:2.40.128.20	SSF50814									
aly3762.16	Lopap	GO:0016504,GO:0005576,GO:0008236,GO:0031409	n/a						PF00061				G3DSA:2.40.128.20	SSF50814									
aly3762.17	Unknown		n/a										G3DSA:2.40.128.20	SSF50814									
aly3762.18	Unknown		n/a																				
aly3762.19	Zinc carboxypeptidase (Fragment)	GO:0006508,GO:0004181,GO:0005576,GO:0008270	CG18585-PA				SM00631		PF02244,PF00246,PF00246		PR00765,PR00765,PR00765,PR00765	PS00133,PS00132,PS00132	G3DSA:3.40.630.10,G3DSA:3.40.630.10,G3DSA:3.30.70.340	SSF53187,SSF53187,SSF54897									
aly3762.2	Adenylosuccinate synthetase	GO:0004019,GO:0005737,GO:0044208,GO:0000287,GO:0006164,GO:0022008,GO:0005525	CG17273-PA	MF_00011			SM00788	TIGR00184	PF00709			PS01266,PS00513	G3DSA:3.40.440.10,G3DSA:3.40.440.10,G3DSA:1.10.300.10,G3DSA:3.90.170.10	SSF52540		00230+6.3.4.4,00250+6.3.4.4	REACT_1698	PWY-7219	UPA00075				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3762.20	Zinc carboxypeptidase A 1	GO:0005615,GO:0007586,GO:0004181,GO:0008270,GO:0006508,GO:0022008	CG17633-PA				SM00631		PF02244,PF00246				G3DSA:3.30.70.340,G3DSA:3.40.630.10	SSF53187,SSF54897									
aly3762.21	Zinc carboxypeptidase A 1	GO:0005615,GO:0007586,GO:0004181,GO:0004180,GO:0008270,GO:0006508	CG4017-PA				SM00631,SM00631		PF00246,PF00246,PF02244		PR00765,PR00765,PR00765,PR00765		G3DSA:3.30.70.340,G3DSA:3.30.70.340,G3DSA:3.40.630.10,G3DSA:3.40.630.10	SSF53187,SSF54897,SSF53187,SSF54897									
aly3762.22	Zinc carboxypeptidase A 1	GO:0007586,GO:0006508,GO:0004181,GO:0008270,GO:0005615	CG7025-PA				SM00631		PF02244,PF00246		PR00765,PR00765,PR00765	PS00133	G3DSA:3.30.70.340,G3DSA:3.40.630.10	SSF53187,SSF54897									
aly3762.23	Zinc carboxypeptidase A 1	GO:0022008,GO:0006508,GO:0004181,GO:0008270,GO:0005615	CG7025-PA				SM00631		PF00246,PF02244		PR00765,PR00765,PR00765,PR00765	PS00133	G3DSA:3.30.70.340,G3DSA:3.40.630.10	SSF53187,SSF54897									
aly3762.24	Zinc carboxypeptidase A 1	GO:0022008,GO:0006508,GO:0004181,GO:0008270,GO:0005615	CG17633-PA				SM00631		PF00246,PF00246,PF02244		PR00765,PR00765		G3DSA:3.40.630.10,G3DSA:3.40.630.10,G3DSA:3.30.70.340	SSF54897,SSF53187,SSF53187									
aly3762.3	SAGA-associated factor 11 homolog	GO:0000124,GO:0008270,GO:0051726,GO:0006325,GO:0005634,GO:0003713,GO:0006355,GO:0045893,GO:0005515,GO:0071819,GO:0007412,GO:0016578,GO:0008347,GO:0006351	CG13379-PB	MF_03047					PF08209														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3762.4	N-acetylneuraminate lyase	GO:0005737,GO:0005975,GO:0016829,GO:0019262,GO:0008152,GO:0008747	n/a			PIRSF001365			PF00701		PR00146,PR00146,PR00146		G3DSA:3.20.20.70	SSF51569									
aly3762.5	N-acetylneuraminate lyase	GO:0005737,GO:0003824,GO:0019262,GO:0005975,GO:0008747	n/a			PIRSF001365			PF00701		PR00146,PR00146,PR00146		G3DSA:3.20.20.70	SSF51569									
aly3762.6	4-hydroxy-tetrahydrodipicolinate synthase	GO:0005737,GO:0016829,GO:0019877,GO:0009089,GO:0008152,GO:0008840	n/a						PF00701				G3DSA:3.20.20.70	SSF51569									
aly3762.7	L-asparaginase	GO:0004622,GO:0006520,GO:0006528,GO:0004067	CG6428-PA			PIRSF001220,PIRSF500176	SM00248,SM00248,SM00248,SM00248,SM00870	TIGR00519	PF12796,PF13857,PF00710	PS50088,PS50088,PS50088,PS51732,PS50297	PR00139,PR00139,PR00139	PS00917	G3DSA:3.40.50.40,G3DSA:1.25.40.20,G3DSA:3.40.50.1170	SSF48403,SSF53774,SSF53774									
aly3762.8	Unknown		n/a						PF14924														
aly3762.9	Unknown	GO:0008157	CG31025-PA						PF16003														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly37657.1	Unknown		n/a																				
aly3766.1	Intraflagellar transport protein 74 homolog	GO:0030992,GO:0007219,GO:0060271,GO:0016023,GO:0005813,GO:0005634,GO:0003334,GO:0042073,GO:0050680,GO:0048487,GO:0042384,GO:0045944,GO:0035735,GO:0005929,GO:0008544,GO:0003682,GO:0072372,GO:0033630	n/a												545~579,390~417,184~282,292~312,494~521,442~483,330~378,147~174,116~143								
aly3766.2	Leucine-rich PPR motif-containing protein, mitochondrial	GO:0035145,GO:0006351,GO:0005634,GO:0006810,GO:0005739,GO:0006355,GO:0003723,GO:0003677,GO:0005488	CG14786-PA					TIGR00756	PF01535,PF01535,PF13812	PS51375,PS51375,PS51375,PS51375,PS51375,PS51375,PS51375,PS51375			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48371,SSF48371,SSF48371,SSF48371	638~658								
aly3766.3	ADP-ribosylation factor 6	GO:0055038,GO:0048149,GO:0006471,GO:0055037,GO:0030036,GO:0030139,GO:0001889,GO:0005925,GO:0048488,GO:0003956,GO:0001726,GO:0090004,GO:0070062,GO:0043209,GO:0034394,GO:0090162,GO:0060998,GO:2000171,GO:0097284,GO:0005525,GO:0005794,GO:0003924,GO:0007283,GO:0005938,GO:0007269,GO:0005886,GO:0007520,GO:0007264,GO:0016197,GO:0051489,GO:0007112,GO:0016192,GO:0005829,GO:0036010,GO:0030866,GO:0031527,GO:0030838,GO:0031529,GO:0033028,GO:0015031,GO:0035020,GO:0005769,GO:0005912	CG8156-PD				SM00175,SM00177,SM00178	TIGR00231	PF00025	PS51417	PR00328,PR00328,PR00328,PR00328		G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3766.4	Unknown		n/a																				
aly3766.5	Fibrous sheath interacting protein 2		CG3345-PA												195~215,282~309								
aly3766.6	Unknown	GO:0008028,GO:0016021,GO:0055085	CG8028-PC										G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly3766.7	Unknown		n/a																				
aly3766.8	Monocarboxylate transporter 9	GO:0015718,GO:0015293,GO:0008028,GO:0016021,GO:0034220,GO:0005886,GO:0055085,GO:0046415	CG8028-PC						PF07690,PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly378.1	Alpha-(1,3)-fucosyltransferase C	GO:0036065,GO:0006486,GO:0016021,GO:0016020,GO:0008417,GO:0005886,GO:0032580,GO:0046920	CG40305-PB						PF00852,PF17039					SSF53756					UPA00378				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly378.10	Nuclear transcription factor Y subunit alpha	GO:0043565,GO:0006909,GO:0016602,GO:0051726,GO:0003700,GO:0001221,GO:0005634,GO:0008134,GO:0006366,GO:0046331,GO:0045466,GO:0045893,GO:0001046,GO:0000976,GO:0048511	CG3891-PA				SM00521		PF02045	PS51152	PR00616,PR00616												
aly378.11	Unknown	GO:0005929	CG31036-PA																				
aly378.12	Homeodomain interacting protein kinase 2	GO:0018107,GO:0018105,GO:0008284,GO:0008587,GO:0008586,GO:0097193,GO:0050821,GO:0010842,GO:0090575,GO:0043524,GO:0035265,GO:0043388,GO:0035332,GO:0005737,GO:0050882,GO:0016605,GO:0016604,GO:0042332,GO:0045747,GO:0005634,GO:0003714,GO:0045766,GO:0004674,GO:0043067,GO:0007179,GO:0004672,GO:0005524,GO:0048749,GO:0006468,GO:0030182,GO:0030218,GO:0019048,GO:0008134,GO:0071456,GO:0032092,GO:0008013,GO:0007628,GO:0046332,GO:0001105,GO:0046330,GO:0001654,GO:0048596,GO:0001102,GO:0061072,GO:0030514,GO:0006978,GO:0030511,GO:0042771,GO:0030578,GO:0051091,GO:0009952,GO:0051726,GO:0060395,GO:0000122,GO:0030177,GO:0007224,GO:0046790,GO:0045944,GO:0060235,GO:0060059,GO:0045893	CG17090-PB				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112,SSF56112										
aly378.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly378.14	Cyclin-dependent kinase inhibitor 1	GO:0007050,GO:0004861,GO:0005634,GO:0071850	n/a						PF02234				G3DSA:4.10.365.10										
aly378.15	Unknown	GO:0007050,GO:0004861,GO:0005634	n/a						PF02234				G3DSA:4.10.365.10										
aly378.16	Unknown		n/a						PF02234				G3DSA:4.10.365.10										
aly378.17	Protein FAM114A2		CG9590-PA						PF05334						297~324,129~149								
aly378.18	Unknown		n/a																				
aly378.19	Protein kibra	GO:0005737,GO:0045177,GO:0016324,GO:0060253,GO:0006355,GO:0006351,GO:0005515,GO:0001745,GO:0035330	CG7552-PA				SM00456,SM00456		PF00397,PF00397	PS50020,PS50020		PS01159	G3DSA:2.20.70.10,G3DSA:2.20.70.10	SSF51045,SSF51045	531~554,302~336,878~898,361~388,237~257,173~200								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly378.2	Alpha-(1,3)-fucosyltransferase C	GO:0036065,GO:0006486,GO:0016021,GO:0016020,GO:0008417,GO:0005886,GO:0032580,GO:0046920	CG40305-PB						PF00852					SSF53756					UPA00378				
aly378.20	Ras association domain-containing protein 10	GO:0005829,GO:0000922,GO:0007165,GO:0005815	CG13875-PA											SSF54236	334~396,298~318,159~186								
aly378.21	Alpha-N-acetylglucosaminidase	GO:0005764,GO:0043202,GO:0005975,GO:0070062,GO:0007399,GO:0046548,GO:0021680,GO:0004561,GO:0060119,GO:0045475,GO:0007040,GO:0030203,GO:0004298,GO:0044281,GO:0006027,GO:0042474	CG13397-PA				SM00948		PF12972,PF00227,PF12971,PF05089,PF10584	PS51475		PS00388	G3DSA:3.60.20.10	SSF56235		00531+3.2.1.50	REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045							
aly378.22	FMRFamide-related peptides	GO:0007218,GO:0005576	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly378.23	Transient receptor potential protein	GO:0050962,GO:0008104,GO:0005262,GO:0009416,GO:0034703,GO:0050908,GO:0008377,GO:0006828,GO:0008355,GO:0008086,GO:0008087,GO:0015279,GO:0016028,GO:0016021,GO:0016027,GO:0010461,GO:0071454,GO:0042802,GO:0042803,GO:0005218,GO:0007608,GO:0019722,GO:0007605,GO:0006816,GO:0007603,GO:0007602,GO:0035997,GO:0005887,GO:0005886,GO:0051480,GO:0005829,GO:0070588,GO:0005622,GO:0030845,GO:0005516,GO:0005515,GO:0046982	CG7875-PA				SM00248,SM00248	TIGR00870	PF12796,PF08344,PF00520	PS50088,PS50297	PR01097,PR01097,PR01097		G3DSA:1.25.40.20	SSF48403			REACT_18266						
aly378.24	Transient-receptor-potential-like protein	GO:0005261,GO:0005262,GO:0030425,GO:0009416,GO:0034703,GO:0050908,GO:0006828,GO:0008086,GO:0015279,GO:0035997,GO:0016021,GO:0019722,GO:0016027,GO:0010461,GO:0071454,GO:0042802,GO:0007589,GO:0007605,GO:0006812,GO:0006811,GO:0006816,GO:0007603,GO:0016028,GO:0005887,GO:0005886,GO:0051480,GO:0005829,GO:0070588,GO:0005622,GO:0015075,GO:0005516,GO:0005515,GO:0046982	CG18345-PA				SM00248,SM00248	TIGR00870	PF00520,PF08344,PF13606,PF12796	PS50088,PS50297	PR01097,PR01097,PR01097		G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403	871~891		REACT_18266						
aly378.25	Probable protein phosphatase 2C T23F11.1	GO:0003824,GO:0048786,GO:0046872,GO:0004722,GO:0006470	CG17746-PA				SM00332		PF00481	PS51746		PS01032	G3DSA:3.60.40.10	SSF81606									
aly378.26	Tryptophan 2,3-dioxygenase	GO:0019441,GO:0019442,GO:0020037,GO:0048072,GO:0006569,GO:0005575,GO:0006727,GO:0004833,GO:0046872	CG2155-PA	MF_01972					PF03301					SSF140959,SSF140959		00380+1.13.11.11			UPA00333				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly378.27	Ecto-NOX disulfide-thiol exchanger 2	GO:0009897,GO:0007624,GO:0016049,GO:0005615,GO:0005829,GO:0000166,GO:0003676,GO:0015035,GO:0040008,GO:0055114,GO:0003729	CG10948-PC				SM00360		PF00076	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928	472~506,367~394								
aly378.28	Cathepsin O	GO:0005764,GO:0003674,GO:0005615,GO:0035071,GO:0051603,GO:0035220,GO:0045169,GO:0005575,GO:0048102,GO:0004197,GO:0008150,GO:0004869,GO:0006508,GO:0022416	CG12163-PA				SM00645,SM00848		PF08246,PF00112		PR00705,PR00705,PR00705	PS00639,PS00139	G3DSA:3.90.70.10	SSF54001									
aly378.29	Aldose 1-epimerase	GO:0005737,GO:0006012,GO:0005975,GO:0070062,GO:0004034,GO:0019318,GO:0030246,GO:0003824,GO:0005576,GO:0006006	CG10467-PA			PIRSF005096			PF01263			PS00545	G3DSA:2.70.98.10	SSF74650		00010+5.1.3.3,00052+5.1.3.3		PWY-6317,PWY-2723,PWY-6737	UPA00242				
aly378.3	Carbonic anhydrase-related protein 10	GO:0004089,GO:0008270,GO:0005576	CG1402-PB				SM01057		PF00194	PS51144			G3DSA:3.10.200.10	SSF51069									
aly378.30	RNA-binding protein 41	GO:0003676,GO:0000398,GO:0000166,GO:0034693,GO:0003723,GO:0005689,GO:0005693,GO:0003729	CG44249-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928	148~168								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly378.31	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	GO:0035060,GO:0003677,GO:0008080,GO:0005634,GO:0043044,GO:0003713,GO:0005654,GO:0016514,GO:0000980,GO:0047485,GO:0017053,GO:0000790,GO:0045892,GO:0045893,GO:0008152,GO:0090544,GO:0016922,GO:0043234,GO:0007399,GO:0006338,GO:0006337,GO:0006355,GO:0071565,GO:0071564,GO:0005515,GO:0003723,GO:0000978,GO:0003682	CG7055-PA				SM00398		PF00505	PS50118			G3DSA:1.10.30.10	SSF47095	294~328,181~201								
aly378.32	Unknown		n/a																				
aly378.33	Unknown		n/a																				
aly378.34	Unknown		CG7669-PA						PF13879														
aly378.35	UHRF1-binding protein 1-like	GO:0005575,GO:0008150,GO:0003674	CG34126-PE						PF12624						1133~1164,1181~1201								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly378.36	Protein kinase C and casein kinase substrate in neurons protein 1	GO:0016020,GO:0060088,GO:0061024,GO:0045887,GO:0045202,GO:0030054,GO:0005543,GO:0000281,GO:0031988,GO:0048812,GO:0048488,GO:0043005,GO:0071212,GO:0008289,GO:0032154,GO:0045211,GO:0007053,GO:0036090,GO:0007269,GO:0005886,GO:0006897,GO:0030100,GO:0032587,GO:0007015,GO:0007112,GO:0007010,GO:0030659,GO:0005829,GO:0008092,GO:0030496,GO:0097320,GO:0005515,GO:0005768	CG33094-PC				SM00055		PF00611	PS51741,PS50002			G3DSA:2.30.30.40	SSF50044,SSF103657										
aly378.37	Myotubularin-related protein 5	GO:0008023,GO:0016311,GO:0055037,GO:0032968,GO:0043086,GO:0043547,GO:0019992,GO:0005634,GO:0000278,GO:0008138,GO:0017137,GO:0017112,GO:0032483,GO:0007283,GO:0019902,GO:0005938,GO:0036313,GO:0030674,GO:0030866,GO:0001558,GO:0032456,GO:0003682,GO:0001691	CG6939-PA						PF06602	PS50003,PS51339			G3DSA:2.30.29.30	SSF52799,SSF52799,SSF52799,SSF50729										
aly378.38	Myotubularin-related protein 13	GO:0008023,GO:0016311,GO:0019208,GO:0005085,GO:0032968,GO:0005737,GO:0019992,GO:0005634,GO:0016020,GO:0055037,GO:0000278,GO:0008138,GO:0017137,GO:0017112,GO:0032483,GO:0019902,GO:0005938,GO:0036313,GO:0030674,GO:0030866,GO:0032456,GO:0003682	CG6939-PA						PF12335,PF02893														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly378.39	Unknown		n/a																				
aly378.4	Alpha-(1,3)-fucosyltransferase C	GO:0036065,GO:0006486,GO:0016021,GO:0016020,GO:0008417,GO:0005886,GO:0032580,GO:0046920	CG40305-PB						PF00852,PF17039					SSF53756					UPA00378				
aly378.40	Unknown		CG13003-PB																				
aly378.41	Unknown		n/a																				
aly378.42	Tektin-1	GO:0007017,GO:0008017,GO:0015630,GO:0000226,GO:0005634,GO:0005874,GO:0005875	CG10541-PA						PF03148		PR00511,PR00511,PR00511,PR00511				294~335,173~200								
aly378.43	UHRF1-binding protein 1-like	GO:0005575,GO:0008150,GO:0003674	CG34126-PE																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly378.5	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9503-PA			PIRSF000137			PF05199,PF00732			PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly378.6	Deoxycytidylate deaminase	GO:0006220,GO:0016787,GO:0070062,GO:0004132,GO:0009165,GO:0008270	CG6951-PB						PF00383	PS51747		PS00903	G3DSA:3.40.140.10	SSF53927									
aly378.7	N-alpha-acetyltransferase 15, NatA auxiliary subunit	GO:0005737,GO:0016020,GO:0072686,GO:0008080,GO:0005634,GO:0030154,GO:0031145,GO:0006474,GO:0043022,GO:0050821,GO:0043066,GO:0045893,GO:0005667,GO:0022008,GO:0001525,GO:0044822,GO:0004596,GO:0006351	CG12202-PA			PIRSF000422	SM00028,SM00028,SM00028,SM00028,SM00028		PF07719,PF12569	PS50005,PS50293,PS50005,PS50293,PS50005,PS50005,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452	592~612								
aly378.8	Unknown		n/a												37~64,2~22,107~134								
aly378.9	Unknown		n/a										G3DSA:3.10.450.50	SSF54427	50~70								
aly37837.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3787.1	Protein PAT1 homolog 2	GO:0005737,GO:0033962,GO:0005634,GO:0000932,GO:0045886,GO:0003723,GO:0017148	CG5208-PA										G3DSA:1.20.120.20		346~366,122~142								
aly379.1	Unknown		n/a																				
aly379.10	Zinc finger protein 624	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0022008,GO:0046872,GO:0006351	CG7386-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57716,SSF57667,SSF57667									
aly379.11	Unknown		CG43861-PC												33~53								
aly379.12	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly379.13	60S ribosomal protein L7a	GO:0005840,GO:0022625,GO:0051297,GO:0042254,GO:0003735,GO:0007052,GO:0000022,GO:0006412,GO:0051298	CG3314-PA						PF01248		PR00882,PR00882,PR00882,PR00882,PR00882,PR00882,PR00882,PR00881,PR00881,PR00881,PR00881	PS01082	G3DSA:3.30.1330.30	SSF55315			REACT_71						
aly379.2	5-hydroxytryptamine receptor 1B	GO:0060179,GO:0007619,GO:0007268,GO:0008144,GO:0042310,GO:0004952,GO:0035690,GO:0007631,GO:0005737,GO:0030818,GO:0016021,GO:0071312,GO:0004993,GO:0060180,GO:0050795,GO:0005887,GO:0005886,GO:0008227,GO:0014063,GO:0051378,GO:0071502,GO:0016543,GO:0007205,GO:0016545,GO:0016546,GO:0007198,GO:0002031,GO:0046849,GO:0007192,GO:0007210	CG12073-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly379.3	Neurogenic locus Notch protein	GO:0007616,GO:0007476,GO:0007615,GO:0008587,GO:0005788,GO:0007293,GO:0045465,GO:0045463,GO:0007297,GO:0007298,GO:0001745,GO:0061382,GO:0045468,GO:0007219,GO:0016021,GO:0005770,GO:0007519,GO:0007451,GO:0042688,GO:0042689,GO:0042686,GO:0005796,GO:0035172,GO:0060250,GO:0035170,GO:0035171,GO:0046331,GO:0007521,GO:0045316,GO:0043234,GO:0007440,GO:0007447,GO:0007446,GO:0045466,GO:0005829,GO:0009608,GO:0046843,GO:0048666,GO:0035165,GO:0035167,GO:0035162,GO:0035003,GO:0010629,GO:0046329,GO:0007346,GO:0008407,GO:0005654,GO:0048803,GO:0016360,GO:0048477,GO:0035153,GO:0035155,GO:0035157,GO:0042067,GO:0060288,GO:0048863,GO:0046666,GO:0046667,GO:0007424,GO:0045165,GO:0009952,GO:0007423,GO:0007422,GO:0007314,GO:0061331,GO:0006351,GO:0001708,GO:0007498,GO:0007450,GO:0005886,GO:0035222,GO:0007419,GO:0010001,GO:0007411,GO:0005737,GO:0050767,GO:0030708,GO:0007252,GO:0000122,GO:0031410,GO:0005634,GO:0030707,GO:0050768,GO:0045747,GO:0005509,GO:0008284,GO:0007015,GO:0050877,GO:0009986,GO:0060429,GO:0045595,GO:0005912,GO:0007403,GO:0007400,GO:0036335,GO:0030718,GO:2000048,GO:0030713,GO:0005622,GO:0045944,GO:0005515,GO:0048542,GO:0003682,GO:0016333,GO:0016330,GO:0007464,GO:0030139,GO:0004872,GO:0008045,GO:0008356,GO:0007478,GO:0007473,GO:0040008,GO:0030720,GO:0007474,GO:1900087,GO:0048749,GO:0035214,GO:0048190,GO:0016348,GO:0042676,GO:0022416,GO:0005887,GO:0048052,GO:0007155,GO:0008340,GO:0007157,GO:0001737,GO:0036099,GO:0008347,GO:0051489,GO:0007398,GO:0007460,GO:0036011,GO:0007391,GO:0005	CG3936-PA			PIRSF002279	SM00179,SM00181,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00004,SM00004,SM00004		PF00023,PF07645,PF07645,PF07645,PF07645,PF12796,PF00008,PF06816,PF13857,PF00066,PF00066,PF00066,PF07684	PS50026,PS50026,PS50026,PS50258,PS50026,PS50026,PS50026,PS50026,PS50088,PS50026,PS50026,PS50088,PS50026,PS50026,PS50026,PS50088,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50297,PS50026,PS50088,PS50258,PS50026,PS50026,PS50026,PS50026,PS50026,PS50258,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026	PR00010,PR00010,PR00010,PR00010,PR01983,PR01983,PR01983,PR01983,PR01983,PR01452,PR01452,PR01452	PS01186,PS00010,PS00022,PS01186,PS01187,PS00022,PS00010,PS01186,PS01187,PS00022,PS01186,PS00022,PS00010,PS00010,PS01186,PS00022,PS01186,PS00022,PS00010,PS01187,PS01186,PS01186,PS00010,PS00022,PS01186,PS00010,PS01187,PS01186,PS01186,PS01187,PS00010,PS01187,PS01186,PS01187,PS01187,PS00022,PS00022,PS01187,PS00010,PS00022,PS01186,PS01186,PS00022,PS01187,PS01186,PS00010,PS00022,PS00010,PS01186,PS00022,PS01186,PS01187,PS00022,PS00022,PS01187,PS00022,PS01187,PS01187,PS00022,PS00010,PS01186,PS00022,PS00022,PS01187,PS01187,PS00022,PS01187,PS01186,PS01186,PS01186,PS01186,PS00022,PS00022,PS01186,PS01186,PS00022,PS00010,PS00022,PS01187,PS00010,PS00010,PS00010,PS00010,PS00022,PS00010,PS00010,PS01186,PS00010,PS01186,PS00022,PS00010,PS00022,PS01187,PS01186,PS00022,PS00010,PS01186,PS00022,PS00022,PS00022,PS00022,PS01187,PS00010,PS00022,PS00022	G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:1.25.40.20,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57184,SSF57196,SSF57196,SSF57196,SSF57196,SSF57184,SSF57184,SSF57196,SSF48403,SSF90193,SSF57184,SSF90193,SSF57196,SSF57196,SSF57196,SSF57184,SSF57184,SSF57184,SSF57196,SSF90193,SSF57196,SSF57196,SSF57196			REACT_71,REACT_299						
aly379.4	Coiled-coil domain-containing protein 151	GO:0036064,GO:0036158,GO:0005814,GO:0005929,GO:0003341,GO:1902017,GO:0005930	CG14127-PA												379~423,206~233,118~145,43~63								
aly379.5	Radial spoke head 14 homolog		n/a										G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly379.6	Neuropathy target esterase sws	GO:0007420,GO:0006643,GO:0007399,GO:0034349,GO:0016021,GO:0005789,GO:0061024,GO:0051402,GO:0005515,GO:0004622,GO:0046470,GO:0007608	CG2212-PA				SM00100,SM00100,SM00100		PF01734,PF00027,PF00027	PS50042,PS50042,PS50042		PS01237	G3DSA:2.60.120.10,G3DSA:2.60.120.10,G3DSA:2.60.120.10,G3DSA:3.40.1090.10	SSF52151,SSF51206,SSF51206,SSF51206									
aly379.7	RNA-binding protein 1	GO:0005515,GO:0005634,GO:0045292,GO:0000398,GO:0000166,GO:0006376,GO:0003676,GO:0035327,GO:0008380,GO:0003729	CG17136-PD				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly379.8	UDP-xylose and UDP-N-acetylglucosamine transporter	GO:0005783,GO:0036084,GO:0015784,GO:0036066,GO:0016021,GO:0008643,GO:0005462,GO:0005461,GO:0005460,GO:0015790,GO:0005464,GO:0005338,GO:0055085,GO:0015788,GO:0015783,GO:0015782,GO:0015787,GO:0015786,GO:0000139,GO:0015012,GO:0005458,GO:0005456,GO:0005457	CG3774-PA						PF08449														
aly379.9	Unknown	GO:0005515	CG8180-PB				SM00192			PS50068		PS01209	G3DSA:4.10.400.10	SSF57424									
aly3799.1	Unknown		n/a																				
aly3799.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly38.1	Kin of IRRE-like protein 1	GO:0045121,GO:0016337,GO:0005515,GO:0007588,GO:0038838,GO:0043198,GO:0016021,GO:0007606,GO:0031253,GO:0005575,GO:0003674,GO:0005911,GO:0001933,GO:0048471,GO:0070062	CG14162-PF				SM00409,SM00409,SM00408		PF13895,PF07686	PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly38.10	Probable malonyl-CoA-acyl carrier protein transacylase, mitochondrial	GO:0006633,GO:0016740,GO:0005739,GO:0004314,GO:0008152	CG7842-PA						PF00698				G3DSA:3.40.366.10	SSF52151									
aly38.11	Unknown	GO:0005575,GO:0007606,GO:0003674	CG14162-PF																				
aly38.2	Cytochrome b5	GO:0005811,GO:0043231,GO:0035206,GO:0051726,GO:0016021,GO:0016020,GO:0005789,GO:0020037,GO:0046872,GO:0009055,GO:0045610,GO:0055114,GO:0002168	CG2140-PB						PF00173	PS50255	PR00363,PR00363,PR00363,PR00363	PS00191	G3DSA:3.10.120.10	SSF55856									
aly38.3	Cytochrome b5	GO:0005811,GO:0043231,GO:0035206,GO:0051726,GO:0016021,GO:0016020,GO:0005789,GO:0020037,GO:0046872,GO:0009055,GO:0045610,GO:0055114,GO:0002168	CG2140-PB						PF00173	PS50255	PR00363,PR00363,PR0363	PS00191	G3DSA:3.10.120.10	SSF55856									
aly38.4	Integrator complex subunit 9	GO:0016180,GO:0016787,GO:0005847,GO:0034472,GO:0005737,GO:0032039,GO:0005654,GO:0006378,GO:0006379	CG5222-PA				SM01027		PF10996				G3DSA:3.60.15.10,G3DSA:3.60.15.10,G3DSA:3.60.15.10	SSF56281,SSF56281,SSF56281									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly38.5	Leucine carboxyl methyltransferase 1	GO:0006479,GO:0006481,GO:0008757,GO:0005829,GO:0031333,GO:0090266,GO:0006464,GO:0010906,GO:0003880,GO:0008168,GO:0032259,GO:0042981	CG3793-PB			PIRSF016305			PF04072				G3DSA:3.40.50.150	SSF53335									
aly38.6	Phospholipase ABHD3	GO:0008970,GO:0006629,GO:0052740,GO:0046470,GO:0005575,GO:0052739,GO:0004623,GO:0016298,GO:0016021	CG8058-PA			PIRSF005211			PF12146				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474									
aly38.7	Unknown		n/a																				
aly38.8	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	GO:0050660,GO:0006635,GO:0005743,GO:0033539,GO:0005811,GO:0000062,GO:0042760,GO:0003995,GO:0004466,GO:0005739,GO:0017099,GO:0005875,GO:0055114	CG7461-PB						PF02771,PF00441,PF02770			PS00072	G3DSA:2.40.110.10,G3DSA:1.10.540.10,G3DSA:1.20.140.10	SSF47203,SSF56645									
aly38.9	Probable malonyl-CoA-acyl carrier protein transacylase, mitochondrial	GO:0006633,GO:0016740,GO:0005739,GO:0004314,GO:0008152	CG7842-PA										G3DSA:3.40.366.10	SSF52151									
aly38104.1	Aminopeptidase N	GO:0004177,GO:0042277,GO:0016021,GO:0030154,GO:0006725,GO:0031983,GO:0008270,GO:0012506,GO:0006508,GO:0001525,GO:0035814,GO:0008237	CG11951-PA						PF11838														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly38104.2	Transmembrane protein 181	GO:0016021,GO:0009405,GO:0015643	CG13409-PA						PF06664														
aly3815.1	BTB/POZ domain-containing protein KCTD1	GO:0045892,GO:0005634,GO:0003714,GO:0051260,GO:0006351	CG10440-PB						PF02214				G3DSA:3.30.710.10	SSF54695									
aly3815.2	Serine/threonine-protein kinase OSR1	GO:0005737,GO:0004674,GO:0006468,GO:0000287,GO:0008362,GO:0004702,GO:0035220,GO:0008065,GO:0008366,GO:0004672,GO:0035556,GO:0007413,GO:0005524	CG7693-PA				SM00220		PF00069,PF12202	PS50011		PS00107	G3DSA:3.30.200.20,G3DSA:3.10.20.90,G3DSA:1.10.510.10	SSF56112									
aly3815.3	Unknown		n/a																				
aly3816.1	Zinc finger protein 26	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872	CG6654-PA				SM00355,SM00355			PS50157		PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667									
aly3816.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3816.3	Cleavage and polyadenylation specificity factor subunit 5	GO:0016787,GO:0042382,GO:0006397,GO:0005813,GO:0005849,GO:0051262,GO:0017091,GO:0006378,GO:0006379,GO:0003729	CG3689-PC						PF13869														
aly3816.4	Tolloid-like protein 1	GO:0004222,GO:0030154,GO:0005576,GO:0008270,GO:0006508,GO:0022008,GO:0005518,GO:0007275,GO:0005509	CG15255-PA				SM00235		PF01400		PR00480,PR00480,PR00480,PR00480		G3DSA:3.40.390.10	SSF55486									
aly3816.5	Unknown		n/a																				
aly3824.1	Protocadherin-like wing polarity protein stan	GO:0016319,GO:0016318,GO:0007409,GO:0016339,GO:0016358,GO:0030177,GO:0007164,GO:0007165,GO:0070593,GO:0007411,GO:0035556,GO:0030178,GO:0004930,GO:0050839,GO:0007367,GO:0005057,GO:0016021,GO:0016020,GO:0004888,GO:0045746,GO:0005509,GO:0042067,GO:0035159,GO:0007218,GO:0048057,GO:0001738,GO:0005887,GO:0005886,GO:0007156,GO:0001736,GO:0005911,GO:0050770,GO:0090175,GO:0016055,GO:0007464,GO:0005622,GO:0051963,GO:0048813,GO:0004872	CG11895-PF				SM00282,SM00282,SM00180,SM00008,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00179,SM00179,SM00303,SM00181,SM00181,SM00181,SM00181		PF00008,PF02793,PF01825,PF16489,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF02210,PF02210,PF00053	PS50026,PS50268,PS50026,PS50025,PS50221,PS50268,PS50027,PS50227,PS50268,PS50025,PS50268,PS50268,PS50268,PS50026,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00022,PS00232,PS00232,PS01248,PS00022,PS01186,PS00232,PS00022,PS00232,PS01186,PS00232,PS01186,PS00232	G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.10.25.10,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49899,SSF49899,SSF49313,SSF49313,SSF49313,SSF49313,SSF57196,SSF49899,SSF49313								
aly3824.10	Facilitated trehalose transporter Tret1-2 homolog	GO:0005355,GO:0035428,GO:0015992,GO:0016021,GO:0016020,GO:0046323,GO:0022857,GO:0005887,GO:0005886,GO:0005351,GO:0055085	CG4797-PB						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473			REACT_15518						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3824.11	Facilitated trehalose transporter Tret1	GO:0022891,GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG4797-PB					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00217,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	438~448		REACT_15518						
aly3824.12	Unknown	GO:0032432,GO:0008407,GO:0030046	CG32397-PD												1111~1138								
aly3824.13	Transposable element Tcb1 transposase	GO:0015074,GO:0005634,GO:0006313,GO:0004803,GO:0003677	n/a						PF01498					SSF46689									
aly3824.2	V-type proton ATPase 21 kDa proteolipid subunit	GO:0015991,GO:0016021,GO:0000220,GO:0016471,GO:0033181,GO:0033179,GO:0007052,GO:0046961,GO:0008553,GO:0005768,GO:0015078,GO:0033177	CG7007-PB						PF00137,PF00137		PR00122,PR00122,PR00122		G3DSA:1.20.120.610	SSF81333,SSF81333	205~205								
aly3824.3	Protein dispatched	GO:0006887,GO:0007224,GO:0016021,GO:0016020,GO:0005623,GO:0007280,GO:0008158,GO:0007275	CG2019-PA						PF02460	PS50156			G3DSA:1.20.1640.10,G3DSA:1.20.1640.10	SSF82866,SSF82866	960~980								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3824.4	IST1 homolog	GO:0008104,GO:0048672,GO:0098779,GO:0003674,GO:0051301,GO:0070062,GO:0016023,GO:0005813,GO:0032403,GO:0005793,GO:0019076,GO:0032509,GO:0045184,GO:0019904,GO:0046745,GO:0090543,GO:0090541,GO:0000910,GO:0009838,GO:0005829,GO:0030496,GO:0002230,GO:0045862,GO:0005768	CG10103-PA						PF03398						8~42								
aly3824.5	Phospholipase A-2-activating protein	GO:0016005,GO:0008150,GO:0005515,GO:0045169	CG5105-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF09070,PF00400,PF00400,PF00400,PF00400,PF00400,PF00400,PF08324	PS51394,PS51396,PS50082,PS50294,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978									
aly3824.6	Calcium uniporter protein, mitochondrial	GO:0007015,GO:0008016,GO:0032024,GO:0006851,GO:0019722,GO:0060027,GO:0005262,GO:0005743,GO:0031305,GO:0042593,GO:0035786,GO:1990246,GO:0003676,GO:0043009,GO:0051561	CG18769-PH						PF04678						160~194								
aly3824.7	Unknown	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG9665-PB						PF00379,PF00379	PS51155,PS51155,PS51155													
aly3824.8	General odorant-binding protein 70	GO:0005549,GO:0006810,GO:0007608,GO:0050896,GO:0007606,GO:0005576	CG13027-PB										G3DSA:1.10.238.20	SSF47565									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3824.9	Aminoacylase-1	GO:0004046,GO:0005737,GO:0006520,GO:0006508,GO:0046872,GO:0008237	CG6465-PA			PIRSF036696		TIGR01880	PF07687,PF01546			PS00759,PS00758	G3DSA:3.40.630.10,G3DSA:3.40.630.10,G3DSA:3.30.70.360	SSF53187,SSF53187,SSF55031		00330+3.5.1.14							
aly38243.1	Unknown	GO:0005575,GO:0003674,GO:0008150	CG3520-PA																				
aly3825.1	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232	PS51257	PR00131,PR00131,PR00131,PR00131,PR00131	PS00653,PS00572	G3DSA:3.20.20.80	SSF51445									
aly383.1	Unknown		n/a																				
aly383.10	Transmembrane protein 198	GO:0016023,GO:0016021,GO:0016055,GO:0012506,GO:0005886,GO:0007275	CG14234-PA						PF13886														
aly383.11	Protein DDI1 homolog 2	GO:0005737,GO:0070628,GO:0005634,GO:0007301,GO:0043130,GO:0004190,GO:0006508	CG4420-PA						PF09668,PF00240	PS50053,PS50175			G3DSA:2.40.70.10,G3DSA:3.10.20.90	SSF50630,SSF54236									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly383.12	Unknown		n/a																				
aly383.13	Unknown		n/a										G3DSA:1.10.8.10										
aly383.14	SH2 domain-containing protein 3C	GO:0005070,GO:0005088,GO:0016020,GO:0005085,GO:0046579,GO:0005622,GO:0005575,GO:0048812,GO:0007165,GO:0005068,GO:0007169,GO:0007264,GO:0005737	CG9098-PA				SM00147,SM00252		PF00017,PF00617	PS50001,PS50009	PR00401,PR00401,PR00401,PR00401		G3DSA:3.30.505.10,G3DSA:1.10.840.10	SSF48366,SSF55550									
aly383.15	Alpha-mannosidase 2	GO:0016799,GO:0030246,GO:0001889,GO:0008270,GO:0060042,GO:0007005,GO:0044267,GO:0001701,GO:0070062,GO:0016021,GO:0016020,GO:0050769,GO:0006013,GO:0018279,GO:0043687,GO:0007585,GO:0035010,GO:0007033,GO:0005975,GO:0006491,GO:0003824,GO:0005801,GO:0000139,GO:0004572,GO:0048286,GO:0004559	CG4606-PA				SM00872		PF09261,PF07748,PF01074				G3DSA:3.20.110.10,G3DSA:2.70.98.30,G3DSA:1.20.1270.50,G3DSA:2.60.40.1180	SSF88713,SSF74650,SSF88688										
aly383.16	ADP-ribosylation factor-like protein 5B	GO:0003924,GO:0005622,GO:0005575,GO:0008150,GO:0007264,GO:0005525	CG7197-PA				SM00177,SM00178	TIGR00231	PF00025	PS51417	PR00328,PR00328,PR00328,PR00328		G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly383.17	Alpha-mannosidase 2	GO:0016799,GO:0030246,GO:0001889,GO:0008270,GO:0060042,GO:0007005,GO:0001701,GO:0070062,GO:0016021,GO:0016020,GO:0050769,GO:0006013,GO:0005794,GO:0015923,GO:0007585,GO:0035010,GO:0007033,GO:0006491,GO:0005801,GO:0000139,GO:0004572,GO:0048286,GO:0004553,GO:0004559	CG4606-PA				SM00872		PF01074,PF09261,PF07748				G3DSA:1.20.1270.50,G3DSA:3.20.110.10,G3DSA:2.70.98.30,G3DSA:2.60.40.1180	SSF88713,SSF88688,SSF74650										
aly383.18	L-galactose dehydrogenase	GO:0019853,GO:0006012,GO:0005829,GO:0010349,GO:0055114,GO:0016491	CG18547-PA						PF00248				G3DSA:3.20.20.100	SSF51430									
aly383.19	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase S	GO:0046989,GO:0046872,GO:0006486,GO:0006688,GO:0016021,GO:0016020,GO:0000139,GO:0030166,GO:0046988,GO:0015020,GO:0015018,GO:0009101,GO:0046987	CG3881-PC						PF03360				G3DSA:3.90.550.10	SSF53448									
aly383.2	Unknown		n/a						PF00567,PF00567	PS51257			G3DSA:2.30.30.140	SSF63748									
aly383.20	Unknown	GO:0046872,GO:0005875	CG11122-PA				SM00355,SM00355,SM00355,SM00355			PS50157		PS00028											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly383.21	Unknown	GO:0046872	n/a							PS50157		PS00028	G3DSA:3.30.160.60		2623~2624								
aly383.22	Unknown	GO:0046872,GO:0005875	CG11122-PA																				
aly383.23	Sensory neuron membrane protein 2	GO:0007608,GO:0050896,GO:0016020,GO:0004888,GO:0005886,GO:0007155,GO:0016021	CG7422-PC						PF01130														
aly383.24	Lysozyme C-1	GO:0005795,GO:0019835,GO:0019730,GO:0000137,GO:0030140,GO:0030141,GO:0016798,GO:0005788,GO:0005737,GO:0003796,GO:0050830,GO:0005576,GO:0050829,GO:0005902,GO:0048237	CG8492-PD				SM00263		PF00062	PS51348	PR00135,PR00135,PR00135	PS00128	G3DSA:1.10.530.10	SSF53955									
aly383.25	Sensory neuron membrane protein 2	GO:0007608,GO:0050896,GO:0016020,GO:0004888,GO:0005886,GO:0007155,GO:0016021	CG7422-PC						PF01130														
aly383.26	Protein AF-10	GO:0005737,GO:0007482,GO:0045433,GO:0003700,GO:0005634,GO:0007591,GO:0005654,GO:0006355,GO:0045944,GO:0008270,GO:0005515,GO:0003677,GO:0002168	CG1070-PP				SM00249,SM00249		PF13831,PF13832	PS50016		PS01359	G3DSA:3.30.40.10	SSF57903	868~870,7 73~793								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly383.27	Proton-coupled amino acid transporter 4	GO:0016021,GO:0015293,GO:0015193,GO:0003333,GO:0015180,GO:0035524,GO:0015827,GO:0015824,GO:0015196,GO:0005774,GO:0015808,GO:0015171	CG43693-PG						PF01490														
aly383.28	Sentrin-specific protease 7	GO:0005737,GO:0005634,GO:0007476,GO:0060997,GO:0016929,GO:0016926,GO:0006508,GO:0008234,GO:0021952	CG12717-PA						PF02902	PS50600			G3DSA:3.30.310.130,G3DSA:3.30.310.130	SSF54001,SSF54001									
aly383.29	PERQ amino acid-rich with GYF domain-containing protein CG11148	GO:0008150,GO:0072686,GO:0003674,GO:0005515,GO:0005813	CG11148-PG				SM00444		PF02213	PS50829			G3DSA:3.30.1490.40	SSF55277	1056~1077								
aly383.3	Zinc finger protein 583	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF00096,PF13912,PF13894	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly383.30	PERQ amino acid-rich with GYF domain-containing protein CG11148	GO:0008150,GO:0072686,GO:0003674,GO:0005813	CG11148-PG												36~56								
aly383.31	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly383.32	Otoferlin	GO:0008021,GO:0010996,GO:0030672,GO:0050885,GO:0030381,GO:0016079,GO:0016021,GO:0035045,GO:0009566,GO:0016323,GO:0009790,GO:0007283,GO:0005509,GO:0005515,GO:0005789,GO:0030054	CG5747-PF				SM00239,SM00239,SM00239,SM00239,SM00239		PF00168,PF00168,PF00168,PF00168,PF00168,PF16165,PF08150,PF08151	PS50004,PS50004,PS50004,PS50004			G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562,SSF49562,SSF49562,SSF49562,SSF49562	321~341								
aly383.33	Otoferlin	GO:0010996,GO:0030672,GO:0050885,GO:0016079,GO:0016021,GO:0005789,GO:0005509,GO:0016323,GO:0030054	n/a																				
aly383.34	Phytanoyl-CoA dioxygenase domain-containing protein 1	GO:0048244,GO:0046872,GO:0001561,GO:0005777,GO:0051213	CG14688-PB						PF05721				G3DSA:2.60.120.620,G3DSA:2.60.120.620	SSF51197,SSF51197									
aly383.35	Unknown		n/a																				
aly383.36	Alpha-mannosidase 2x	GO:0004572,GO:0044267,GO:0018279,GO:0016021,GO:0016799,GO:0030246,GO:0000139,GO:0006013,GO:0035010,GO:0008270,GO:0043687,GO:0004559	CG4606-PA						PF01074				G3DSA:3.20.110.10	SSF88713									
aly383.37	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly383.38	Unknown		n/a																				
aly383.4	Ubiquitin-conjugating enzyme E2 G2	GO:0070936,GO:0045089,GO:0007619,GO:0016874,GO:0007283,GO:0005524,GO:0030433,GO:0050829,GO:0008049,GO:0004842,GO:0018279,GO:0007140	CG4443-PA				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				
aly383.5	Autophagy-related protein 13 homolog	GO:0019901,GO:0045850,GO:0000407,GO:0019887,GO:0006914,GO:0070969,GO:0034273,GO:0032147,GO:0035096,GO:0003674,GO:0000045,GO:0010506,GO:0005829	CG7331-PA						PF10033														
aly383.6	Unknown		n/a																				
aly383.7	Unknown		n/a																				
aly383.8	Unknown		n/a												679~679								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly383.9	Nostrin	GO:0005856,GO:0050999,GO:0030666,GO:0006897,GO:0005634,GO:0005543,GO:0005575,GO:0008150,GO:0007165,GO:0005886,GO:0003677,GO:0045892,GO:0046209,GO:0044281	CG42388-PH				SM00055,SM00326		PF00611,PF14604	PS51741,PS50002	PR00452,PR00452,PR00452,PR00452		G3DSA:2.30.30.40	SSF103657,SSF50044	274~301,226~246,419~439								
aly38324.1	Leucine-rich repeat serine/threonine-protein kinase 1	GO:0050808,GO:0032418,GO:0018105,GO:0048489,GO:0005737,GO:0007264,GO:0048846,GO:1900242,GO:0004674,GO:0004672,GO:0046872,GO:0043025,GO:0031902,GO:0005524,GO:0005525,GO:0005794,GO:0034613,GO:0017137,GO:1901215,GO:0006979,GO:0005765,GO:0034976	CG5483-PD				SM00369,SM00369,SM00369		PF08477	PS51450,PS51450,PS51424,PS51450	PR00449,PR00449,PR00449		G3DSA:3.40.50.300,G3DSA:3.30.70.1390,G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52540									
aly3839.1	Trypsin-4	GO:0007586,GO:0004252,GO:0008236,GO:0005576,GO:0006508	CG4812-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly3839.10	Unknown		n/a										G3DSA:1.10.287.770										
aly3839.11	Probable U3 small nucleolar RNA-associated protein 11	GO:0032040,GO:0005732,GO:0005730,GO:0003674,GO:0006364,GO:0022008,GO:0006412	CG1789-PA			PIRSF015952			PF03998														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3839.12	Endothelin-converting enzyme 1	GO:0004222,GO:0016021,GO:0005886,GO:0016485,GO:0006508,GO:0046872,GO:0008237	CG5905-PB						PF05649,PF01431,PF01431		PR00786,PR00786,PR00786		G3DSA:3.40.390.10,G3DSA:3.40.390.10,G3DSA:3.40.390.10	SSF55486,SSF55486	116~136								
aly3839.13	Zinc finger matrin-type protein CG9776	GO:0005634,GO:0046872	CG9776-PA				SM00451,SM00451								555~575,168~202								
aly3839.14	Unknown		n/a																				
aly3839.15	Glycine N-methyltransferase	GO:0017174,GO:0005542,GO:0051289,GO:0008757,GO:0005829,GO:0005634,GO:0051262,GO:0006544,GO:0046498,GO:0046655,GO:0046500,GO:1901052,GO:0016594	CG6188-PA			PIRSF000385			PF12847	PS51600			G3DSA:3.40.50.150,G3DSA:3.40.50.150,G3DSA:3.30.46.10	SSF53335									
aly3839.16	Protein transport protein Sec61 subunit gamma	GO:0008565,GO:0005784,GO:0015450,GO:0016021,GO:0016020,GO:0045047,GO:0006616,GO:0030176,GO:0015031,GO:0005789,GO:0010507	CG14214-PC	MF_00422				TIGR00327	PF00584			PS01067	G3DSA:1.20.5.820	SSF103456									
aly3839.17	Exocyst complex component 7	GO:0016192,GO:0000145,GO:0016081,GO:0016080,GO:0005326,GO:0006887,GO:0008013,GO:0005546,GO:0007269,GO:0015031	CG7127-PA						PF03081					SSF74788,SSF74788									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3839.18	Unknown		n/a						PF10505						130~150								
aly3839.19	Translation initiation factor eIF-2B subunit beta	GO:0005737,GO:0051716,GO:0019509,GO:0001541,GO:0005851,GO:0005829,GO:0005085,GO:0007417,GO:0046523,GO:0071456,GO:0014003,GO:0042552,GO:0005525,GO:0006413,GO:0006446,GO:0005524,GO:0003743	CG2677-PA						PF01008				G3DSA:3.40.50.10470,G3DSA:3.40.50.10470	SSF100950,SSF100950		00270+5.3.1.23		PWY-7174,PWY-4361	UPA00904				
aly3839.2	Beta-1,4-glucuronyltransferase 1	GO:0005794,GO:0035269,GO:0008532,GO:0016021,GO:0000139,GO:0015020,GO:0046872	CG3253-PA						PF13896														
aly3839.20	Solute carrier family 22 member 1	GO:0005333,GO:0005277,GO:0006855,GO:0015651,GO:0005329,GO:0010248,GO:0015874,GO:0016021,GO:0016020,GO:0051260,GO:0016323,GO:0048241,GO:0015101,GO:0044281,GO:0005887,GO:0005886,GO:0015872,GO:0015695,GO:0008513,GO:0055085	CG7442-PA						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly3839.21	Solute carrier family 22 member 1	GO:0005333,GO:0005277,GO:0006855,GO:0015651,GO:0005329,GO:0010248,GO:0006812,GO:0016021,GO:0051260,GO:0016323,GO:0048241,GO:0015101,GO:0005887,GO:0015874,GO:0015872,GO:0008513,GO:0055085	CG7458-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3839.22	Bile salt-activated lipase	GO:0030157,GO:0009062,GO:0044281,GO:0044241,GO:0005737,GO:0070062,GO:0018350,GO:0004771,GO:0047372,GO:0016787,GO:0006707,GO:0006629,GO:0006641,GO:0052689,GO:0030299,GO:0008150,GO:0008152,GO:0044258,GO:0008201,GO:0005615,GO:0004806,GO:0003824,GO:0005575,GO:0005576	CG10175-PD						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly3839.23	Juvenile hormone esterase	GO:0004453,GO:0052689	CG6414-PA						PF00135,PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly3839.24	Forkhead box protein L2	GO:0030154,GO:0009790,GO:0001077,GO:0003677,GO:0042703,GO:0009653,GO:0048048,GO:0007389,GO:0001541,GO:0000122,GO:0005634,GO:0006309,GO:0043065,GO:0043028,GO:0048806,GO:0043280,GO:0003690,GO:0000981,GO:0060014,GO:0019101,GO:0008134,GO:0009888,GO:0008301,GO:0045893,GO:0031624,GO:0051090,GO:0003700,GO:0003705,GO:0048813,GO:0006357,GO:0000976,GO:0005667,GO:0045892,GO:0000978,GO:0002074	CG44123-PC				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00658	G3DSA:1.10.10.10	SSF46785									
aly3839.25	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3839.26	Solute carrier family 22 member 3	GO:0015651,GO:0019534,GO:0051615,GO:0005329,GO:0032098,GO:0016021,GO:1901998,GO:0008513,GO:0022857,GO:0015101,GO:0015697,GO:0015872,GO:0015695,GO:0098655,GO:0072488,GO:0055085,GO:1903146	CG8654-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly3839.27	Unknown		n/a																				
aly3839.28	Trypsin	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG18735-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly3839.29	Esterase FE4	GO:0005575,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly3839.3	Ribosomal RNA-processing protein 8	GO:0005737,GO:0046015,GO:0006351,GO:0000183,GO:0005730,GO:0008757,GO:0005634,GO:0035064,GO:0071158,GO:0033553,GO:0005677,GO:0006364,GO:0005886,GO:0042149,GO:0008168,GO:0044822,GO:0016568,GO:0072332	CG7137-PA						PF05148				G3DSA:3.40.50.150	SSF53335	237~257								
aly3839.4	Helicase POLQ-like	GO:0005730,GO:0008026,GO:0009951,GO:0009994,GO:0009949,GO:0007294,GO:0030532,GO:0016321,GO:0030717,GO:0004386,GO:0005654,GO:0000724,GO:0008298,GO:0003676,GO:0006417,GO:0048477,GO:0005682,GO:0005524	CG7972-PA				SM00487		PF00270	PS51192			G3DSA:1.10.150.20,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF158702,SSF52540	832~855								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3839.5	Troponin T	GO:0030239,GO:0006937,GO:0007498,GO:0006874,GO:0030240,GO:0046716,GO:0045214,GO:0005509,GO:0005523,GO:0005865,GO:0048644,GO:0005861,GO:0007005	CG7107-PA						PF00992				G3DSA:1.20.5.350	SSF90250	16~119,134~154,331~360		REACT_17044						
aly3839.6	Coatomer subunit beta	GO:0005794,GO:0006890,GO:0006909,GO:0016192,GO:0006886,GO:0005198,GO:0010883,GO:0050829,GO:0045089,GO:0030126,GO:0000902	CG6223-PA						PF07718,PF14806				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371			REACT_11123						
aly3839.7	Coatomer subunit beta	GO:0005794,GO:0006890,GO:0006909,GO:0016192,GO:0006886,GO:0045089,GO:0005198,GO:0030117,GO:0050829,GO:0010883,GO:0030126,GO:0000902	CG6223-PA						PF01602				G3DSA:1.25.10.10	SSF48371									
aly3839.8	E3 ubiquitin-protein ligase TM129	GO:0006986,GO:0016021,GO:0005789,GO:0016567,GO:0046872,GO:0016874	CG14646-PA						PF10272										UPA00143				
aly3839.9	Sodium channel protein Nach (Fragment)	GO:0035002,GO:0016021,GO:0016020,GO:0005272,GO:0006814	CG10858-PB						PF00858														
aly38412.1	Unknown		n/a												99~119,136~177								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3842.1	Synaptotagmin 15	GO:0008021,GO:0006810,GO:0016192,GO:0005215,GO:0016021,GO:0016020,GO:0005544,GO:0048791,GO:0005764,GO:0016528,GO:0030276,GO:0005509,GO:0005515,GO:0016079,GO:0007269,GO:0019905,GO:0005886,GO:0017158,GO:0031982	CG2381-PA				SM00239		PF00168,PF00168	PS50004			G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562										
aly3842.2	Unknown		n/a																				
aly3842.3	Basic juvenile hormone-suppressible protein 2	GO:0046331,GO:0005811,GO:0005616,GO:0045735,GO:0005576	CG4178-PA						PF00372,PF03722,PF03723		PR00187,PR00187,PR00187,PR00187	PS00209,PS00210	G3DSA:2.60.40.1520,G3DSA:1.10.1280.10,G3DSA:1.20.1370.10	SSF81296,SSF48050,SSF48056									
aly3842.4	Basic juvenile hormone-suppressible protein 2	GO:0046331,GO:0005811,GO:0005616,GO:0045735,GO:0005576	CG4178-PA						PF03722,PF03723,PF00372		PR00187,PR00187,PR00187,PR00187	PS00210,PS00209	G3DSA:1.20.1370.10,G3DSA:2.60.40.1520,G3DSA:1.10.1280.10	SSF81296,SSF48050,SSF48056									
aly3850.1	Serine/threonine-protein phosphatase 2A regulatory subunit B" subunit alpha	GO:0090090,GO:0000159,GO:0090263,GO:0006470,GO:0045732,GO:0034047,GO:0046331,GO:0005509,GO:0001754,GO:0090249,GO:0008601,GO:0061053,GO:0007525,GO:0090244	CG4733-PB						PF13499	PS50222,PS50222		PS00018	G3DSA:1.10.238.10	SSF47473									
aly3850.10	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3850.11	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689	CG4382-PB						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly3850.12	Esterase FE4	GO:0005575,GO:0008150,GO:0052689	CG4382-PB						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly3850.13	Esterase FE4	GO:0005575,GO:0008150,GO:0052689	CG4382-PB						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly3850.14	Unknown	GO:0008601,GO:0046331,GO:0005509	CG4733-PB																				
aly3850.2	Ribonuclease H1	GO:0090502,GO:0000287,GO:0005739,GO:0043137,GO:0004523,GO:0003676,GO:0006369	CG8729-PA			PIRSF036852			PF00075,PF01693	PS50879			G3DSA:3.30.420.10,G3DSA:3.40.970.10	SSF55658,SSF53098									
aly3850.3	Protein kinase C-binding protein 1	GO:0000122,GO:0005080,GO:0005634,GO:0001106,GO:0008270,GO:0005515,GO:0070491	CG1815-PC				SM00293,SM00297,SM00249		PF00439,PF00855	PS50014,PS50812,PS50016,PS50865		PS01359,PS01360	G3DSA:1.20.920.10,G3DSA:2.30.30.160,G3DSA:3.30.40.10	SSF47370,SSF57903,SSF63748,SSF144232	1740~1760,731~751								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3850.4	Myotubularin-related protein 9	GO:0016311,GO:0005737,GO:0030234,GO:0008138	CG5026-PA						PF06602	PS51339			G3DSA:2.30.29.30	SSF50729,SSF52799	520~540								
aly3850.5	Replication factor C subunit 4	GO:0005737,GO:0005634,GO:0017111,GO:0031122,GO:0005654,GO:0005663,GO:0046331,GO:0006260,GO:0006261,GO:0003677,GO:0005875,GO:0005524	CG8142-PA				SM00382		PF00004,PF08542				G3DSA:1.10.8.60,G3DSA:3.40.50.300,G3DSA:1.20.272.10	SSF52540,SSF48019			REACT_152,REACT_216,REACT_22172,REACT_383,REACT_1538						
aly3850.6	Ribonuclease H2 subunit B	GO:0006401,GO:0005634,GO:0032299	CG11164-PA						PF09468														
aly3850.7	YTH domain-containing family protein 2	GO:1990247,GO:0044822,GO:0000932,GO:0043488	CG6422-PA						PF04146	PS50882													
aly3850.8	Heparan-sulfate 6-O-sulfotransferase 1	GO:0048666,GO:0007424,GO:0090097,GO:0016021,GO:0008587,GO:0007428,GO:0008146,GO:0015012,GO:0022416,GO:0017095,GO:0045570,GO:0008543,GO:0060828	CG4451-PA						PF03567					SSF52540									
aly3850.9	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689	CG4382-PB						PF00135,PF00135			PS00122,PS00122	G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3855.1	Phosphoglucomutase-2	GO:0008973,GO:0005975,GO:0046386,GO:0005980,GO:0005978,GO:0005829,GO:0000287,GO:0016052,GO:0004614,GO:0044281,GO:0004615,GO:0016868,GO:0006006,GO:0019388,GO:0070062	CG8073-PA						PF02880,PF02879				G3DSA:3.40.120.10,G3DSA:3.40.120.10	SSF53738,SSF53738		00520+5.4.2.10		PWY-6749					
aly3856.1	Protein vreteno	GO:0005737,GO:0043186,GO:0070725,GO:0007293,GO:0060966,GO:0005515,GO:0051321,GO:0010526,GO:0034587,GO:0048477	CG4771-PA				SM00333		PF00567	PS50304			G3DSA:2.30.30.140	SSF63748									
aly3856.2	Unknown		n/a												139~159,189~209								
aly3856.3	Unknown	GO:0005515	n/a				SM00256		PF12937	PS50181			G3DSA:1.20.1280.50	SSF81383									
aly3856.4	Unknown		n/a																				
aly3856.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3856.6	Protein yellow	GO:0060179,GO:0004167,GO:0006583,GO:0048066,GO:0048067,GO:0005576,GO:0042438,GO:0042435,GO:0007275	CG8063-PA						PF03022				G3DSA:2.120.10.30										
aly3856.7	Unknown		n/a																				
aly38595.1	Unknown		n/a						PF14529				G3DSA:3.60.10.10	SSF56219									
aly386.1	Unknown		n/a																				
aly386.10	Unknown		n/a																				
aly386.11	YEATS domain-containing protein 4	GO:0005737,GO:0005730,GO:0008022,GO:0005200,GO:0006351,GO:0000123,GO:0043967,GO:0006325,GO:0005634,GO:0043968,GO:0003700,GO:0005654,GO:0006355,GO:0035267,GO:0006367,GO:0003677,GO:0005669,GO:0007067,GO:0016363,GO:0040008,GO:0045893	CG9207-PA						PF03366	PS51037					195~222								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly386.12	Unknown		CG15760-PB																				
aly386.13	DnaJ homolog subfamily C member 1	GO:0006457,GO:0005783,GO:0032781,GO:0016021,GO:0016020,GO:0031965,GO:0005789,GO:0005886,GO:0003677,GO:0006417,GO:0050708,GO:0045861,GO:0003682,GO:0001671	CG7556-PA				SM00271,SM00717		PF00226	PS50090,PS50076	PR00625,PR00625,PR00625	PS00636	G3DSA:1.10.287.110	SSF46565,SSF46689	207~234,368~394								
aly386.14	Hemocytin	GO:0007599,GO:0042381,GO:0008270,GO:0030246,GO:0042060,GO:0005576,GO:0035006,GO:0008061,GO:0003676,GO:0007155,GO:0006030,GO:0042803	CG7002-PA				SM00041		PF01826,PF00093	PS01225,PS50184		PS01185	G3DSA:2.10.25.10	SSF57603,SSF57567									
aly386.2	Death-associated protein kinase related	GO:0002009,GO:0006468,GO:0007480,GO:0004683,GO:0007476,GO:0005575,GO:0004674,GO:0008360,GO:0007155,GO:0042981,GO:0005524	CG32666-PE				SM00220		PF00069	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly386.3	Protein HIRA	GO:0006338,GO:0006336,GO:0005634,GO:0003714,GO:0035042,GO:0035041,GO:0006355,GO:0042585,GO:0006351,GO:0005515,GO:0003682,GO:0001673,GO:0016568	CG12153-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF07569,PF00400,PF00400,PF00400,PF00400,PF09453	PS50294,PS50082,PS50082,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978,SSF101898,SSF101898									
aly386.4	Solute carrier family 2, facilitated glucose transporter member 1	GO:0022891,GO:0005355,GO:0006461,GO:0042470,GO:0016021,GO:0016020,GO:0030864,GO:0015758,GO:0005887,GO:0055085,GO:0043621	CG7882-PA					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171,PR00171,PR00171	PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly386.5	Solute carrier family 25 member 35	GO:0005743,GO:0005740,GO:0016021,GO:0022857,GO:0006810	CG8323-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly386.6	Solute carrier family 25 member 35	GO:0005743,GO:0005740,GO:0016021,GO:0022857,GO:0006810	CG8323-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly386.7	Unknown		n/a						PF14924,PF16003						963~983								
aly386.8	Unknown		n/a						PF16003						492~512								
aly386.9	Solute carrier family 25 member 35	GO:0005743,GO:0022857,GO:0016021,GO:0005740,GO:0006810	CG18327-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly38694.1	Guanine nucleotide-binding protein-like 1	GO:0005615,GO:0005829,GO:0003924,GO:0042254,GO:0005198,GO:0006974,GO:0007165,GO:0008152,GO:0002456,GO:0005634,GO:0005525	CG9320-PA						PF01926		PR00326,PR00326		G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly38704.1	Glutamate--cysteine ligase	GO:0005515,GO:0004357,GO:0017109,GO:0006974,GO:0006749,GO:0006750,GO:0048471,GO:0005634,GO:0005524	CG2259-PA						PF03074					SSF55931		00480+6.3.2.2		PWY-7255,PWY-6840	UPA00142				
aly3875.1	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG4920-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly3875.10	Unknown		n/a																				
aly3875.2	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG4920-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly3875.3	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG4920-PA				SM00020,SM00680		PF12032,PF12032,PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly3875.4	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG4920-PA				SM00680,SM00680,SM00020		PF12032,PF12032,PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3875.5	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG4920-PA				SM00020,SM00680,SM00680		PF00089,PF12032,PF12032	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly3875.6	Serine protease easter	GO:0004252,GO:0006909,GO:0009950,GO:0031638,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG9737-PA				SM00020,SM00680		PF00089,PF12032	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly3875.7	Serine protease easter	GO:0004252,GO:0006909,GO:0009950,GO:0031638,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG9737-PA				SM00020,SM00680		PF00089,PF12032	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly3875.8	Unknown		n/a																				
aly3875.9	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3881.1	Exosome complex exonuclease RRP44	GO:0071027,GO:0005085,GO:0090305,GO:0043547,GO:0005730,GO:0005634,GO:0016020,GO:0005654,GO:0006364,GO:0005652,GO:0006402,GO:0010468,GO:0071034,GO:0022008,GO:0090503,GO:0016075,GO:0004519,GO:0000176,GO:0000177,GO:0000175,GO:0003723,GO:0006397	CG6413-PA				SM00670		PF13638				G3DSA:3.40.50.1010	SSF88723,SSF50249										
aly3881.2	Niemann-Pick C1 protein	GO:0005783,GO:0030301,GO:0010004,GO:0004872,GO:0007041,GO:0006486,GO:0016021,GO:0005635,GO:0048471,GO:0031902,GO:0016328,GO:0016324,GO:0005887,GO:0005886,GO:0042632,GO:0008206,GO:0008158,GO:0008203,GO:0015485,GO:0005764,GO:0005765,GO:0005576	CG11212-PA						PF02460,PF02460	PS50156			G3DSA:1.20.1640.10,G3DSA:1.20.1640.10	SSF82866,SSF82866										
aly3881.3	Probable cytochrome P450 304a1	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0017143,GO:0055114,GO:0009055	CG7241-PA						PF00067,PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly3881.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3881.5	Odorant receptor 67c	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG14156-PA						PF02949														
aly3881.6	Uncharacterized protein C15orf61	GO:0005576	CG34148-PB						PF15031														
aly3881.7	Nuclear factor NF-kappa-B p110 subunit	GO:0006963,GO:0003677,GO:0006967,GO:0006964,GO:0045429,GO:0001077,GO:0010628,GO:0007165,GO:0008063,GO:0050829,GO:0005737,GO:0043565,GO:0005719,GO:0005634,GO:0009617,GO:0006366,GO:0034198,GO:2000647,GO:0000981,GO:0045089,GO:0045088,GO:0045087,GO:0006974,GO:0006955,GO:0061057,G	CG11992-PC				SM00248,SM00248,SM00248,SM00248		PF16179,PF12796	PS50088,PS50297	PR00057,PR00057		G3DSA:1.25.40.20,G3DSA:2.60.40.10	SSF81296,SSF48403									
aly38926.1	Unknown	GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG12926-PA										G3DSA:3.40.525.10	SSF52087									
aly3894.1	Hemicentin-2	GO:0050896,GO:0005509,GO:0005578	n/a						PF13519				G3DSA:3.40.50.410	SSF53300									
aly3894.2	Hemicentin-1	GO:0005604,GO:0005515,GO:0070062,GO:0030054,GO:0007601,GO:0005509,GO:0005887,GO:0007155,GO:0050896,GO:0042802,GO:0005938	CG42330-PI				SM00892,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408,SM00408		PF07679,PF13927,PF01223,PF13895,PF13895	PS50835,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.40.570.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF54060,SSF48726,SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3894.3	Hemicentin-1	GO:0005604,GO:0070062,GO:0050896,GO:0007601,GO:0005509,GO:0030054,GO:0005938	n/a											SSF53300									
aly38987.1	Eukaryotic translation initiation factor 2-alpha kinase 4	GO:0006446,GO:0004686,GO:0022626,GO:0045793,GO:0030968,GO:0071011,GO:0005829,GO:0017148,GO:0006468,GO:0000398,GO:0004674,GO:0010998,GO:0009267,GO:0004672,GO:0006417,GO:0071013,GO:0005524,GO:0004694	CG1609-PC				SM00220,SM00591		PF05773,PF00069,PF00069,PF00069	PS50908,PS50011,PS50011		PS00108,PS00109	G3DSA:3.30.200.20,G3DSA:3.30.200.20,G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10,G3DSA:3.10.110.10,G3DSA:1.10.510.10	SSF56112,SSF56112,SSF54495,SSF56112	511~531									
aly38987.2	Unknown		n/a																				
aly38987.3	Unknown		n/a																				
aly390.1	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0006694,GO:0005506,GO:0055114,GO:0009055	CG11715-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly390.10	NUAK family SNF1-like kinase 1	GO:0005737,GO:0030155,GO:0006468,GO:0031588,GO:0005730,GO:0042127,GO:2000772,GO:0005634,GO:0042149,GO:0006974,GO:0004674,GO:0015630,GO:0035507,GO:0007155,GO:0035556,GO:0046872,GO:0002039,GO:0032007,GO:0005524	CG43143-PI				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10	SSF56112	1309~1329,814~834								
aly390.11	Inactive pancreatic lipase-related protein 1	GO:0004806,GO:0006629,GO:0016042,GO:0005575,GO:0005576,GO:0005509,GO:0016298	CG6847-PA						PF00151		PR00821,PR00821,PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly390.12	Poly [ADP-ribose] polymerase	GO:0042393,GO:0006471,GO:0051287,GO:0008270,GO:0003677,GO:0003950,GO:0007000,GO:0051457,GO:0005719,GO:0005730,GO:0005634,GO:0043484,GO:0006963,GO:0005694,GO:0045087,GO:0035363,GO:0009303,GO:0035079,GO:0015030,GO:0051276,GO:0005703,GO:0005700,GO:0030576,GO:0006355,GO:0048812,GO:0007552,GO:0035080	CG40411-PB				SM00773		PF05406,PF00645,PF00645,PF00644,PF02877,PF00533,PF08063	PS50064,PS51059,PS50172,PS50064,PS51060			G3DSA:2.20.140.10,G3DSA:3.40.50.10190,G3DSA:1.20.142.10,G3DSA:3.90.228.10,G3DSA:3.30.1740.10,G3DSA:3.30.1740.10	SSF57716,SSF142921,SSF56399,SSF57716,SSF47587,SSF52113										
aly390.13	RuvB-like helicase 1	GO:0035060,GO:0017025,GO:0031011,GO:0030111,GO:0010628,GO:0035267,GO:0003678,GO:0005875,GO:0007049,GO:0005634,GO:0003713,GO:0051301,GO:0043141,GO:0005524,GO:0042127,GO:0006281,GO:0008013,GO:0006310,GO:0006355,GO:0090307,GO:0006351,GO:0007095,GO:0016568	CG4003-PA				SM00382		PF06068				G3DSA:1.10.8.60,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly390.14	Importin-13	GO:0005737,GO:0042331,GO:0006606,GO:0006886,GO:0008536,GO:0050804,GO:0007270,GO:0005634	CG7212-PA				SM00913		PF08389,PF03810	PS50166			G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371									
aly390.15	Unknown		n/a																				
aly390.16	E3 ubiquitin-protein ligase sina	GO:0005737,GO:0042802,GO:0007423,GO:0010498,GO:0005634,GO:0007465,GO:0000151,GO:0007601,GO:0045676,GO:0016567,GO:0016874,GO:0006511,GO:0008270,GO:0005515,GO:0006508,GO:0004842,GO:0050896,GO:0043621	CG9949-PA						PF03145	PS50089			G3DSA:3.30.40.10,G3DSA:3.90.890.10,G3DSA:2.60.210.10	SSF57850,SSF49599					UPA00143				
aly390.17	Sphingomyelin synthase-related 1	GO:0007030,GO:0016021,GO:0060305,GO:0047493,GO:0030176,GO:0003674,GO:0033188,GO:0006686,GO:2000303,GO:0046513	CG32380-PA						PF14360				G3DSA:1.10.150.50	SSF47769	517~520								
aly390.18	SH3 domain-binding glutamic acid-rich protein homolog	GO:0005575,GO:0003674,GO:0008150	CG8582-PE						PF04908				G3DSA:3.40.30.10	SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly390.19	Golgi-associated PDZ and coiled-coil motif-containing protein	GO:0016333,GO:0016332,GO:0008105,GO:0008104,GO:0016336,GO:0016335,GO:0016334,GO:0007617,GO:0005886,GO:0045197,GO:0045196,GO:0030425,GO:0031594,GO:0045887,GO:0051124,GO:0045202,GO:0005794,GO:0046956,GO:0044325,GO:0008049,GO:0043195,GO:0005920,GO:0061176,GO:0005856,GO:0002009,GO:0042332,GO:0051260,GO:0019991,GO:0045179,GO:0005737,GO:0005198,GO:0008022,GO:0030054,GO:0048471,GO:0042803,GO:0042127,GO:0008285,GO:0050790,GO:0016328,GO:0005154,GO:0030140,GO:0051294,GO:0006914,GO:0016327,GO:0004385,GO:0045175,GO:0045211,GO:0001738,GO:0014069,GO:0045475,GO:0007268,GO:0007289,GO:0007010,GO:0016020,GO:0016323,GO:0005918,GO:0043234,GO:0045167,GO:0008283,GO:0000132,GO:0007399,GO:0042734,GO:0051726,GO:0030710,GO:0007391,GO:0000139,GO:0005109,GO:0030695,GO:0005515,GO:0015031,GO:0019905,GO:0005938	CG1725-PM				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156										
aly390.2	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0006694,GO:0005506,GO:0055114,GO:0009055	CG11715-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463		G3DSA:1.10.630.10	SSF48264	1~21		REACT_13433						
aly390.20	Unknown		n/a												84~111,312~332								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly390.21	Golgi-associated PDZ and coiled-coil motif-containing protein	GO:0008022,GO:0030425,GO:0045202,GO:0044325,GO:0030054,GO:0005737,GO:0016020,GO:0051260,GO:0042803,GO:0005794,GO:0030140,GO:0006914,GO:0050790,GO:0045211,GO:0014069,GO:0005886,GO:0007289,GO:0043234,GO:0030695,GO:0000139,GO:0005109,GO:0015031,GO:0019905	n/a																				
aly390.22	GTP-binding protein Rheb homolog	GO:0051124,GO:0035264,GO:0030307,GO:0000082,GO:0005789,GO:0007165,GO:0042594,GO:0007411,GO:0016049,GO:0042331,GO:0016020,GO:0042254,GO:0045727,GO:0010506,GO:0010507,GO:0005525,GO:0006629,GO:0003924,GO:2000377,GO:0006184,GO:0007264,GO:0045793,GO:0046872,GO:0005975,GO:0007446,GO:0090070,GO:0000139,GO:0005575,GO:0032008,GO:0005829	CG1081-PA				SM00173,SM00175,SM00174	TIGR00231	PF00071	PS51421	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly390.23	Vacuolar protein sorting associated protein VTA1 homolog	GO:0010008,GO:0015031,GO:0005771,GO:0032509,GO:0001671	CG7967-PA						PF04652				G3DSA:1.20.5.420,G3DSA:1.25.40.270		60~80								
aly390.24	Transmembrane protein 35	GO:0016023,GO:0016021,GO:0005778	CG13920-PA						PF13564														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly390.25	Unknown	GO:0003677	n/a				SM00384,SM00384,SM00384,SM00384		PF02178,PF02178,PF02178,PF02178		PR00930,PR00930,PR00930,PR00930,PR00929,PR00929,PR00929,PR00929												
aly390.26	Afadin	GO:0016318,GO:0008022,GO:0045216,GO:0034332,GO:0007267,GO:0007163,GO:0007165,GO:0005926,GO:0046328,GO:0090557,GO:0019904,GO:0032880,GO:0005737,GO:0005654,GO:0007254,GO:0007219,GO:0043547,GO:0003779,GO:0030054,GO:0048749,GO:0045177,GO:0017016,GO:0005915,GO:0048598,GO:0005912,GO:0005911,GO:0005886,GO:0007155,GO:0007265,GO:0034329,GO:0000132,GO:0005829,GO:0007394,GO:0007391,GO:0005515,GO:0048730,GO:0005913,GO:0005938	CG42312-PE				SM00228,SM00314,SM00314,SM00240		PF01843,PF00788,PF00788,PF00498,PF00595	PS50200,PS50200,PS51126,PS50106			G3DSA:2.60.200.20,G3DSA:2.30.42.10,G3DSA:3.10.20.90	SSF54236,SSF54236,SSF49879,SSF50156	1214~1234								
aly390.27	Dual specificity protein phosphatase Mpk3	GO:0005737,GO:0042127,GO:0043409,GO:0016791,GO:0008138,GO:0006470,GO:0005829,GO:0007428,GO:0017017,GO:0035160,GO:0007474,GO:0016337,GO:0000188,GO:0004725,GO:0002385	CG14080-PC				SM00195,SM00450		PF00782,PF00581	PS50054,PS50056,PS50206	PR01764,PR01764,PR01764,PR01764,PR01764		G3DSA:3.40.250.10,G3DSA:3.90.190.10	SSF52821,SSF52799									
aly390.28	Unknown	GO:0006398,GO:0035363,GO:0071204,GO:0005515	CG4616-PA												10~65								
aly390.29	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly390.3	Cytochrome P450 4d2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG3466-PA						PF00067				G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly390.30	Kelch-like ECH-associated protein 1	GO:0005737,GO:0006355,GO:0005634,GO:0005703,GO:0010499,GO:0003779,GO:0016567,GO:0006351,GO:0005515,GO:0031463,GO:0006979	CG3962-PB				SM00612,SM00612,SM00612,SM00612,SM00612,SM00875,SM00225		PF01344,PF01344,PF01344,PF01344,PF01344,PF07707,PF00651	PS50097			G3DSA:3.30.710.10,G3DSA:2.130.10.80	SSF117281,SSF54695										
aly390.31	Ran-binding protein 3	GO:0005737,GO:0051168,GO:0046907,GO:0006611,GO:0005634,GO:0015031,GO:0030178	CG10225-PA				SM00160		PF00638	PS50196			G3DSA:2.30.29.30	SSF50729									
aly390.32	Odorant receptor 46a, isoform A	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG6679-PA						PF02949														
aly390.33	Putative protein kinase C delta type homolog	GO:0006468,GO:0019992,GO:0005622,GO:0004674,GO:0035556,GO:0046872,GO:0004697,GO:0005524	CG42349-PE			PIRSF000551	SM00133,SM00220,SM00109,SM00109		PF00130,PF00130,PF00069,PF00433	PS51285,PS50081,PS50081,PS50011	PR00008,PR00008,PR00008,PR00008	PS00107,PS00108,PS00479,PS00479	G3DSA:3.30.60.20,G3DSA:3.30.60.20,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF57889,SSF57889			REACT_14797						
aly390.34	Unknown	GO:0005515	n/a				SM00256		PF12937	PS50181			G3DSA:1.20.1280.50	SSF81383									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly390.35	Pre-mRNA-splicing factor ISY1 homolog	GO:0071011,GO:0071013,GO:0000398,GO:0008380,GO:0005681,GO:0006397	CG9667-PA						PF06246					SSF140102	71~91								
aly390.36	Cyclin-G-associated kinase	GO:0005795,GO:0005794,GO:0006468,GO:0007219,GO:0005925,GO:0030332,GO:0016191,GO:0004674,GO:0007291,GO:0007049,GO:0004672,GO:0048471,GO:0001745,GO:0005524	CG1107-PA				SM00220,SM00271		PF10409,PF00069	PS50076,PS51182,PS50011,PS51181		PS00108	G3DSA:1.10.510.10,G3DSA:3.90.190.10,G3DSA:2.60.40.1110,G3DSA:1.10.287.110,G3DSA:3.30.200.20	SSF52799,SSF46565,SSF56112,SSF49562									
aly390.37	E3 ubiquitin-protein ligase NRDP1	GO:0017160,GO:0008285,GO:0097191,GO:0017022,GO:0016881,GO:0008270,GO:0000209,GO:0043408,GO:0061630,GO:2000114,GO:0051896,GO:0010468,GO:0005135,GO:0030336,GO:2000379,GO:0006914,GO:2000377,GO:0005128,GO:0004842,GO:0051445,GO:0051091,GO:0010498,GO:0016567,GO:0051865,GO:0045619,GO:0005515,GO:0031386,GO:0045637	CG17033-PA				SM00184,SM00504		PF00097,PF08941	PS50089		PS00518	G3DSA:3.90.890.10,G3DSA:3.30.40.10	SSF49599,SSF160088,SSF57850	135~169				UPA00143				
aly390.38	Proteasome-associated protein ECM29 homolog	GO:0005319,GO:0005737,GO:0006869,GO:0005634,GO:0003674,GO:0000502,GO:0008150	CG8858-PA						PF13001				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48431,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371			REACT_22258						
aly390.39	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0006694,GO:0005506,GO:0055114,GO:0009055	CG11715-PA						PF00067		PR00463,PR00463,PR00463		G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly390.4	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264			REACT_13433							
aly390.40	Probable cytochrome P450 313a1	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0017143,GO:0055114,GO:0009055	CG3360-PA						PF00067				G3DSA:1.10.630.10	SSF48264			REACT_13433							
aly390.41	Unknown	GO:0004674,GO:0006468,GO:0005524	CG43143-PI												273~297									
aly390.42	Unknown		n/a																					
aly390.43	Unknown		n/a																					
aly390.44	Unknown	GO:0006468,GO:0019992,GO:0004674,GO:0035556,GO:0004697,GO:0005524	CG42349-PE												583~603,1250~1252									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly390.45	Unknown		n/a						PF14924						196~223								
aly390.5	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly390.6	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly390.7	Unknown		n/a																				
aly390.8	Rho GTPase-activating protein 39	GO:0005856,GO:0005737,GO:0030675,GO:0051056,GO:0005829,GO:0016199,GO:0032855,GO:0005515,GO:0005100,GO:0007411,GO:0007264,GO:0005634	CG3421-PA				SM00324,SM00139		PF00620,PF00397,PF00784	PS50020,PS50238,PS51016			G3DSA:2.20.70.10,G3DSA:1.10.555.10	SSF51045,SSF48350			REACT_11044						
aly390.9	Dipeptidyl peptidase 3	GO:0005829,GO:0016020,GO:0008239,GO:0005886,GO:0006508,GO:0046872,GO:0016021,GO:0008237	CG7415-PC			PIRSF007828			PF03571														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3900.1	Unknown		n/a										G3DSA:2.40.10.10	SSF50494									
aly3905.1	Unknown		n/a																				
aly3905.10	Clavesin-1	GO:0008431,GO:0005802,GO:0080025,GO:0005215,GO:0006810,GO:0005622,GO:0007040,GO:0005768,GO:0031901,GO:0030136	CG3823-PA				SM00516		PF00650	PS50191			G3DSA:3.40.525.10	SSF52087,SSF46938	245~265								
aly3905.11	Astacin-like metalloendopeptidase	GO:0005737,GO:0060473,GO:0004222,GO:2000360,GO:0009566,GO:0030133,GO:0070001,GO:0017090,GO:0070002,GO:0008270,GO:0060468,GO:0005886,GO:0007155,GO:0006508,GO:0008233,GO:0010954,GO:0008237	CG6696-PA				SM00235		PF01400,PF01400		PR00480,PR00480,PR00480,PR00480,PR00480		G3DSA:3.40.390.10,G3DSA:3.40.390.10	SSF55486									
aly3905.12	Protein windbeutel	GO:0040014,GO:0009950,GO:0000042,GO:0005788,GO:0009306,GO:0009792,GO:0007313,GO:0012505,GO:0005515,GO:0008063,GO:0016485,GO:0042803,GO:0005783	CG7225-PA						PF07749,PF07912				G3DSA:3.40.30.10,G3DSA:1.20.1150.12	SSF52833,SSF47933	168~188								
aly3905.13	Ran-specific GTPase-activating protein	GO:0046907,GO:0005643,GO:0006606,GO:0005811,GO:0008536,GO:0006607,GO:0005622,GO:0005096,GO:0008270,GO:0005875,GO:0007184	CG11856-PB				SM00160		PF00638	PS50229,PS50196			G3DSA:2.30.29.30	SSF50729									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3905.14	Leucine-zipper-like transcriptional regulator 1	GO:0003700,GO:0006355,GO:0005634,GO:0009653	CG3711-PD				SM00225,SM00225,SM00612,SM00612,SM00612,SM00612		PF07646,PF13415,PF00651,PF00651,PF01344	PS50097,PS50097			G3DSA:3.30.710.10,G3DSA:3.30.710.10,G3DSA:3.30.710.10,G3DSA:2.120.10.80,G3DSA:2.120.10.80	SSF50965,SSF54695,SSF54695,SSF50965,SSF54695									
aly3905.15	Cytochrome b-c1 complex subunit 9	GO:0070062,GO:0005750,GO:0008121,GO:0006122,GO:0005739,GO:0005743,GO:0007286	CG8764-PA						PF05365				G3DSA:1.20.5.260	SSF81514									
aly3905.16	Unknown		n/a																				
aly3905.17	Unknown		n/a																				
aly3905.2	Unconventional myosin-XVIIIa	GO:0031032,GO:0030017,GO:0005903,GO:0042641,GO:0005856,GO:0000146,GO:0042623,GO:0090164,GO:0016020,GO:0090161,GO:0016459,GO:0016477,GO:0003774,GO:0005524,GO:0048194,GO:0005793,GO:0044822,GO:0043066,GO:0030898,GO:0008150,GO:0051015,GO:0043531,GO:0007030,GO:0050714,GO:0005802,GO:0000139	CG31045-PB										G3DSA:4.10.270.10		390~477,169~323,639~666,484~567,333~381,44~85,582~609,114~148								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3905.3	AP-1 complex subunit beta-1	GO:0008021,GO:0006901,GO:0061024,GO:0005905,GO:0030131,GO:0030119,GO:0030135,GO:0030136,GO:0008565,GO:0016183,GO:0006886,GO:0030669,GO:0048749,GO:0019886,GO:0005215,GO:0050690,GO:0019901,GO:0030659,GO:0032588,GO:0007269,GO:0005886,GO:0030122,GO:0030121,GO:0006892,GO:0016192,GO:0005829,GO:0005802,GO:0000139,GO:0005765,GO:0016032	CG12532-PA				SM01020		PF09066,PF01602				G3DSA:2.60.40.1150,G3DSA:2.60.40.1150,G3DSA:1.25.10.10,G3DSA:3.30.310.10	SSF55711,SSF49348,SSF48371			REACT_6185						
aly3905.4	PAX-interacting protein 1	GO:0009880,GO:0006281,GO:0008134,GO:0007448,GO:0006355,GO:0016571,GO:0006351,GO:0051568,GO:0044666,GO:0005634,GO:0002805	CG32133-PA				SM00292,SM00292,SM00292,SM00292,SM00292,SM00292		PF12738,PF12738	PS50172,PS50172,PS50172,PS50172,PS50172			G3DSA:3.40.50.10190,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190	SSF52113,SSF52113,SSF52113,SSF52113,SSF52113,SSF52113	476~500,431~458								
aly3905.5	Serine protease gd	GO:0004252,GO:0009950,GO:0009620,GO:0009617,GO:0005575,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG33329-PC				SM00020		PF16030,PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly3905.6	N-glycosylase/DNA lyase	GO:0009314,GO:0033158,GO:0009416,GO:0016607,GO:0032355,GO:0005634,GO:0033683,GO:0005739,GO:0005654,GO:0043066,GO:0016363,GO:0006284,GO:0006285,GO:0006281,GO:0006289,GO:0003906,GO:0045471,GO:0034039,GO:0002526,GO:0071276,GO:0006979,GO:0043234,GO:0006974,GO:0045007,GO:0007568,GO:0051593,GO:0004519,GO:0042493,GO:0045008,GO:0008534,GO:0006355,GO:1901291,GO:0003684	CG1795-PA				SM00478		PF07934,PF00730				G3DSA:3.30.310.40,G3DSA:1.10.1670.10,G3DSA:1.10.340.30	SSF55945,SSF48150			REACT_216						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3905.7	N-chimaerin	GO:0048749,GO:0030675,GO:0016337,GO:0005622,GO:0007480,GO:0019992,GO:0043087,GO:0005096,GO:0050770,GO:0032314,GO:0005575,GO:0032855,GO:0046872,GO:0008045,GO:0048013,GO:0034334,GO:0046875,GO:0035556,GO:0043408	CG3208-PA				SM00252,SM00109,SM00324		PF00017,PF00130,PF00620	PS50081,PS50001,PS50238	PR00008,PR00008,PR00008,PR00008	PS00479	G3DSA:1.10.555.10,G3DSA:3.30.60.20,G3DSA:3.30.505.10	SSF48350,SSF57889,SSF55550			REACT_11044						
aly3905.8	Phospholipase A2	GO:0004623,GO:0006644,GO:0005576,GO:0005509,GO:0016042	CG30503-PA						PF05826			PS00118	G3DSA:1.20.90.10	SSF48619		00564+3.1.1.4,00590+3.1.1.4,00592+3.1.1.4,00591+3.1.1.4,00565+3.1.1.4		PWY-7409,PWY-7417,PWY-6803,PWY-7416					
aly3905.9	RIMS-binding protein 2	GO:0048789,GO:0048788,GO:0010923,GO:0045202,GO:0005886,GO:0007274,GO:0030054	CG43073-PF				SM00326,SM00326,SM00326,SM00060,SM00060		PF07653,PF07653	PS50853,PS50853,PS50002,PS50002,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.30.30.40,G3DSA:2.30.30.40,G3DSA:2.30.30.40	SSF49265,SSF50044,SSF49265,SSF50044,SSF50044	175~202,134~168,229~249								
aly39100.1	Cytoplasmic aconitate hydratase	GO:0005783,GO:0009791,GO:0006099,GO:0010040,GO:0005737,GO:0070062,GO:0005739,GO:0005506,GO:0046872,GO:0010468,GO:0005794,GO:0006879,GO:0006447,GO:0030350,GO:0007370,GO:0051539,GO:0005829,GO:0050892,GO:0006101,GO:0003723,GO:0006417,GO:0003994,GO:0003729	CG4900-PA						PF00330		PR00415,PR00415	PS01244,PS00450	G3DSA:3.30.499.10	SSF53732		00290+4.2.1.33			UPA00048				
aly39165.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly39244.1	Unknown		n/a												126~153								
aly39245.1	Acetyl-CoA carboxylase 1	GO:0006633,GO:0005737,GO:0006084,GO:0000902,GO:0051289,GO:0005829,GO:0005811,GO:0042493,GO:0009374,GO:0019900,GO:0014070,GO:0003989,GO:0004075,GO:0046872,GO:0005524,GO:2001295	CG11198-PA						PF02786			PS00867	G3DSA:3.30.470.20	SSF56059									
aly39269.1	Protein glass	GO:0010780,GO:0008270,GO:0003676,GO:0003677,GO:0007126,GO:0005634,GO:0046872,GO:0000977,GO:0007605,GO:0007601,GO:0035271,GO:0000790,GO:0009649,GO:0010114,GO:0007131,GO:0001752,GO:0003700,GO:0003705,GO:0006355,GO:0045944,GO:0006351,GO:0043153	CG4413-PA				SM00355,SM00355			PS50157,PS50157		PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667									
aly393.1	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0007155,GO:0007156,GO:0005887,GO:0042802,GO:0048812	CG42330-PI				SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409		PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF00041,PF00041,PF00041,PF00041,PF00041	PS50853,PS50835,PS50835,PS50835,PS50835,PS50853,PS50835,PS50853,PS50853,PS50835,PS50853,PS50835,PS50835,PS50853,PS50835	PR00014,PR00014,PR00014,PR00014		G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF49265,SSF48726,SSF48726								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly393.10	Ras-related protein Rab-2A	GO:0005794,GO:0007030,GO:0042470,GO:0031982,GO:0005765,GO:0033116,GO:0006886,GO:0003924,GO:0005634,GO:0070062,GO:0000139,GO:0008152,GO:0032482,GO:0019003,GO:0005515,GO:0015031,GO:0005789,GO:0043025,GO:0016192,GO:0005525	CG3269-PA				SM00173,SM00175,SM00174,SM00176	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly393.11	Unknown		n/a						PF13092														
aly393.12	Peroxisomal multifunctional enzyme type 2	GO:0005778,GO:0005782,GO:0006635,GO:0060009,GO:0008210,GO:0044281,GO:0003857,GO:0044255,GO:0001649,GO:0016491,GO:0044594,GO:0080023,GO:0004300,GO:0016020,GO:0005777,GO:0005739,GO:0033540,GO:0042803,GO:0036109,GO:0008209,GO:0008152,GO:0000038,GO:0008206,GO:0055114,GO:0016853,GO:0033989,GO:0043231,GO:0036111,GO:0036112,GO:0016508,GO:0006699,GO:0005102,GO:0033559	CG3415-PA				SM00822		PF02036,PF00106,PF01575		PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.10.129.10,G3DSA:3.40.50.720,G3DSA:3.10.129.10,G3DSA:3.30.1050.10	SSF51735,SSF54637,SSF54637,SSF55718										
aly393.13	Growth arrest-specific protein 1	GO:0008284,GO:0008589,GO:0021904,GO:0050680,GO:0060021,GO:0046658,GO:0045880,GO:0007411,GO:0048589,GO:0016020,GO:0060628,GO:0043066,GO:2001240,GO:0048598,GO:0045930,GO:0048706,GO:0048701,GO:0042733,GO:0048592,GO:0045879,GO:0007050,GO:0012501,GO:0005886,GO:0010955,GO:0050679,GO:0021587,GO:0042473,GO:0045165,GO:0009953,GO:0042474,GO:0042476,GO:0002053,GO:0030308,GO:0043010	n/a						PF02351														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly393.14	Membralin	GO:0005737,GO:0016021,GO:0048190	CG8405-PA						PF09746														
aly393.15	Carboxypeptidase B	GO:0006508,GO:0004181,GO:0004180,GO:0008270,GO:0005576	CG8560-PA				SM00631,SM00631		PF00246,PF00246		PR00765,PR00765,PR00765	PS00132	G3DSA:3.40.630.10,G3DSA:3.40.630.10	SSF53187,SSF53187										
aly393.16	Mast cell carboxypeptidase A (Fragment)	GO:0006508,GO:0004181,GO:0008270,GO:0030133	CG3097-PA				SM00631		PF00246				G3DSA:3.40.630.10	SSF53187									
aly393.17	Dystroglycan	GO:0017166,GO:0034453,GO:0019048,GO:0015631,GO:0030175,GO:0030336,GO:0051898,GO:0070938,GO:0009279,GO:0043409,GO:0005737,GO:0005654,GO:0005925,GO:0070062,GO:0016021,GO:0016020,GO:0003779,GO:0060441,GO:0060445,GO:0006509,GO:0005509,GO:0005856,GO:0042169,GO:0051393,GO:0042383,G	n/a				SM00736						G3DSA:3.30.70.1040,G3DSA:2.60.40.10	SSF111006,SSF49313										
aly393.18	Dystroglycan	GO:0016334,GO:0060025,GO:0045197,GO:0046716,GO:0031594,GO:0007293,GO:0007163,GO:0030010,GO:0007295,GO:0007309,GO:0030018,GO:0005737,GO:0035088,GO:0005615,GO:0031532,GO:0016021,GO:0016020,GO:0007474,GO:0005654,GO:0005509,GO:0006110,GO:0009925,GO:0016203,GO:0005856,GO:0042383,GO:0030315,GO:0045211,GO:0008307,GO:0007314,GO:0045214,GO:0005886,GO:0007016,GO:0030054,GO:0007411,GO:0016010,GO:0005515	CG18250-PD				SM00736,SM00736		PF05454,PF05454	PS51699,PS51699			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49313,SSF49313										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly393.19	Angiogenic factor with G patch and FHA domains 1	GO:0005737,GO:0001570,GO:0005515,GO:0071011,GO:0000398,GO:0001938,GO:0005576,GO:0045766,GO:0003676,GO:0007155,GO:0048471,GO:0001525,GO:0006396	CG8079-PA				SM00240		PF00498,PF01585	PS50006,PS50174			G3DSA:2.60.200.20	SSF49879	378~398,47~67								
aly393.2	CWF19-like protein 1	GO:0008419,GO:0005575,GO:0008150,GO:0003824	CG7741-PA						PF04676,PF04677				G3DSA:3.30.428.10	SSF54197									
aly393.20	Unknown		n/a												9~36								
aly393.3	Negative elongation factor B	GO:0006351,GO:0034244,GO:0032021,GO:0017053,GO:0000122,GO:0005634,GO:0045892,GO:0003723,GO:0045944,GO:0005694,GO:0007070,GO:0003729	CG32721-PA						PF06209														
aly393.4	Uncharacterized protein PFA0635c	GO:0007605,GO:0050954,GO:0016021,GO:0031012,GO:0048813,GO:0005576	CG13207-PA				SM00473,SM00473,SM00473,SM00473,SM00241		PF00024,PF00024,PF00024,PF00024	PS50948,PS51034,PS50948,PS50948,PS50948,PS50948			G3DSA:3.50.4.10,G3DSA:3.50.4.10,G3DSA:3.50.4.10	SSF57414,SSF57414,SSF57414,SSF57414									
aly393.5	Farnesyl pyrophosphate synthase	GO:0005737,GO:0004161,GO:0035220,GO:0045337,GO:0008299,GO:0004337,GO:0006695,GO:0033384,GO:0046872,GO:0008354	CG12389-PA						PF00348			PS00444	G3DSA:1.10.600.10	SSF48576									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly393.6	Farnesyl pyrophosphate synthase 2	GO:0004161,GO:0005829,GO:0035220,GO:0045337,GO:0008299,GO:0004337,GO:0006695,GO:0033384,GO:0046872,GO:0008354	CG12389-PA						PF00348			PS00723	G3DSA:1.10.600.10	SSF48576									
aly393.7	Farnesyl pyrophosphate synthase 1, mitochondrial	GO:0004161,GO:0005829,GO:0035220,GO:0045337,GO:0008299,GO:0004337,GO:0006695,GO:0005739,GO:0033384,GO:0046872,GO:0008354	CG12389-PA						PF00348				G3DSA:1.10.600.10	SSF48576									
aly393.8	Farnesyl pyrophosphate synthase	GO:0005737,GO:0004161,GO:0035220,GO:0045337,GO:0008299,GO:0004337,GO:0006695,GO:0016032,GO:0033384,GO:0046872,GO:0008354	CG12389-PA						PF00348			PS00723,PS00444	G3DSA:1.10.600.10	SSF48576									
aly393.9	Unknown		n/a																				
aly3931.1	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0005515,GO:0048812,GO:0005887,GO:0005886,GO:0007155,GO:0007156,GO:0042802	CG31190-PE				SM00408,SM00408,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00060,SM00060,SM00060,SM00060,SM00060		PF00047,PF07679,PF07679,PF07679,PF00041,PF00041,PF00041,PF00041,PF00041,PF13927	PS50835,PS50853,PS50835,PS50853,PS50853,PS50835,PS50853,PS50835,PS50853,PS50835,PS50853,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF49265,SSF48726,SSF48726,SSF49265,SSF48726,SSF49265,SSF48726,SSF48726									
aly3931.2	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0005515,GO:0048812,GO:0005887,GO:0005886,GO:0007155,GO:0007156,GO:0042802	CG31190-PE				SM00060,SM00060,SM00060,SM00060,SM00060,SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408,SM00408		PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF00041,PF00041,PF00041	PS50835,PS50835,PS50853,PS50853,PS50853,PS50835,PS50853,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3931.3	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0005515,GO:0048812,GO:0005887,GO:0005886,GO:0007155,GO:0007156,GO:0042802	CG31190-PE				SM00060,SM00060		PF00041	PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF48726									
aly3931.4	Unknown		n/a																				
aly39331.1	Unknown		n/a																				
aly3936.1	Unknown	GO:0019028	CG42598-PB						PF03067														
aly3936.2	Phagocyte signaling-impaired protein	GO:0005737,GO:0010592,GO:0002253,GO:0045087,GO:0097374,GO:0006959,GO:0006911,GO:0005764,GO:0043524,GO:0005515,GO:0006955,GO:0007298,GO:0031416	CG4845-PA						PF09797	PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452									
aly3936.3	TBC1 domain family member 10B	GO:0005737,GO:0043547,GO:0007430,GO:0032313,GO:0005096,GO:0005097,GO:0035149,GO:0030175,GO:0060439,GO:0042147,GO:0005886,GO:0043087	CG5344-PA				SM00164		PF00566	PS50086			G3DSA:1.10.8.270	SSF47923,SSF47923									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3936.4	Protein suppressor of white apricot	GO:0016607,GO:0006351,GO:0005634,GO:0000398,GO:0006355,GO:0006396,GO:0006397,GO:0008380,GO:0005681,GO:0003723	CG3019-PA				SM00648,SM00648		PF09750,PF01805,PF01805	PS50128,PS50128				SSF109905,SSF109905	876~899,969~971,746~780									
aly3936.5	Inositol oxygenase	GO:0005737,GO:0019310,GO:0008199,GO:0050113,GO:0005506,GO:0055114	CG6910-PB						PF05153					SSF109604		00053+1.13.99.1,00562+1.13.99.1		PWY-4841	UPA00111				
aly3936.6	Inositol oxygenase	GO:0005737,GO:0019310,GO:0008199,GO:0005506,GO:0050113,GO:0055114	CG6910-PB						PF05153					SSF109604		00053+1.13.99.1,00562+1.13.99.1		PWY-4841	UPA00111				
aly3936.7	Inositol oxygenase	GO:0005737,GO:0019310,GO:0008199,GO:0050113,GO:0005506,GO:0055114	CG6910-PB						PF05153					SSF109604		00053+1.13.99.1,00562+1.13.99.1		PWY-4841	UPA00111				
aly3936.8	Cytospin-A	GO:0005737,GO:0005819,GO:0035220,GO:0048802,GO:0045214,GO:0051301,GO:0005921,GO:0048734,GO:0007049,GO:0007527	CG13366-PB				SM00033		PF00307	PS50021			G3DSA:1.10.418.10	SSF47576	662~696,509~536,579~620,358~419								
aly3936.9	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3959.1	Unknown		n/a																				
aly3959.2	Unknown		n/a																				
aly3959.3	Unknown		n/a																				
aly3962.1	Octopamine receptor beta-3R	GO:0004930,GO:0010579,GO:0016021,GO:0007606,GO:0007612,GO:0007189,GO:0001963,GO:0005887,GO:0007191,GO:0004989,GO:0007186,GO:0008227,GO:0060158	CG42244-PF						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly39629.1	Unknown		n/a																				
aly3964.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly3966.1	Sex peptide receptor	GO:0045434,GO:0008528,GO:0004930,GO:0016021,GO:0005886,GO:0048042,GO:0008188,GO:0007186	CG13229-PA						PF10324	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly3967.1	Acid sphingomyelinase-like phosphodiesterase 3a	GO:0016787,GO:0006685,GO:0004767,GO:0005615,GO:0016798	CG32052-PC						PF00149				G3DSA:3.60.21.10	SSF56300									
aly3967.2	LisH domain-containing protein FOPNL	GO:0036064,GO:0042384,GO:0034453,GO:0031514,GO:0034451,GO:0005515	n/a						PF09398	PS50896													
aly3967.3	Unknown		n/a																				
aly3969.1	Unknown		n/a																				
aly39779.1	Unknown		n/a												9~36								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly398.1	Unknown	GO:0008080	n/a						PF00583				G3DSA:3.40.630.30	SSF55729									
aly398.10	Attacin-E	GO:0045087,GO:0005576,GO:0042742	n/a						PF03769,PF03768														
aly398.11	Attacin-A	GO:0019731,GO:0045087,GO:0050830,GO:0005576,GO:0042742,GO:0031201	CG7629-PA						PF03769														
aly398.2	Unknown		n/a																				
aly398.3	E3 ubiquitin-protein ligase MARCH2	GO:0006897,GO:0005783,GO:0016567,GO:0031410,GO:0016021,GO:0005789,GO:0005765,GO:0004842,GO:0008270,GO:0016874,GO:0010008	CG13442-PA				SM00744		PF12906	PS51292			G3DSA:3.30.40.10	SSF57850					UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly398.4	Nuclear pore glycoprotein p62	GO:0006909,GO:0019221,GO:0030159,GO:0008285,GO:0034605,GO:0019058,GO:0046578,GO:0042059,GO:0031074,GO:0043407,GO:0010827,GO:0019083,GO:0044281,GO:0007166,GO:0051028,GO:0000922,GO:0005487,GO:0008219,GO:0005737,GO:0044267,GO:0046930,GO:0009966,GO:0008645,GO:0005635,GO:0044613,GO:0030529,GO:0015758,GO:0010467,GO:0043066,GO:0045742,GO:0043069,GO:0043123,GO:0009755,GO:0042169,GO:0017056,GO:0000278,GO:0006606,GO:0043687,GO:0031965,GO:0046966,GO:0007283,GO:0046580,GO:0007077,GO:0016925,GO:0090543,GO:0043231,GO:0005975,GO:0007569,GO:0055085,GO:0005643,GO:1900034,GO:0043130,GO:0006351,GO:0016032,GO:0003682,GO:0045893	CG6251-PA						PF05064						374~394,332~352,429~463,491~518								
aly398.5	Checkpoint protein HUS1	GO:0033314,GO:0009790,GO:0009411,GO:0044778,GO:0005737,GO:0071479,GO:0031573,GO:0005730,GO:0005634,GO:0005654,GO:0006260,GO:0030896,GO:0006468,GO:0035038,GO:0006281,GO:0006289,GO:0006974,GO:0008156,GO:0000077,GO:0051332,GO:0035861,GO:0000724,GO:0001932	CG2525-PA			PIRSF011312			PF04005				G3DSA:3.70.10.10	SSF55979									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly398.6	Myb protein	GO:0008284,GO:0007307,GO:0030261,GO:0001077,GO:0003677,GO:0007067,GO:0005719,GO:0090282,GO:0005634,GO:0000281,GO:0006366,GO:0007088,GO:0045931,GO:0000278,GO:0008283,GO:0051297,GO:0007051,GO:0007052,GO:0000910,GO:0007030,GO:0045792,GO:0003700,GO:0031523,GO:0010971,GO:0005700,GO:0006355,GO:0090307,GO:0007098,GO:0007099,GO:0003682	CG9045-PA				SM00717,SM00717,SM00717		PF00249,PF00249,PF00249,PF09316	PS51294,PS51294,PS51294			G3DSA:1.10.10.60,G3DSA:1.10.10.60,G3DSA:1.10.10.60	SSF46689,SSF46689									
aly398.7	Unknown		n/a																				
aly398.8	Gloverin	GO:0045087,GO:0005576,GO:0042742	n/a						PF10793														
aly398.9	Attacin-A	GO:0045087,GO:0005576,GO:0042742	n/a						PF03769														
aly3990.1	GTPase-activating protein CdGAPr	GO:0043547,GO:0005096,GO:0005622,GO:0005575,GO:0007165,GO:0005100,GO:0007266,GO:0031290	CG10538-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly39944.1	Thioredoxin-related transmembrane protein 2 homolog	GO:0016021,GO:0005623,GO:0005575,GO:0008150,GO:0003674,GO:0045454	CG11007-PA						PF00085	PS51352			G3DSA:3.40.30.10	SSF52833	125~145								
aly40.1	Alpha-1,6-mannosyl-glycoprotein 2 beta-N-acetylglucosaminyltransferase	GO:0008455,GO:0005795,GO:0005797,GO:0006487,GO:0016021,GO:0030246,GO:0009312,GO:0008375,GO:0000139,GO:0018279	CG7921-PA						PF05060,PF05060				G3DSA:3.90.550.10,G3DSA:3.90.550.10	SSF53448,SSF53448		00513+2.4.1.143,00510+2.4.1.143		PWY-7426	UPA00378				
aly40.2	Unknown		n/a																				
aly40.3	Unknown		n/a																				
aly40.4	Unknown		n/a																				
aly4003.1	Actin-binding LIM protein 2	GO:0030016,GO:0007010,GO:0015629,GO:0030036,GO:0003779,GO:0045944,GO:0008270,GO:0007411,GO:0006351	CG31332-PC				SM00153,SM00132,SM00132,SM00132,SM00132		PF00412,PF00412,PF00412,PF00412,PF02209	PS50023,PS50023,PS50023,PS51089,PS50023		PS00478,PS00478,PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:1.10.950.10	SSF57716,SSF47050,SSF57716,SSF57716,SSF57716,SSF57716										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4003.2	Mitoferrin	GO:0016021,GO:0005740,GO:0005739,GO:0055072,GO:0005743,GO:0022857,GO:0048250,GO:0048515,GO:0005381,GO:0034755,GO:0055085	CG4963-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10,G3DSA:1.50.40.10	SSF103506,SSF103506									
aly4003.3	Unknown		n/a																				
aly4003.4	Unknown		n/a																				
aly4003.5	General odorant-binding protein 69a	GO:0005549,GO:0007606,GO:0005576,GO:0008145,GO:0005550	CG10436-PA				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly4007.1	Ankyrin repeat domain-containing protein SOWAHC	GO:0005575,GO:0003674,GO:0008150	CG10632-PG				SM00248,SM00248		PF12796	PS50088,PS50297			G3DSA:1.25.40.20	SSF48403									
aly4007.10	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4007.2	Homeobox protein araucan	GO:0043565,GO:0045317,GO:0003700,GO:0005634,GO:0007476,GO:0003705,GO:0007474,GO:0006355,GO:0048813,GO:0045944,GO:0045893,GO:0006352,GO:0003677,GO:0042693,GO:0001745,GO:0035310,GO:0006351	CG10571-PA				SM00389,SM00548		PF05920	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689										
aly4007.3	Homeobox protein caupolican	GO:0006909,GO:0097374,GO:0003677,GO:0001745,GO:0043565,GO:0001700,GO:0000122,GO:0005634,GO:0007476,GO:0007474,GO:0000981,GO:0042803,GO:0045893,GO:0045317,GO:0007422,GO:0003700,GO:0007224,GO:0003705,GO:0006355,GO:0045944,GO:0006351,GO:0042693,GO:0046843	CG10601-PC				SM00389,SM00548		PF05920	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689										
aly4007.4	Glycerol kinase	GO:0004370,GO:0005737,GO:0006641,GO:0019563,GO:0005975,GO:0045471,GO:0016773,GO:0016310,GO:0005634,GO:0005741,GO:0042493,GO:0005739,GO:0005575,GO:0046167,GO:0042393,GO:0006071,GO:0009409,GO:0010033,GO:0005524	CG18374-PA			PIRSF000538		TIGR01311	PF00370,PF02782			PS00933,PS00445	G3DSA:3.30.420.40,G3DSA:3.30.420.40	SSF53067,SSF53067		00561+2.7.1.30		PWY-4261	UPA00618				
aly4007.5	Probable cytochrome P450 305a1	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG8733-PA						PF00067,PF00067		PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly4007.6	Sodium-dependent nutrient amino acid transporter 1	GO:0017032,GO:0005328,GO:0003333,GO:0016021,GO:0006814,GO:0015804,GO:0005283,GO:1903825,GO:0005887,GO:0006836,GO:0042940,GO:0042943,GO:0015175,GO:0005326	CG1698-PA						PF00209					SSF161070									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4007.7	Gamma-aminobutyric acid receptor subunit beta	GO:0006836,GO:0030425,GO:0030424,GO:0034707,GO:0009612,GO:0030285,GO:0090328,GO:0030054,GO:0008503,GO:0016021,GO:0016020,GO:0007214,GO:0042749,GO:0004890,GO:0005254,GO:0006811,GO:0005230,GO:0001505,GO:0005216,GO:0045211,GO:0050805,GO:0007268,GO:0005886,GO:0046682,GO:0042493,GO:0030431	CG10537-PG					TIGR00860	PF02931,PF02932		PR01160,PR01160,PR01160,PR01160,PR00252,PR00252,PR00252,PR00252,PR00253,PR00253,PR00253,PR00253	PS00236	G3DSA:1.20.58.390,G3DSA:1.20.58.390,G3DSA:2.70.170.10	SSF90112,SSF63712										
aly4007.8	JNK-interacting protein 1	GO:0005737,GO:0008432,GO:0007254,GO:0019894,GO:2000331,GO:0005078,GO:0009967,GO:0030424,GO:0019901,GO:0048812,GO:0048491,GO:0048490,GO:0005515,GO:0046328,GO:0019896,GO:0042802	CG1200-PB				SM00462,SM00326		PF14604,PF00640	PS01179,PS50002			G3DSA:2.30.29.30,G3DSA:2.30.30.40	SSF50729,SSF50044									
aly4007.9	Tryptophan 5-hydroxylase 1	GO:0004510,GO:0005737,GO:0004505,GO:0016714,GO:0045600,GO:0006568,GO:0045187,GO:0009072,GO:0042427,GO:0005506,GO:0016597,GO:0055114,GO:0046849	CG9122-PA						PF00351,PF01842	PS51671,PS51410			G3DSA:1.10.800.10	SSF56534,SSF55021									
aly40082.1	Unknown		n/a												34~53								
aly40089.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly40182.1	28S ribosomal protein S18c, mitochondrial	GO:0070126,GO:0032543,GO:0070124,GO:0070125,GO:0005840,GO:0005622,GO:0003735,GO:0005743,GO:0006996,GO:0005763,GO:0006412	CG9688-PA					TIGR00165	PF01084				G3DSA:4.10.640.10	SSF46911									
aly4022.1	UDP-glucuronosyltransferase 1-1	GO:0052695,GO:0052696,GO:0052697,GO:0071385,GO:0019899,GO:0005789,GO:0001889,GO:0042594,GO:0005887,GO:0004857,GO:0043086,GO:0005783,GO:0034663,GO:0070069,GO:0015020,GO:2001030,GO:0042803,GO:0032496,GO:0031100,GO:0007584,GO:0006953,GO:0032870,GO:0008152,GO:0005496,GO:0051552,GO:0043231,GO:0071361,GO:0070980,GO:0042493,GO:0009813,GO:0001972,GO:0046982	CG6658-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly4022.10	UDP-glucuronosyltransferase 3A2	GO:0043231,GO:0052696,GO:0016021,GO:0009813,GO:0071412,GO:0032870,GO:0008152,GO:0016758,GO:0015020,GO:0008194	CG6658-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly4022.11	UDP-glucuronosyltransferase 3A2	GO:0043231,GO:0052696,GO:0016021,GO:0009813,GO:0071412,GO:0032870,GO:0008152,GO:0016758,GO:0015020,GO:0008194	CG18578-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly4022.12	UDP-glucuronosyltransferase 2B7	GO:0043231,GO:0006629,GO:0052695,GO:0052696,GO:0016021,GO:0016020,GO:0009813,GO:0005789,GO:0032870,GO:0008209,GO:0008152,GO:0016758,GO:0015020,GO:0070062	CG6658-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756,SSF53756									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4022.2	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0003851,GO:0008152	CG4739-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756,SSF53756									
aly4022.3	UDP-glucuronosyltransferase 2C1 (Fragment)	GO:0016758,GO:0015020,GO:0016021,GO:0008152,GO:0005789	CG18578-PA						PF00201,PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly4022.4	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG6633-PB						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756,SSF53756									
aly4022.5	Unknown		n/a											SSF53756									
aly4022.6	UDP-glucuronosyltransferase 2B13	GO:0016758,GO:0015020,GO:0016021,GO:0008152,GO:0005789	CG6633-PB						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly4022.7	UDP-glucuronosyltransferase 2B7	GO:0043231,GO:0006629,GO:0052695,GO:0052696,GO:0016021,GO:0016020,GO:0009813,GO:0005789,GO:0032870,GO:0008209,GO:0008152,GO:0016758,GO:0015020,GO:0070062	CG6633-PB						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756,SSF53756									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4022.8	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG6633-PB						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly4022.9	UDP-glucuronosyltransferase 2B15	GO:0043231,GO:0052696,GO:0016021,GO:0042493,GO:0009813,GO:0005789,GO:0032870,GO:0008152,GO:0019439,GO:0016758,GO:0015020	CG6633-PB						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756,SSF53756									
aly4036.1	Protein prickle	GO:0005737,GO:0045184,GO:0008104,GO:0009948,GO:0042067,GO:0016020,GO:0016348,GO:0045746,GO:0045185,GO:0007163,GO:0007164,GO:0008270,GO:0005515,GO:0005886,GO:0001737,GO:0001736,GO:0001738	CG11084-PC																				
aly4036.2	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0046331,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9518-PA			PIRSF000137			PF05199,PF00732			PS00624,PS00623	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly4036.3	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9503-PA			PIRSF000137			PF00732,PF05199				G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly4036.4	General odorant-binding protein 1	GO:0005549,GO:0050896,GO:0006810,GO:0007608	n/a			PIRSF015604	SM00708		PF01395		PR00484,PR00484,PR00484,PR00484,PR00484,PR00484		G3DSA:1.10.238.20	SSF47565									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4036.5	Pheromone-binding protein	GO:0005549,GO:0006810,GO:0019236,GO:0005550	n/a			PIRSF015604	SM00708		PF01395		PR00484,PR00484,PR00484,PR00484,PR00484,PR00484		G3DSA:1.10.238.20	SSF47565									
aly4036.6	General odorant-binding protein 1	GO:0005549,GO:0050896,GO:0006810,GO:0007608	n/a				SM00708		PF01395		PR00484,PR00484,PR00484,PR00484,PR00484		G3DSA:1.10.238.20	SSF47565									
aly4036.7	Pheromone-binding protein	GO:0005549,GO:0006810,GO:0019236,GO:0005550	n/a			PIRSF015604	SM00708		PF01395		PR00484,PR00484,PR00484,PR00484,PR00484,PR00484		G3DSA:1.10.238.20	SSF47565									
aly4036.8	General odorant-binding protein 2	GO:0005549,GO:0050896,GO:0006810,GO:0007608	n/a			PIRSF015604	SM00708		PF01395		PR00484,PR00484,PR00484,PR00484,PR00484,PR00484		G3DSA:1.10.238.20	SSF47565									
aly4036.9	Solute carrier family 22 member 1	GO:0005329,GO:0015874,GO:0072488,GO:0015651,GO:0048241,GO:0008504,GO:0016021,GO:0051260,GO:0015101,GO:0015697,GO:0015695,GO:0042802,GO:0042803,GO:0005333,GO:0005277,GO:0006855,GO:0015844,GO:0016323,GO:0005887,GO:0006836,GO:1901374,GO:0015872,GO:0055085,GO:0010248,GO:0008513,GO:0098655	CG7442-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4039.1	Alpha-1,3-mannosyl-glycoprotein 2 beta-N-acetylglucosaminyltransferase	GO:0016319,GO:0006049,GO:0005797,GO:0001701,GO:0005975,GO:0070062,GO:0006486,GO:0046872,GO:0018279,GO:0016021,GO:0016020,GO:0000139,GO:0043687,GO:0035010,GO:0003827,GO:0008375,GO:0008340,GO:1903561,GO:0044267,GO:0008344	CG13431-PA						PF03071				G3DSA:3.90.550.10	SSF53448					UPA00378				
aly40512.1	Unknown	GO:0006508,GO:0004190	n/a									PS00141											
aly4053.1	DNA-binding protein Ets97D	GO:0043565,GO:0003700,GO:0005634,GO:0030154,GO:0006355,GO:0006357,GO:0010821,GO:0003677,GO:0000981,GO:0045451	CG6338-PB				SM00251,SM00413		PF00178,PF11620,PF02198	PS50061,PS51433	PR00454,PR00454,PR00454,PR00454	PS00346,PS00345	G3DSA:1.10.150.50,G3DSA:1.10.10.10	SSF47769,SSF46785									
aly40536.1	Cathepsin L	GO:0051603,GO:0005615,GO:0035071,GO:0007586,GO:0045169,GO:0005764,GO:0048102,GO:0004197,GO:0030163,GO:0006508,GO:0008233,GO:0007275	CG6692-PC				SM00645		PF00112				G3DSA:3.90.70.10	SSF54001									
aly4054.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly407.1	Unknown		n/a						PF00159	PS50276			G3DSA:1.20.5.570										
aly408.1	Solute carrier family 2, facilitated glucose transporter member 12	GO:0005355,GO:0035428,GO:0015992,GO:0016021,GO:0016020,GO:0015758,GO:0046323,GO:0012505,GO:0005887,GO:0005351,GO:0055085	CG1208-PC						PF00083,PF00083	PS50850	PR00171,PR00171,PR00171,PR00171		G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473			REACT_15518						
aly408.2	Long-chain fatty acid transport protein 1	GO:0006655,GO:0006654,GO:0006656,GO:0005783,GO:0005324,GO:0032049,GO:0031957,GO:0006659,GO:0005901,GO:0032868,GO:0071902,GO:0031652,GO:0031410,GO:0016021,GO:0016020,GO:0000166,GO:0006646,GO:0004467,GO:0006661,GO:0071072,GO:0042803,GO:0033211,GO:0015909,GO:0015908,GO:0003824,GO:0008152,GO:0005886,GO:0001676,GO:0001579,GO:0009409,GO:0005743,GO:0015245	CG3394-PA						PF13193,PF00501			PS00455	G3DSA:2.30.38.10,G3DSA:3.30.300.30,G3DSA:3.40.50.980	SSF56801									
aly408.3	Facilitated trehalose transporter Tret1	GO:0005355,GO:0004252,GO:0004175,GO:0015574,GO:0015771,GO:0005215,GO:0016021,GO:0005886,GO:0006508,GO:0055085	CG6484-PA						PF00083,PF00083	PS50850,PS50850		PS00216,PS00216,PS00216,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473,SSF103473									
aly408.4	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0046427,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG10960-PB						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly408.5	Glycosylphosphatidylinositol anchor attachment 1 protein	GO:0016020,GO:0003923,GO:0005783,GO:0016021,GO:0006506,GO:0042996,GO:0005887,GO:0034235,GO:0042765,GO:0016255,GO:0045313	CG3033-PA						PF04114										UPA00196				
aly408.6	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0046427,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG10960-PB						PF00083	PS50850		PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly408.7	Facilitated trehalose transporter Tret1-2 homolog	GO:0005355,GO:0035428,GO:0015992,GO:0046427,GO:0016021,GO:0016020,GO:0046323,GO:0005887,GO:0005886,GO:0005351,GO:0055085	CG10960-PB						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly408.8	Trypsin	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG10405-PB				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly408.9	Serine protease 38	GO:0004252,GO:0005576,GO:0006508	CG11192-PB				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494	300~320								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4091.1	Histone acetyltransferase KAT7	GO:0009996,GO:0003713,GO:0043982,GO:0008270,GO:0010485,GO:0005737,GO:0000123,GO:0005634,GO:0004402,GO:0005654,GO:0016458,GO:0006260,GO:0016747,GO:0016360,GO:0046529,GO:0048666,GO:0048190,GO:0043966,GO:0008134,GO:0022416,GO:0045892,GO:0003700,GO:0043983,GO:0043981,GO:0006355,GO:0048813,GO:0045944,GO:0006351	CG5229-PA						PF01853,PF01853,PF01530	PS51726			G3DSA:3.40.630.30,G3DSA:3.40.630.30,G3DSA:3.30.60.60	SSF55729,SSF103637										
aly4091.2	TBC1 domain family member 15	GO:0005737,GO:0070062,GO:0032313,GO:0005096,GO:0005097,GO:0005739,GO:0005576,GO:0043087,GO:0043547	CG11490-PA				SM00164		PF12068,PF00566	PS50086			G3DSA:1.10.8.270	SSF47923,SSF47923									
aly4091.3	PR domain zinc finger protein 5	GO:0005737,GO:0043565,GO:0005819,GO:0000278,GO:0006351,GO:0000122,GO:0003700,GO:0005634,GO:0016575,GO:0044212,GO:0045892,GO:0008270,GO:0003676,GO:0051567,GO:0008168,GO:0000978,GO:0046872,GO:0001078,GO:0005876,GO:0070491	CG8474-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776,PF12874,PF12874,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57716,SSF57667,SSF57667									
aly4091.4	Unknown		n/a						PF15348						138~162								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4091.5	Protein dachsous	GO:0016318,GO:0018149,GO:0016337,GO:0004871,GO:0016339,GO:0035222,GO:0045198,GO:0007164,GO:0004872,GO:0030010,GO:0007157,GO:0000904,GO:0016021,GO:0008283,GO:0007476,GO:0050839,GO:0005509,GO:0035159,GO:0007480,GO:0042067,GO:0048592,GO:0005887,GO:0005886,GO:0007155,GO:0044331,GO:0045317,GO:0007156,GO:0001737,GO:0001736,GO:0090176,GO:0090175,GO:0045296,GO:0007165	CG17941-PA				SM00112,SM00112,SM00112,SM00112,SM00112		PF00028,PF00028,PF00028,PF00028,PF00028	PS50268,PS50268,PS50268,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00232,PS00232,PS00232,PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313										
aly4091.6	Unknown		n/a																				
aly4091.7	Retrovirus-related Pol polyprotein from transposon TNT 1-94	GO:0004519,GO:0015074,GO:0004190,GO:0008270,GO:0003676,GO:0003964	n/a				SM00343		PF00098,PF07727	PS50158			G3DSA:4.10.60.10	SSF57756		00240+2.7.7.7,00230+2.7.7.7							
aly40917.1	Unknown		n/a																				
aly4096.1	Circadian clock-controlled protein	GO:0007623,GO:0005615,GO:0032504	CG10407-PA				SM00700		PF06585														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4096.2	Unknown		n/a																				
aly4096.3	Circadian clock-controlled protein	GO:0007623,GO:0005615,GO:0032504	CG10407-PA				SM00700		PF06585														
aly4096.4	PDZ and LIM domain protein 4	GO:0008270,GO:0005515	CG15617-PA				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156									
aly4096.5	Allatostatin-A receptor	GO:0004930,GO:0016021,GO:0008261,GO:0042923,GO:0007218,GO:0005887,GO:0008188,GO:0005886,GO:0007186,GO:0042562	CG2872-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00663,PR00663,PR00663,PR00663	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly40964.1	Unknown		n/a																				
aly4097.1	Probable RNA directed DNA polymerase from transposon BS	GO:0003964,GO:0006278,GO:0006313	n/a						PF00078	PS50878				SSF56672									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4097.2	Unknown		n/a																				
aly40989.1	Serine protease 3	GO:0004252,GO:0022008,GO:0004175,GO:0006508	CG8869-PA						PF00089	PS50240		PS00135	G3DSA:2.40.10.10	SSF50494									
aly4105.1	5-hydroxytryptamine receptor 1	GO:0060180,GO:0004930,GO:0007619,GO:0016021,GO:0016543,GO:0016545,GO:0016546,GO:0008227,GO:0004952,GO:0005887,GO:0005886,GO:0060179,GO:0007192,GO:0007186,GO:0007210,GO:0004993	CG12073-PA						PF00001	PS50262	PR00242,PR00242,PR00242,PR00242,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly41077.1	Unknown		n/a																				
aly4118.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4118.2	Glutathione S-transferase theta-1	GO:0005737,GO:0004364,GO:0006749	CG1702-PB						PF00043,PF02798	PS50404,PS50405			G3DSA:3.40.30.10,G3DSA:1.20.1050.10	SSF47616,SSF52833									
aly4118.3	DNA transposase THAP9	GO:0006310,GO:0043565,GO:0006313,GO:0004803,GO:0015074,GO:0016740,GO:0003676,GO:0046872	n/a				SM00980		PF05485	PS50950				SSF57716									
aly4118.4	Ubiquitin carboxyl-terminal hydrolase 5	GO:0071108,GO:0032436,GO:0048812,GO:0043161,GO:0008242,GO:0004221,GO:0005764,GO:0006511,GO:0008270,GO:0061136,GO:0004197,GO:0016579,GO:0004843	CG12082-PA																				
aly4118.5	Unknown		n/a																				
aly412.1	39S ribosomal protein L40, mitochondrial	GO:0005730,GO:0044822,GO:0003735,GO:0005761,GO:0005762,GO:0022008,GO:0006412	CG5242-PA						PF09812						59~86								
aly412.10	RAB6A-GEF complex partner protein 2	GO:0043234,GO:0043547,GO:1903363,GO:0034066,GO:0005829,GO:0016020,GO:0017137,GO:0017112,GO:0042147	CG1116-PD						PF08737,PF08737														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly412.11	Unknown		n/a				SM00595		PF10545	PS51029					134~154								
aly412.12	Rho GTPase-activating protein 11A	GO:0007494,GO:0008258,GO:0008586,GO:0035024,GO:0007165,GO:0007274,GO:0007264,GO:0033109,GO:0051056,GO:0005096,GO:0008289,GO:0035160,GO:0007173,GO:0005938,GO:0035277,GO:0007266,GO:0016323,GO:0007443,GO:0007424,GO:0007427,GO:0005829,GO:0007391,GO:0005622,GO:0048814,GO:0005100	CG34389-PC				SM00324		PF00620	PS50238			G3DSA:1.10.555.10	SSF48350	400~420		REACT_11044						
aly412.13	F-box only protein 11	GO:0005737,GO:0016274,GO:0005730,GO:0007605,GO:0005694,GO:0005634,GO:0000151,GO:0006464,GO:0060966,GO:0035246,GO:0008270,GO:0005515,GO:0048471,GO:0004842,GO:0070923	CG9461-PA				SM00256,SM00396,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00710,SM00722,SM00722,SM00722	TIGR03804,TIGR03804	PF12937,PF13229,PF13229,PF05048,PF02207	PS51157,PS50181			G3DSA:1.20.1280.50,G3DSA:2.160.20.10,G3DSA:2.160.20.10	SSF51126,SSF51126,SSF81383,SSF51126									
aly412.14	CAAX prenyl protease 2	GO:0016787,GO:0004222,GO:0016021,GO:0016020,GO:0005789,GO:0030176,GO:0006508	CG4852-PA						PF02517														
aly412.15	BTB/POZ domain-containing protein KCTD3	GO:0055114,GO:0051260,GO:0016620,GO:0005515	CG9467-PA				SM00320,SM00320,SM00225		PF02214	PS50097			G3DSA:3.30.710.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF54695									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly412.16	Dolichyl-diphosphoolig osaccharide--protein glycosyltransfe rase subunit STT3B	GO:0016020,GO:0005783,GO:0006486,GO:0018279,GO:0016021,GO:0043686,GO:0008250,GO:0006986,GO:0004576,GO:0030433,GO:0006516,GO:0004579,GO:0043687	CG7748-PA						PF02516										UPA00378				
aly412.17	Zinc finger protein 541	GO:0046872,GO:0005634,GO:0030154,GO:0000118,GO:0006355,GO:0007283,GO:0006351,GO:0003677,GO:0003682,GO:0007275	CG16779-PA				SM00717,SM00355,SM00355,SM00355,SM00355,SM00355		PF01448,PF13912,PF13912,PF13912	PS50157,PS50157,PS50157,PS51156,PS51293,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF46689										
aly412.18	Unknown		n/a																				
aly412.19	Unknown		n/a																				
aly412.2	5-hydroxytrypta mine receptor 1A	GO:0042053,GO:0001609,GO:0042428,GO:0042310,GO:0001662,GO:0090281,GO:0016021,GO:0035640,GO:0007186,GO:0004993,GO:0008283,GO:0050795,GO:0008306,GO:0005887,GO:0007268,GO:0022008,GO:0014062,GO:0007198,GO:0046883,GO:0001973,GO:0006109,GO:0007210	CG9753-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly412.3	Carboxypeptidase B	GO:0006508,GO:0004181,GO:0004180,GO:0008270,GO:0005576	CG8560-PA				SM00631		PF00246		PR00765,PR00765,PR00765,PR00765	PS00132	G3DSA:3.40.630.10	SSF53187									
aly412.4	Autophagy-related protein 2 homolog B	GO:0006995,GO:0000407,GO:0000422,GO:0035069,GO:0006914,GO:0005811,GO:0016236,GO:0042060,GO:0000045,GO:0034045,GO:0044804,GO:0019898,GO:0010506	CG1241-PA						PF09333,PF12624														
aly412.5	28S ribosomal protein S5, mitochondrial	GO:0044822,GO:0006412,GO:0003735,GO:0005743,GO:0003723,GO:0005763,GO:0032543	CG40049-PC						PF03719,PF00333	PS50881		PS00585	G3DSA:3.30.160.20,G3DSA:3.30.230.10	SSF54768,SSF54211									
aly412.6	Zinc finger protein-like 1	GO:0005794,GO:0033227,GO:0016192,GO:0016021,GO:0005575,GO:0008270,GO:0005515	CG5382-PB				SM00184		PF13639	PS50089			G3DSA:3.30.40.10	SSF57850									
aly412.7	Tubulin--tyrosine ligase like protein 12	GO:0004835,GO:0006464	CG1550-PA						PF03133	PS51221													
aly412.8	DDB1- and CUL4-associated factor 5	GO:0016567,GO:0005739,GO:0080008,GO:0005515	CG2112-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400	PS50082,PS50082,PS50294			G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly412.9	RRP15-like protein	GO:0005730,GO:0005634,GO:0005739,GO:0005575,GO:0003674,GO:0022008	CG3817-PA						PF07890														
aly41207.1	Metabotropic glutamate receptor	GO:0005886,GO:0004930,GO:0015485,GO:0042734,GO:0001641,GO:0038038,GO:0007200,GO:0016021,GO:0045121,GO:0007216,GO:0030425,GO:0007528,GO:0008066,GO:0051966,GO:0001642,GO:0005887,GO:0017085,GO:0008343,GO:0072553,GO:0016595,GO:0007196	CG30361-PG								PR00248,PR00248,PR00248		G3DSA:3.40.50.2300	SSF53822			REACT_14797						
aly41207.2	Unknown		n/a																				
aly41267.1	Unknown		n/a																				
aly4135.1	Peroxidase mlt7	GO:0018149,GO:0020037,GO:0002119,GO:0042338,GO:0006979,GO:0040032,GO:0046872,GO:0004601,GO:0055114	CG5873-PA						PF03098,PF03098,PF03098	PS50292			G3DSA:1.10.640.10,G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4135.2	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0006979,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0004601,GO:0055114	CG3477-PA						PF03098	PS50292	PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10	SSF48113									
aly41365.1	Protein downstream neighbor of son homolog	GO:0008283,GO:0005634,GO:0033260,GO:0003674,GO:0007307,GO:0007275,GO:0051301	CG2669-PA																				
aly4138.1	Zonadhesin	GO:2000359,GO:0050840,GO:0016021,GO:0007339,GO:0005886,GO:0007155	n/a												364~384								
aly4138.2	Pro-resilin	GO:0040003,GO:0032992,GO:0005214,GO:0030023,GO:0008010,GO:0031012,GO:0005576,GO:0008061,GO:0042302	CG9036-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly4138.3	Pro-resilin	GO:0040003,GO:0032992,GO:0005214,GO:0030023,GO:0008010,GO:0031012,GO:0005576,GO:0008061,GO:0042302	CG9036-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly4138.4	Spherulin-2A		n/a										G3DSA:2.170.15.10	SSF56973									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4138.5	Spherulin-2A		n/a																				
aly4138.6	Monoacylglycerol lipase ABHD12	GO:0046464,GO:0016021,GO:0047372	CG15111-PB						PF12695				G3DSA:3.40.50.1820	SSF53474									
aly4138.7	Jerky protein homolog-like	GO:0005634,GO:0003677	CG12346-PA				SM00674		PF04218,PF03221,PF03184	PS51253,PS50960			G3DSA:1.10.10.60,G3DSA:1.10.10.60	SSF46689,SSF46689									
aly4138.8	Monoacylglycerol lipase ABHD12	GO:0046464,GO:0016021,GO:0047372	CG15111-PB										G3DSA:3.40.50.1820	SSF53474									
aly414.1	Unknown		n/a																				
aly41476.1	Fatty acid-binding protein, muscle	GO:0005737,GO:0007616,GO:0005215,GO:0006810,GO:0008289,GO:0005504,GO:0005875	CG6783-PC										G3DSA:2.40.128.20	SSF50814									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly41545.1	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0005534,GO:0030246	CG42295-PB				SM00034		PF00059	PS50041			G3DSA:3.10.100.10	SSF56436,SSF56436									
aly416.1	Unknown		n/a																				
aly41646.1	Beta-1,3-glucan-binding protein	GO:0045087,GO:0005975,GO:0045088,GO:0008329,GO:0009620,GO:0009986,GO:0002758,GO:0005576,GO:0004553,GO:0052736,GO:0032491,GO:0001872	CG5008-PA						PF00722,PF15886				G3DSA:2.60.120.200	SSF49899,SSF49899,SSF49899									
aly41646.2	Beta-1,3-glucan-binding protein (Fragment)	GO:0005975,GO:0045088,GO:0008329,GO:0002758,GO:0045087,GO:0004553,GO:0030247,GO:0001530,GO:0050832,GO:0046658,GO:0050830,GO:0005576,GO:0001872,GO:0005515,GO:0009253,GO:0050829,GO:0052736,GO:0042834,GO:0006955,GO:0042742	CG6895-PA						PF00722,PF15886				G3DSA:2.60.120.200	SSF49899,SSF49899									
aly41664.1	Unknown		n/a																				
aly41673.1	Methionine--tRNA ligase, mitochondrial	GO:0005759,GO:0004825,GO:0006431,GO:0005739,GO:0005524	CG31322-PA										G3DSA:2.170.220.10										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly41850.1	Phenylalanine-tRNA ligase alpha subunit	GO:0005737,GO:0004826,GO:0000049,GO:0006450,GO:0006432,GO:0009328,GO:0004812,GO:0043039,GO:0002161,GO:0005524	CG2263-PA						PF01409	PS50862			G3DSA:3.30.930.10	SSF55681		00970+6.1.1.20	REACT_71						
aly41850.2	GDP-L-fucose synthase	GO:0050662,GO:0033227,GO:0016853,GO:0042356,GO:0042350,GO:0042351,GO:0005575,GO:0050577	CG3495-PA										G3DSA:3.90.25.10	SSF51735									
aly419.1	Neuroligin-1	GO:0009897,GO:0002087,GO:0032433,GO:0097091,GO:0016339,GO:0005886,GO:0061002,GO:0030425,GO:0010841,GO:0045202,GO:0031175,GO:2000809,GO:0030054,GO:0032230,GO:0048789,GO:0048511,GO:1900029,GO:0051932,GO:0051260,GO:0051491,GO:0097104,GO:0097120,GO:0006605,GO:0060999,GO:0007416,GO:0097119,GO:2000310,GO:2000311,GO:0005794,GO:0042043,GO:0016080,GO:0009986,GO:1902474,GO:2000463,GO:0052689,GO:0051290,GO:0045184,GO:0045211,GO:0030165,GO:0023041,GO:0030431,GO:0005887,GO:0060076,GO:1902533,GO:0007157,GO:0050839,GO:0046983,GO:0097481,GO:0045664,GO:0007399,GO:0043197,GO:0060291,GO:0043198,GO:0072553,GO:0097105,GO:0035418,GO:2000302,GO:0097114,GO:0097115,GO:0097110,GO:0051965,GO:0097113,GO:0017146,GO:0007158,GO:0051968,GO:1900244,GO:0004872	CG34139-PD						PF00135,PF00135				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474	561~581								
aly419.2	Unknown	GO:0005549	n/a						PF01395				G3DSA:1.10.238.20	SSF47565									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly419.3	Cytochrome P450 6l1	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG13977-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly419.4	Cytochrome P450 6j1	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0035220,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG11466-PA						PF00067		PR00385,PR00385,PR00385,PR00359,PR00359,PR00359,PR00359	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly419.5	Cytochrome P450 6B7	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0040040,GO:0005506,GO:0055114,GO:0009055	CG10241-PA						PF00067				G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly419.6	Cytochrome P450 6B5 (Fragment)	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0070330,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA						PF00067		PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly4192.1	Leucine-rich repeat-containing protein 24	GO:0005515,GO:0016021,GO:0042059,GO:0005887,GO:0005886,GO:0030510	CG12199-PB				SM00409,SM00369,SM00369,SM00369,SM00369,SM00369,SM00408,SM00082		PF00560,PF07679,PF13855,PF13855	PS51450,PS50835,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:2.60.40.10	SSF52058,SSF48726									
aly4192.10	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4192.11	Unknown		n/a																				
aly4192.2	Unknown		n/a																				
aly4192.3	Zinc carboxypeptidase A 1	GO:0005615,GO:0007586,GO:0004181,GO:0004180,GO:0008270,GO:0006508	CG18417-PA				SM00631		PF00246,PF00246,PF02244		PR00765,PR00765,PR00765,PR00765	PS00132	G3DSA:3.30.70.340,G3DSA:3.40.630.10,G3DSA:3.40.630.10	SSF53187,SSF53187,SSF54897									
aly4192.4	Unknown		n/a										G3DSA:3.40.630.10	SSF53187									
aly4192.5	Carboxypeptidase A4	GO:0004181,GO:0004180,GO:0005576,GO:0008270,GO:0016573,GO:0006508	CG8560-PA				SM00631		PF00246,PF02244		PR00765,PR00765,PR00765,PR00765		G3DSA:3.30.70.340,G3DSA:3.40.630.10	SSF54897,SSF53187									
aly4192.6	Carboxypeptidase A2	GO:0007039,GO:0005773,GO:0004181,GO:0004180,GO:0005576,GO:0008270,GO:0006508	CG8560-PA				SM00631		PF00246,PF02244		PR00765,PR00765,PR00765,PR00765		G3DSA:3.30.70.340,G3DSA:3.40.630.10	SSF53187,SSF54897									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4192.7	Zinc carboxypeptidase (Fragment)	GO:0006508,GO:0004181,GO:0005576,GO:0008270	CG18417-PA				SM00631		PF00246				G3DSA:3.40.630.10	SSF53187									
aly4192.8	Unknown		n/a						PF14529						177~179								
aly4192.9	Unknown		n/a						PF00078	PS50878				SSF56672									
aly4196.1	Unknown		n/a																				
aly4196.2	Unknown		n/a																				
aly4196.3	Protein SERAC1	GO:0005783,GO:0008654,GO:0006886,GO:0016788,GO:0005578,GO:0005654,GO:0030198,GO:0006505,GO:0005739,GO:0008340,GO:0016021	CG10383-PA										G3DSA:1.25.10.10,G3DSA:3.40.50.1820	SSF53474,SSF53474,SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.1	Unknown		n/a																				
aly420.10	Putative serine/threonine-protein kinase haspin homolog	GO:0005737,GO:0006468,GO:0005634,GO:0005575,GO:0004674,GO:0004672,GO:0035556,GO:0005524	CG40080-PA				SM00220		PF12330	PS50011			G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:3.30.200.20	SSF56112,SSF56112									
aly420.11	Unknown		n/a																				
aly420.12	Max dimerization protein 4	GO:0008285,GO:0000122,GO:0005634,GO:0003714,GO:0006351,GO:0003677,GO:0046983	n/a						PF00010	PS50888			G3DSA:4.10.280.10	SSF47459	72~106								
aly420.13	Unknown		n/a																				
aly420.14	DALR anticodon-binding domain-containing protein 3	GO:0004812,GO:0004814,GO:0006420,GO:0000166,GO:0006418,GO:0005524	CG8097-PA				SM00836		PF05746				G3DSA:1.10.730.10	SSF47323	513~513		REACT_71						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.15	DnaJ homolog subfamily C member 25 homolog	GO:0005575,GO:0008150,GO:0016021,GO:0003674,GO:0012505	CG7872-PA				SM00271		PF00226	PS50076	PR00625,PR00625,PR00625	PS00636	G3DSA:1.10.287.110	SSF46565	74~94,171~198								
aly420.16	Unknown		n/a																				
aly420.17	Blood vessel epicardial substance	GO:0042391,GO:0034446,GO:0060973,GO:2001135,GO:0043087,GO:0005923,GO:0060931,GO:0016021,GO:0016020,GO:0005198,GO:0002027,GO:0002244,GO:0001921,GO:0016328,GO:0031253,GO:0048278,GO:0008360,GO:0005886,GO:0090136,GO:0030552,GO:0016192,GO:0040017	CG32513-PA						PF04831				G3DSA:2.60.120.10	SSF51206									
aly420.18	Unknown	GO:0048598,GO:0072669	n/a						PF15323														
aly420.19	cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A	GO:0004118,GO:0047555,GO:0004115,GO:0004112,GO:0008144,GO:0007165,GO:0006198,GO:0046068,GO:0046069,GO:0005737,GO:0043204,GO:0016020,GO:0046872,GO:0043025,GO:0046058,GO:0043949,GO:0046331,GO:0030553,GO:0030552,GO:0005575,GO:0005515,GO:0010738	CG34341-PF				SM00065,SM00065		PF13185,PF01590,PF00233		PR00387,PR00387,PR00387,PR00387,PR00387,PR00387	PS00126	G3DSA:1.10.1300.10,G3DSA:3.30.450.40,G3DSA:3.30.450.40	SSF55781,SSF55781,SSF109604									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.2	Protein TANC2	GO:0005737,GO:0001701,GO:0061327,GO:0009986,GO:0008270,GO:0005515,GO:0007520,GO:0007298,GO:0005912	CG32096-PB				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796,PF12796	PS50293,PS50088,PS50088,PS50089,PS50088,PS50088,PS50297			G3DSA:1.25.40.20,G3DSA:1.25.40.10,G3DSA:3.30.40.10,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF57850,SSF52540,SSF48403,SSF48452									
aly420.20	Sorting nexin-12	GO:0006909,GO:0090263,GO:0035220,GO:0019898,GO:0050821,GO:0010629,GO:0042177,GO:0051224,GO:0070062,GO:0030100,GO:0006886,GO:0061357,GO:0061355,GO:2000642,GO:0061359,GO:0060070,GO:0019899,GO:0010955,GO:0006897,GO:0035091,GO:0016050,GO:0030904,GO:0015031,GO:0005769	CG6359-PA				SM00312		PF00787	PS50195			G3DSA:3.30.1520.10	SSF64268									
aly420.21	Pre-mRNA-splicing factor Slu7	GO:0016607,GO:0030628,GO:0000389,GO:0000398,GO:0007052,GO:0008270,GO:0003676,GO:0008380,GO:0005681	CG1420-PA						PF11708						323~343,490~530,178~201								
aly420.22	Kinesin-like protein subito	GO:0000089,GO:0016887,GO:0005871,GO:0007067,GO:0005873,GO:0005875,GO:0007140,GO:0005737,GO:0000922,GO:0005876,GO:0003774,GO:0005524,GO:0000278,GO:0000212,GO:0008017,GO:0016321,GO:0000090,GO:0007052,GO:0051233,GO:0040016,GO:0007018,GO:0051257,GO:0003777,GO:0007091	CG12298-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380		G3DSA:3.40.850.10,G3DSA:3.40.850.10	SSF52540,SSF52540	1238~1258,527~582,1059~1079								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.23	Adhesion G protein-coupled receptor A3	GO:0009897,GO:0004930,GO:0007186,GO:0016021,GO:0005515	CG15744-PA				SM00082,SM00369,SM00369,SM00369		PF13895,PF00002,PF13855	PS51450,PS50261,PS50835,PS51450,PS51450,PS50227,PS51450			G3DSA:3.80.10.10,G3DSA:2.60.40.10	SSF111418,SSF48726,SSF52058									
aly420.24	Unknown		n/a												82~102								
aly420.25	Epoxide hydrolase 4	GO:0016787,GO:0016021	n/a						PF12697				G3DSA:3.40.50.1820	SSF53474									
aly420.26	Protein Optix	GO:0048749,GO:0043565,GO:0007458,GO:0003700,GO:0005634,GO:0006355,GO:0048813,GO:0003677,GO:0001745,GO:0001751	CG18455-PC				SM00389		PF00046,PF16878	PS50071			G3DSA:1.10.10.60	SSF46689									
aly420.27	Integrator complex subunit 7	GO:0005737,GO:0016180,GO:0034472,GO:0005634,GO:0032039,GO:0006974,GO:0003674,GO:0005488,GO:0005694	CG18176-PA										G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371									
aly420.28	Solute carrier family 41 member 2	GO:0006812,GO:0016021,GO:0008324,GO:0005886	CG33181-PC						PF01769,PF01769				G3DSA:1.10.357.20,G3DSA:1.10.357.20	SSF161093,SSF161093									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.29	Integrator complex subunit 7	GO:0005737,GO:0016180,GO:0071479,GO:0000077,GO:0034472,GO:0005634,GO:0032039,GO:0003674,GO:0005694	CG18176-PA																				
aly420.3	Unknown	GO:0005549	n/a										G3DSA:1.10.238.20										
aly420.30	Leucine-rich repeat-containing protein 70	GO:0016021	CG4781-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00082		PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly420.31	Unknown		n/a																				
aly420.32	Vang-like protein 1	GO:0016328,GO:0090175,GO:0042067,GO:0016021,GO:0001736,GO:0005109,GO:0007163,GO:0005515,GO:0005886,GO:0070593,GO:0007298,GO:0007275,GO:0001738	CG8075-PB			PIRSF007991			PF06638														
aly420.33	Monocarboxylate transporter 14	GO:0015718,GO:0015293,GO:0034220,GO:0008028,GO:0016021,GO:0015355,GO:0005886,GO:0055085	CG8271-PA										G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.34	SCY1-like protein 2	GO:0090090,GO:0005794,GO:0006468,GO:0032504,GO:2000286,GO:2000370,GO:0008333,GO:0002092,GO:0004672,GO:0048471,GO:0010008,GO:0005102,GO:0005524,GO:0030136	CG1951-PA				SM00220		PF00069	PS50011			G3DSA:3.30.200.20,G3DSA:1.25.10.10,G3DSA:1.10.510.10	SSF48371,SSF56112	597~617								
aly420.35	TM2 domain-containing protein CG11103	GO:0005575,GO:0003674,GO:0016021,GO:0008150	CG11103-PB						PF05154														
aly420.36	40S ribosomal protein S13	GO:0005737,GO:0005840,GO:0005730,GO:0005622,GO:0003735,GO:0007052,GO:0000022,GO:0000228,GO:0006412,GO:0022627	CG13389-PB	MF_01343_A					PF00312,PF08069			PS00362		SSF47060			REACT_71						
aly420.37	NADH dehydrogenase [ubiqui] 1 beta subcomplex subunit 4	GO:0070062,GO:0008137,GO:0016021,GO:0031965,GO:0005739,GO:0006120,GO:0005654,GO:0005747,GO:0006979,GO:0003954	CG12859-PA						PF07225														
aly420.38	Trafficking protein particle complex subunit 5	GO:0005794,GO:0006888,GO:0005783,GO:0017112,GO:0030008,GO:0016192	CG10153-PA			PIRSF017479			PF04051				G3DSA:3.30.1380.20	SSF111126									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.39	Ras-related protein Rab-39A	GO:0006914,GO:0005794,GO:0031982,GO:0030670,GO:0090385,GO:0006886,GO:0005770,GO:0003924,GO:0006913,GO:0090383,GO:0005764,GO:0032482,GO:0045335,GO:0016192,GO:0007165,GO:0005886,GO:0045202,GO:0043025,GO:0015031,GO:0005525	CG12156-PA				SM00176,SM00175,SM00174,SM00173	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly420.4	Activator of 90 kDa heat shock protein ATPase homolog 1	GO:0005737,GO:0005783,GO:0070062,GO:0005829,GO:0051087,GO:0006950,GO:0032781,GO:0001671	CG1416-PA				SM01000		PF09229,PF08327				G3DSA:3.30.530.20	SSF55961,SSF103111									
aly420.40	THAP domain containing protein 1	GO:0043565,GO:0003700,GO:0005634,GO:0005654,GO:0006355,GO:0048813,GO:0008270,GO:0003676,GO:0046872,GO:0007049,GO:0006351	CG10431-PA				SM00980,SM00692		PF05485	PS50950				SSF57716									
aly420.41	Unknown		n/a												47~95								
aly420.42	FERM and PDZ domain-containing protein 4	GO:0005856,GO:0043197,GO:0005546,GO:0007165,GO:0005515,GO:0051835	CG42788-PB				SM00295,SM00456,SM00456,SM00228		PF00373,PF00397,PF00595	PS50020,PS50057,PS50020,PS50200,PS50106			G3DSA:2.30.42.10,G3DSA:2.20.70.10,G3DSA:2.20.70.10,G3DSA:3.10.20.90	SSF51045,SSF51045,SSF47031,SSF54236,SSF50156									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.43	WD and tetratricopeptide repeats protein 1	GO:0001701,GO:0005975,GO:0006629,GO:0000122,GO:0005829,GO:0006006,GO:0008361,GO:0005575,GO:0010891,GO:0032869,GO:0003674,GO:0035264,GO:0016567,GO:0009269,GO:0010883,GO:0055082,GO:0005634,GO:0004857,GO:0045717	CG5124-PA				SM00028,SM00028,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF13414,PF00400,PF00400	PS50293,PS50082,PS50294,PS50294,PS50082			G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:1.25.40.10	SSF48452,SSF50978,SSF50978,SSF50978										
aly420.44	Coiled-coil domain-containing protein 130 homolog	GO:0005575,GO:0008150,GO:0003674	CG15084-PA						PF04502														
aly420.45	Vacuolar protein sorting associated protein 13A	GO:0007626,GO:0008104,GO:0007399,GO:0006895,GO:0035176,GO:0045053,GO:0006623,GO:0019898,GO:0031045,GO:0005622	CG2093-PA						PF16908,PF12624,PF16910,PF06650,PF16909														
aly420.46	Transmembrane protein 183	GO:0016021,GO:0031647,GO:0009952,GO:0005515,GO:0019005	CG12765-PA										G3DSA:1.20.1280.50										
aly420.47	Liprin-alpha-3	GO:0048675,GO:0008594,GO:0051124,GO:0031290,GO:0009986,GO:0048786,GO:0005737,GO:0048841,GO:0045467,GO:0048172,GO:0045202,GO:0005515,GO:0007411,GO:0007269,GO:0043234,GO:0007412,GO:0005925,GO:0007416,GO:0048490	CG11199-PE												49~76								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.48	Liprin-alpha-2	GO:0048675,GO:0051124,GO:0007160,GO:0045202,GO:0045467,GO:0007411,GO:0007412,GO:0005925,GO:0007416,GO:0005737,GO:0070062,GO:0048786,GO:0048841,GO:0031290,GO:0009986,GO:0008594,GO:0048490,GO:0007269,GO:0007268,GO:0043234,GO:0014047,GO:0005829,GO:0005515	CG11199-PE				SM00454,SM00454,SM00454		PF07647,PF00536,PF00536	PS50105,PS50105,PS50105			G3DSA:1.10.150.50,G3DSA:1.10.150.50	SSF47769,SSF47769	403~444,13~61,183~308,315~370,527~568,105~139								
aly420.49	Ribosome biogenesis protein bms1	GO:0005737,GO:0072686,GO:0005730,GO:0042255,GO:0005634,GO:0003924,GO:0042254,GO:0005739,GO:0006364,GO:0022008,GO:0005524,GO:0005525	CG7728-PA				SM00785		PF08142,PF04950	PS51714			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	373~393,1075~1107								
aly420.5	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	GO:0006631,GO:0050660,GO:0070062,GO:0005739,GO:0005759,GO:0034641,GO:0055114,GO:0003995,GO:0016937,GO:0009083,GO:0044281	CG3902-PA			PIRSF016578			PF02770,PF00441,PF02771			PS00072,PS00073	G3DSA:1.10.540.10,G3DSA:1.20.140.10,G3DSA:2.40.110.10	SSF56645,SSF47203									
aly420.50	GRAM domain-containing protein 1B	GO:0016021,GO:0016020	CG3304-PC				SM00568		PF16016,PF02893														
aly420.51	Unknown		n/a																				
aly420.52	Ubiquitin-40S ribosomal protein S27a	GO:0022627,GO:0005634,GO:0006412,GO:0003735,GO:0046872,GO:0005875,GO:0005840	CG5271-PA						PF01599					SSF57829									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.53	Ribosome biogenesis protein NSA2 homolog	GO:0006909,GO:0005730,GO:0044822,GO:0030529,GO:0006364,GO:0022008,GO:0005634	CG5277-PB						PF01201						51~78								
aly420.54	E3 ubiquitin-protein ligase Mdm2	GO:0005737,GO:0000122,GO:0005730,GO:0005654,GO:0016567,GO:0043066,GO:0008270,GO:0016874,GO:0071157	n/a						PF13920				G3DSA:3.30.40.10	SSF90209									
aly420.55	Thymosin beta 12	GO:0005737,GO:0007015,GO:0007010,GO:0007420,GO:0005829,GO:0005856,GO:0035193,GO:0003779,GO:0042989,GO:0003785	CG4944-PA				SM00152,SM00152,SM00152,SM00152		PF01290,PF01290,PF01290,PF01290				G3DSA:1.20.5.520,G3DSA:1.20.5.520,G3DSA:1.20.5.520,G3DSA:1.20.5.520										
aly420.56	Protein ovarian tumor locus	GO:0005737,GO:0051276,GO:0019099,GO:0018992,GO:0016579,GO:0007281,GO:0032877,GO:0048477,GO:0004843,GO:0048134	CG12743-PB						PF02338	PS50802				SSF54001									
aly420.57	Regucalcin	GO:0019853,GO:0005737,GO:0005615,GO:0032504,GO:0006874,GO:0030234,GO:0005811,GO:0004341,GO:0050848,GO:0005576,GO:0005509,GO:0032781,GO:0005634,GO:0008270	CG1803-PD						PF08450		PR01791,PR01791,PR01791,PR01790,PR01790,PR01790,PR01790,PR01790,PR01790		G3DSA:2.120.10.30	SSF63829		00030+3.1.1.17,00053+3.1.1.17,00930+3.1.1.17		PWY-2221,PWY-5530,PWY-7165					
aly420.58	Regucalcin	GO:0019853,GO:0005737,GO:0005615,GO:0032504,GO:0006874,GO:0030234,GO:0005811,GO:0004341,GO:0050848,GO:0005576,GO:0005509,GO:0032781,GO:0005634,GO:0008270	CG1803-PD						PF08450		PR01791,PR01791,PR01791,PR01791,PR01790,PR01790,PR01790,PR01790,PR01790,PR01790		G3DSA:2.120.10.30	SSF63829		00030+3.1.1.17,00053+3.1.1.17,00930+3.1.1.17		PWY-2221,PWY-5530,PWY-7165					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.59	WD repeat-containing protein 6	GO:0005737,GO:0008285,GO:0044822,GO:0007050,GO:0005515,GO:0005886,GO:0010507	CG33172-PB				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50294,PS50082			G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978,SSF50978									
aly420.6	SRR1-like protein	GO:0048511	CG34117-PA						PF07985														
aly420.60	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	GO:0005947,GO:0016624,GO:0005739,GO:0003826,GO:0046949,GO:0008152,GO:0017086,GO:0003863,GO:0046872,GO:0009083	CG8199-PA						PF00676				G3DSA:3.40.50.970	SSF52518									
aly420.61	Cyclin-K	GO:0044828,GO:0006974,GO:0006468,GO:0001701,GO:0006355,GO:0000079,GO:2001165,GO:0019901,GO:0016538,GO:0002945,GO:0006351,GO:0004693,GO:0008353,GO:0022008,GO:0005634,GO:0002944,GO:0007067,GO:0051301,GO:0071157	CG15218-PA				SM00385,SM00385		PF00134				G3DSA:1.10.472.10	SSF47954,SSF47954									
aly420.62	Tyrosine-protein phosphatase non-receptor type 14	GO:0005856,GO:0005737,GO:0045177,GO:0006351,GO:0008092,GO:0006470,GO:0004725,GO:0030971,GO:0003712,GO:0001946,GO:0005654,GO:0006355,GO:0046825,GO:0005938,GO:0035335,GO:2000647,GO:0005634,GO:0035331,GO:0008285	CG9493-PA				SM00295		PF00373,PF09379,PF09380	PS50057,PS50055	PR00935,PR00935,PR00935	PS00661	G3DSA:1.20.80.10,G3DSA:3.90.190.10,G3DSA:2.30.29.30,G3DSA:3.10.20.90	SSF50729,SSF54236,SSF47031,SSF52799									
aly420.63	Oxygen-dependent coproporphyrinogen-III oxidase	GO:0006783,GO:0006782,GO:0004109,GO:0005739,GO:0006779,GO:0055114,GO:0042803	CG3433-PA						PF01218		PR00073,PR00073,PR00073,PR00073,PR00073	PS01021	G3DSA:3.40.1500.10	SSF102886		00860+1.3.3.3		PWY-5531,PWY-7159	UPA00251				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.64	Basic juvenile hormone-suppressible protein 1	GO:0016201,GO:0005616,GO:0005811,GO:0005576,GO:0045735,GO:0008045	CG6806-PA						PF03723,PF03722,PF00372		PR00187,PR00187,PR00187,PR00187	PS00210,PS00209	G3DSA:1.10.1280.10,G3DSA:2.60.40.1520,G3DSA:1.20.1370.10	SSF48056,SSF81296,SSF48050	771~771								
aly420.65	Syntaxin-binding protein 5	GO:0008021,GO:0045921,GO:0007616,GO:0005892,GO:0007163,GO:0015031,GO:0030054,GO:0016021,GO:0006887,GO:0017075,GO:0010468,GO:0030141,GO:0016082,GO:0030659,GO:0007269,GO:0022008,GO:0006893,GO:0031594,GO:0016079,GO:1900073,GO:0030193,GO:0000149	CG17762-PC				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF08366,PF00957	PS50892	PR00962,PR00962,PR00962,PR00962	PS00678	G3DSA:1.20.5.110,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF58038,SSF50978,SSF50978,SSF50978									
aly420.66	Unknown		n/a																				
aly420.67	Probable ATP-dependent RNA helicase DDX10	GO:0008026,GO:0044822,GO:0004004,GO:0003724,GO:0005524,GO:0003676,GO:0022008,GO:0010501,GO:0007526	CG5800-PA				SM00487,SM00490		PF00271,PF00270,PF13959	PS51192,PS51194		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	580~611								
aly420.68	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly420.69	Unknown		n/a																				
aly420.7	Unknown		CG6040-PA																				
aly420.70	Unknown		n/a																				
aly420.8	Sideroflexin-2	GO:0008324,GO:0016021,GO:0006281,GO:0006812,GO:0006811,GO:0016020,GO:0015075,GO:0005743,GO:0055072,GO:0003677,GO:0055085	CG6812-PA					TIGR00798	PF03820														
aly420.9	PWWP domain-containing protein 2A		n/a				SM00293		PF00855	PS50812			G3DSA:2.30.30.160	SSF63748									
aly4200.1	Serine protease 3	GO:0004252,GO:0004175,GO:0006508	CG6457-PA						PF00089			PS00135	G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4201.1	STE20-like serine/threonine-protein kinase	GO:0032147,GO:0010800,GO:0042981,GO:0046777,GO:0023014,GO:0005737,GO:0007346,GO:0000902,GO:0000281,GO:0004674,GO:0042801,GO:0042802,GO:0042803,GO:0033109,GO:0006468,GO:0008283,GO:0006915,GO:0032154,GO:1990023,GO:0007052,GO:0005938,GO:0032879,GO:0070062,GO:0000132,GO:0031098,GO:0005524,GO:0004702,GO:0007091	CG4527-PD						PF12474,PF12474						343~395,155~191,67~94,275~305								
aly4201.2	Interleukin enhancer-binding factor 2 homolog	GO:0005730,GO:0071011,GO:0071013,GO:0006955,GO:0000398,GO:0016740,GO:0003725,GO:0045893,GO:0003677,GO:0005634,GO:0005524,GO:0006351	CG5641-PA				SM00572		PF07528	PS50152,PS51703			G3DSA:3.30.460.10	SSF81301										
aly4201.3	Probable Golgi transport protein 1	GO:0016192,GO:0016021,GO:0000139,GO:0005575,GO:0003674,GO:0015031	CG32576-PB						PF04178														
aly4201.4	Unknown		n/a																				
aly42060.1	Cyclin-dependent kinase 9	GO:0004693,GO:0006468,GO:0009408,GO:0008024,GO:0000278,GO:0006355,GO:0006368,GO:0005634,GO:0032783,GO:0005703,GO:0005700,GO:0004674,GO:0008360,GO:0006351,GO:0004672,GO:0007155,GO:0008353,GO:0022008,GO:0005524	CG5179-PA				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly42060.2	RE1-silencing transcription factor	GO:0001047,GO:0071385,GO:0010629,GO:0035690,GO:0200798,GO:0046676,GO:0003677,GO:0003700,GO:0001078,GO:0070933,GO:0005654,GO:0000122,GO:0006325,GO:0006355,GO:0005634,GO:0002244,GO:0050768,GO:0045665,GO:0045955,GO:2000740,GO:0043280,GO:0046872,GO:2000706,GO:0008285,GO:0071257,GO:0017053,GO:0060379,GO:0008134,GO:0045892,GO:0045893,GO:0043922,GO:0001046,GO:0044212,GO:0032348,GO:0005829,GO:2000065,GO:0001228,GO:0071805,GO:0043065,GO:0003682,GO:0015271	CG7928-PA				SM00980,SM00355,SM00355,SM00355,SM00355,SM00355		PF13909,PF13909,PF05485	PS50157,PS50950,PS50157				SSF57667,SSF57716	148~190,219~239									
aly42060.3	Gamma-interferon-inducible lysosomal thiol reductase	GO:0005764,GO:0042590,GO:0005576,GO:0016667	CG9796-PA						PF03227				G3DSA:3.40.30.10	SSF52833,SSF52833									
aly42060.4	Unknown		n/a																				
aly4212.1	Unknown		n/a																				
aly4226.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4226.2	Monocarboxylate transporter 12	GO:0005308,GO:0035879,GO:0015129,GO:0008028,GO:0016021,GO:1902598,GO:0015293,GO:0005887,GO:0055085	CG10019-PB						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly4226.3	Unknown		n/a																				
aly4226.4	Unknown		n/a																				
aly423.1	Intersectin-2	GO:0005089,GO:0005070,GO:0006897,GO:0070062,GO:0007480,GO:0005813,GO:0005085,GO:0045179,GO:0009967,GO:0005737,GO:0035025,GO:0005509,GO:0035277,GO:0035023,GO:0007411,GO:0002121,GO:1903861	CG32239-PA				SM00325		PF00621	PS50010,PS50003			G3DSA:1.20.900.10	SSF48065	1415~1435,1361~1381								
aly423.10	Unknown		n/a																				
aly423.11	GTP-binding protein Rhes	GO:0031681,GO:0043949,GO:0007626,GO:0016020,GO:0003924,GO:0005622,GO:0005575,GO:0008150,GO:0001963,GO:0008152,GO:0031397,GO:0015031,GO:0006184,GO:0005886,GO:0007264,GO:0051897,GO:0033235,GO:0005525	CG8641-PA				SM00175,SM00174,SM00173	TIGR00231	PF00071	PS51421	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly423.12	Unknown	GO:0003677	CG4404-PA				SM00595		PF10545,PF02944	PS51031,PS51029													
aly423.13	Brain protein I3	GO:0016021	CG12012-PA						PF10164														
aly423.14	Protein N-terminal asparagine amidohydrolase	GO:0005737,GO:0008418,GO:0004067	CG5473-PA						PF14736														
aly423.15	Serine/threonine-protein kinase SBK1	GO:0005737,GO:0006468,GO:0007498,GO:0004672,GO:0004674,GO:0004702,GO:0005524	CG4945-PB				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly423.16	Protein ELYS	GO:0005643,GO:0005575,GO:0003674,GO:0003677,GO:0015031,GO:0008150,GO:0051028	CG14215-PA						PF16687,PF13934						1881~1915,757~757								
aly423.17	Putative sodium-coupled neutral amino acid transporter 10	GO:0003333,GO:0006865,GO:0016021,GO:0015171,GO:0006814	CG30394-PA						PF01490						568~602,646~673								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly423.18	Zinc finger protein 184	GO:0051726,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG11247-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	591~611								
aly423.19	Unknown		CG13634-PA												64~84								
aly423.2	Contactin-associated protein-like 2	GO:0019226,GO:0071109,GO:0031175,GO:0007612,GO:0030425,GO:0030424,GO:0021761,GO:0021987,GO:0043204,GO:0016021,GO:0016020,GO:0044224,GO:0043025,GO:0042297,GO:0021794,GO:0005794,GO:0007420,GO:0035176,GO:0021756,GO:0009986,GO:0008076,GO:0008038,GO:0019899,GO:0004867,GO:0007155,GO:0045163,GO:0030534,GO:0030673,GO:0071205,GO:0005576,GO:0071625,GO:0005769	CG43225-PG				SM00179,SM00179,SM00181,SM00181,SM00181,SM00282,SM00282,SM00282,SM00282,SM00282,SM00282		PF00008,PF02210,PF02210,PF02210,PF02210,PF02210,PF02210	PS50026,PS50026,PS50025,PS50025,PS50025,PS50025,PS50026,PS50026,PS50025,PS50025		PS01186,PS00010	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.60.120.200,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.60.120.200	SSF49899,SSF49899,SSF49899,SSF49899,SSF49899,SSF49899,SSF49899,SSF49899,SSF49899,SSF49899									
aly423.20	Mitochondrial thiamine pyrophosphate carrier	GO:0015619,GO:0030974,GO:0016021,GO:0022857,GO:0005743,GO:0005740,GO:0005634,GO:0055085	CG6608-PB						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920	PR00926,PR00926,PR00926,PR00926,PR00926		G3DSA:1.50.40.10	SSF103506									
aly423.21	Mediator of RNA polymerase II transcription subunit 10	GO:0006367,GO:0003713,GO:0001104,GO:0006357,GO:0006351,GO:0005515,GO:0006366,GO:0016592	CG5057-PC						PF09748						7~27								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly423.22	Mitochondrial cardiolipin hydrolase	GO:0030719,GO:0007126,GO:0034587,GO:0035755,GO:0043046,GO:0016021,GO:0007286,GO:0016042,GO:0008053,GO:0005741,GO:0004519,GO:0046872,GO:0042803	n/a						PF13091				G3DSA:3.30.870.10	SSF56024									
aly423.23	Exonuclease 1	GO:0006310,GO:0008409,GO:0006281,GO:0004518,GO:0005634,GO:0008852,GO:0006298,GO:0045145,GO:0090305,GO:0048256,GO:0003677,GO:0046872,GO:0051908	CG10387-PA				SM00484,SM00485,SM00279		PF00752,PF00867		PR00853,PR00853,PR00853,PR00853,PR00853	PS00841,PS00842	G3DSA:3.40.50.1010	SSF88723,SSF47807									
aly423.24	Tyrosine-protein phosphatase Lar	GO:0048675,GO:0051124,GO:0006470,GO:0035335,GO:0030424,GO:0045467,GO:0008045,GO:0007411,GO:0007412,GO:0005925,GO:0005875,GO:0001700,GO:0032093,GO:0016021,GO:0048841,GO:0031290,GO:0048477,GO:0008594,GO:0007283,GO:0008360,GO:0005886,GO:0007155,GO:0008201,GO:1903386,GO:0007399,GO:0004725,GO:0005001	CG10443-PF				SM00194,SM00194,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00408,SM00408,SM00408,SM00404,SM00404,SM00409,SM00409,SM00409		PF00102,PF00102,PF07679,PF07679,PF07679,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041	PS50853,PS50853,PS50835,PS50853,PS50056,PS50835,PS50853,PS50853,PS50056,PS50835,PS50835,PS50853,PS50853,PS50853,PS50853,PS50853,PS50055,PS50055	PR00700,PR00700,PR00700,PR00700,PR00700,PR00700,PR00700	PS00383,PS00383	G3DSA:3.90.190.10,G3DSA:3.90.190.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF52799,SSF49265,SSF48726,SSF49265,SSF48726,SSF49265,SSF49265,SSF49265,SSF52799	2165~2167								
aly423.25	Opsin-3	GO:0008020,GO:0004930,GO:0016028,GO:0009881,GO:0009588,GO:0016038,GO:0016021,GO:0007601,GO:0018298,GO:0007602,GO:0007605,GO:0009416,GO:0007186	CG5279-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00238,PR00238,PR00238,PR00577,PR00577,PR00577,PR005	PS00237,PS00238	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly423.26	Protein FAM195A		CG34159-PA						PF14799														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly423.27	THO complex subunit 1	GO:0016607,GO:0007165,GO:0000347,GO:0003677,GO:0005737,GO:0005654,GO:0045171,GO:0005634,GO:0048297,GO:0046784,GO:0016363,GO:0031297,GO:0008380,GO:0006406,GO:0006351,GO:0043234,GO:0005515,GO:0006915,GO:0032784,GO:0032786,GO:0000445,GO:0031990,GO:0000018,GO:0000346,GO:0003723,GO:2000002,GO:0006396,GO:0006397	CG2031-PA				SM00005		PF11957,PF00531	PS50017			G3DSA:1.10.533.10	SSF47986										
aly423.28	Large subunit GTPase 1 homolog	GO:0005737,GO:0051168,GO:0005783,GO:0030307,GO:0005829,GO:0003924,GO:0042254,GO:0046626,GO:0040008,GO:0008152,GO:0015030,GO:0000054,GO:0009267,GO:0040018,GO:0015031,GO:0006184,GO:0007275,GO:0005525	CG14788-PA						PF01926	PS51721	PR00326,PR00326		G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	269~289								
aly423.29	Trimethylguanosine synthase	GO:0005737,GO:0071164,GO:0005615,GO:0036261,GO:0008283,GO:0005634,GO:0006355,GO:0009452,GO:0005654,GO:0008173,GO:0015030,GO:0006351,GO:0001510,GO:0008168	CG44890-PB						PF09445				G3DSA:3.40.50.150	SSF53335									
aly423.3	Mitochondrial carrier homolog 2	GO:0070585,GO:0070062,GO:0016021,GO:0005739,GO:0005743,GO:0022857,GO:0005741,GO:0097284,GO:0005634,GO:1902108	CG6851-PB						PF00153,PF00153	PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly423.30	Small nuclear ribonucleoprotein F	GO:0005732,GO:0030532,GO:0071011,GO:0071013,GO:0000398,GO:0007052,GO:0003723,GO:0005685,GO:0005681	CG16792-PA			PIRSF006609	SM00651		PF01423				G3DSA:2.30.30.100	SSF50182									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly423.31	Phosducin-like protein	GO:0005575,GO:0003674,GO:0007602	CG7650-PA						PF02114		PR00677,PR00677,PR00677,PR00677,PR00677,PR00677		G3DSA:1.10.168.10,G3DSA:3.40.30.10	SSF52833	99~126								
aly423.32	SUMO-activating enzyme subunit 2	GO:0005737,GO:0051092,GO:0016925,GO:0019948,GO:0005634,GO:0031510,GO:0008641,GO:0019950,GO:0046872,GO:0004839,GO:0005515,GO:0006959,GO:0005524	CG7528-PA			PIRSF039133			PF10585,PF14732,PF00899	PS51257		PS00865	G3DSA:3.10.290.20,G3DSA:1.10.3240.10,G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF69572					UPA00886				
aly423.33	Unknown		n/a									PS60019											
aly423.34	Calmodulin	GO:0051383,GO:0042052,GO:0046716,GO:0031476,GO:0031475,GO:0005875,GO:0005737,GO:0016028,GO:0016062,GO:0016061,GO:0016060,GO:0005814,GO:0000922,GO:0005509,GO:0007099,GO:0032036,GO:0006468,GO:0007605,GO:0072499,GO:0030048,GO:0007052,GO:0005819,GO:2001020,GO:0031489,GO:0070855,GO:0016059,GO:0016056,GO:0030496,GO:0051533,GO:0005513,GO:0046331,GO:0005516,GO:0005515	CG8472-PA										G3DSA:1.10.238.10	SSF47473	205~238								
aly423.35	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly423.36	Unknown		n/a						PF01391														
aly423.4	U3 small nucleolar RNA-associated protein 6 homolog	GO:0034388,GO:0032040,GO:0005730,GO:0005622,GO:0000462,GO:0005515,GO:0022008,GO:0030515,GO:0006396	CG7246-PA				SM00386,SM00386,SM00386,SM00386,SM00386,SM00386		PF08640				G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452	2~22								
aly423.5	Tonsoku-like protein	GO:0005575,GO:0003674,GO:0008150	CG7457-PA				SM00248,SM00248,SM00248,SM00028,SM00028,SM00028,SM00028,SM00028		PF13181,PF13181,PF13181,PF13637	PS50088,PS50088,PS50297,PS50293,PS50293,PS50088			G3DSA:3.80.10.10,G3DSA:1.25.40.20,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48403,SSF52047,SSF48452,SSF48452									
aly423.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly423.7	Tyrosine-protein kinase Src64B	GO:0016319,GO:0007616,GO:0034332,GO:0030154,GO:0008335,GO:0030036,GO:0007611,GO:0008064,GO:0007301,GO:0045886,GO:0030717,GO:0007169,GO:0007411,GO:0008355,GO:0007254,GO:0007435,GO:0038083,GO:0045172,GO:0007349,GO:0030723,GO:0004715,GO:0004713,GO:0005886,GO:0016477,GO:0048477,GO:0005524,GO:0042127,GO:0006468,GO:0045087,GO:0030708,GO:0036058,GO:0018108,GO:0008302,GO:0090136,GO:0031234,GO:0030046,GO:0007424,GO:0007300,GO:0007293,GO:0005829,GO:0007391,GO:0005102,GO:0045860	CG7524-PK				SM00252,SM00326		PF00017,PF00018	PS50011,PS50002,PS50001	PR00401,PR00401,PR00401,PR00401,PR00401,PR00401,PR00452,PR00452,PR00452		G3DSA:3.30.200.20,G3DSA:2.30.30.40,G3DSA:3.30.505.10	SSF50044,SSF55550									
aly423.8	Adenosine 3'-phospho 5'-phosphosulfate transporter 2	GO:1902559,GO:0005783,GO:0000137,GO:0016021,GO:0000139,GO:0015012,GO:0046964,GO:0046963,GO:0005794,GO:0007275,GO:0055085	CG7853-PA						PF08449					SSF103481										
aly423.9	E3 ubiquitin-protein ligase MARCH6	GO:0000835,GO:1904264,GO:0004842,GO:0016021,GO:0016020,GO:0010498,GO:0036503,GO:0019899,GO:0030176,GO:0008270,GO:0070936,GO:0016874,GO:0031624	CG1317-PB				SM00744		PF12906	PS51292			G3DSA:3.30.40.10	SSF57850					UPA00143				
aly4237.1	Protein CLEC16A	GO:0016197,GO:0008333,GO:0016021,GO:0005770,GO:0005765,GO:0006914,GO:0010008	CG12753-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly42383.1	Vacuolar protein sorting associated protein 35	GO:0008565,GO:0016021,GO:0006897,GO:0016192,GO:1990126,GO:0097422,GO:0005829,GO:0005770,GO:0045056,GO:0006624,GO:0030904,GO:0005765,GO:1902823,GO:0042147,GO:0006886,GO:0015031,GO:0097481,GO:0005768,GO:0005769,GO:0070062	CG5625-PB						PF03635														
aly4244.1	Unknown		n/a																				
aly4244.2	Unknown		n/a																				
aly425.1	Unknown		n/a												88~108,52~72								
aly425.10	MKI67 FHA domain-interacting nucleolar phosphoprotein-like	GO:0005730,GO:0010923,GO:0000166,GO:0003723,GO:0003676,GO:0022008,GO:0003729	CG6937-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928	153~197								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly425.11	PCI domain-containing protein 2	GO:0005737,GO:0005844,GO:0005829,GO:0047499,GO:0005515	CG7351-PA				SM00753		PF01399														
aly425.12	Unknown		CG9813-PG																				
aly425.13	NAD-dependent protein deacylase sirtuin-5, mitochondrial	GO:2000378,GO:0005829,GO:0036048,GO:0005739,GO:0036055,GO:0034979,GO:0005743,GO:0010566,GO:0070403,GO:0036046,GO:0005759,GO:0005758,GO:0036054,GO:0005634,GO:0008270	CG3187-PC	MF_01121					PF02146	PS50305			G3DSA:3.30.1600.10,G3DSA:3.30.1600.10,G3DSA:3.40.50.1220,G3DSA:3.40.50.1220,G3DSA:3.40.50.1220	SSF52467										
aly425.14	Putative ATP-dependent RNA helicase DDX11-like protein 8	GO:0006139,GO:0016818,GO:0008026,GO:0005730,GO:0004003,GO:0032508,GO:0004386,GO:0003723,GO:0003676,GO:0003677,GO:0006289,GO:0005524	CG11403-PA				SM00491,SM00488	TIGR00604	PF13307,PF06733	PS51193			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	58~85,102~132,498~518								
aly425.15	Dynactin subunit 6	GO:0005813,GO:0045502,GO:0007018,GO:0005739,GO:0003824,GO:0007052,GO:0005869,GO:0008610,GO:0007005,GO:0000777	CG17347-PA										G3DSA:2.160.10.10	SSF51161									
aly425.16	Phosphatidylinositol 4-kinase beta	GO:0007111,GO:0007110,GO:0007112,GO:0090175,GO:0000916,GO:0004430,GO:0016310,GO:0030726,GO:0005741,GO:0030867,GO:0043147,GO:0007283,GO:0008340,GO:0046854,GO:0006661,GO:0048015,GO:0048137,GO:0005524	CG7004-PB				SM00146		PF00454,PF00454	PS51545,PS50290		PS00915	G3DSA:3.30.1010.10,G3DSA:3.30.1010.10,G3DSA:1.10.1070.11,G3DSA:1.25.40.70	SSF56112,SSF56112										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly425.17	ATP-dependent RNA helicase DDX54	GO:0016070,GO:0003714,GO:0030331,GO:0005730,GO:0006396,GO:0005634,GO:0016020,GO:0005102,GO:0004004,GO:0004386,GO:0006355,GO:1903507,GO:0003723,GO:0022008,GO:0010501,GO:0044822,GO:0005524,GO:0006351	CG32344-PA				SM00487,SM00490		PF00270,PF00271,PF08147	PS51192,PS51194,PS51195		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	730~748								
aly425.18	Unknown		n/a																				
aly425.19	Unknown		n/a																				
aly425.2	Unknown	GO:0005575,GO:0008150,GO:0003674	CG11791-PA																				
aly425.20	Peptidoglycan recognition protein	GO:0008745,GO:0045087,GO:0009253,GO:0042834,GO:0006952,GO:0005576,GO:0008270,GO:0005887,GO:0006955,GO:0005875	CG9681-PA				SM00701,SM00644		PF01510				G3DSA:3.40.80.10	SSF55846									
aly425.21	Peptidoglycan recognition protein	GO:0032500,GO:0005887,GO:0005515,GO:0008329,GO:0008745,GO:0045087,GO:0006955,GO:0006965,GO:0008063,GO:0006952,GO:0016045,GO:0050830,GO:0005576,GO:0008270,GO:0008592,GO:0009253,GO:0032494,GO:0016019,GO:0042834	CG11709-PA				SM00644,SM00701		PF01510				G3DSA:3.40.80.10	SSF55846									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly425.22	Peptidoglycan recognition protein 3	GO:0044117,GO:0032827,GO:0002221,GO:0008745,GO:0045087,GO:0009253,GO:0042834,GO:0006952,GO:0016045,GO:0050830,GO:0005576,GO:0008270,GO:0005887,GO:0006955,GO:0032689,GO:0016019,GO:0005875	CG9681-PA				SM00701,SM00701,SM00644		PF01510				G3DSA:3.40.80.10,G3DSA:3.40.80.10	SSF55846,SSF55846										
aly425.23	Peptidoglycan recognition protein	GO:0032500,GO:0005887,GO:0005515,GO:0008329,GO:0008745,GO:0045087,GO:0006955,GO:0006965,GO:0008063,GO:0006952,GO:0016045,GO:0050830,GO:0005576,GO:0008270,GO:0008592,GO:0009253,GO:0032494,GO:0016019,GO:0042834	CG11709-PA			PIRSF037945	SM00644,SM00701		PF01510				G3DSA:3.40.80.10	SSF55846										
aly425.24	E3 ubiquitin-protein ligase MARCH2	GO:0006897,GO:0005783,GO:0016567,GO:0031410,GO:0016021,GO:0005789,GO:0005765,GO:0004842,GO:0008270,GO:0030097,GO:0016874,GO:0010008	CG13442-PA				SM00744		PF12906	PS51292			G3DSA:3.30.40.10	SSF57850					UPA00143				
aly425.25	Tachykinin-like peptides receptor 86C	GO:0004930,GO:0006935,GO:0016021,GO:0007218,GO:0007217,GO:0004950,GO:0005887,GO:0008188,GO:0004995,GO:0002121,GO:0007186	CG6515-PB						PF00001	PS50262	PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly425.3	Unknown		n/a																				
aly425.4	Serine protease gd	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG1505-PD				SM00020		PF00089	PS50240		PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly425.5	Sterile alpha motif domain-containing protein 5	GO:0005070,GO:0007608	CG31163-PI				SM00454,SM00454,SM00326		PF07653,PF00536,PF00536	PS50105,PS50105			G3DSA:1.10.150.50,G3DSA:1.10.150.50,G3DSA:2.30.30.40	SSF47769,SSF47769,SSF50044	407~427								
aly425.6	Pyruvate kinase	GO:0030955,GO:0000287,GO:0016310,GO:0005829,GO:0005811,GO:0004743,GO:0006096,GO:0005524	CG7070-PA						PF02887				G3DSA:3.40.1380.20	SSF52935		00230+2.7.1.40,00010+2.7.1.40,00620+2.7.1.40	REACT_474	PWY-1042,PWY-2221,PWY-6901,PWY-7218,PWY-7383,PWY-6886,PWY-5723,PWY-6142,PWY-5484,PWY-7003	UPA00109				
aly425.7	Pyruvate kinase	GO:0004743,GO:0000287,GO:0006096,GO:0030955,GO:0005524	CG2964-PA						PF02887,PF00224		PR01050,PR01050,PR01050,PR01050		G3DSA:2.40.33.10,G3DSA:3.20.20.60,G3DSA:3.40.1380.20	SSF51621,SSF50800,SSF52935		00230+2.7.1.40,00010+2.7.1.40,00620+2.7.1.40	REACT_474	PWY-1042,PWY-2221,PWY-6901,PWY-7218,PWY-7383,PWY-6886,PWY-5723,PWY-6142,PWY-5484,PWY-7003	UPA00109				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly425.8	Pyruvate kinase	GO:0030955,GO:0000287,GO:0043186,GO:0016310,GO:0005829,GO:0005811,GO:0007525,GO:0007520,GO:0004743,GO:0006096,GO:0005524	CG7070-PA					TIGR01064	PF00224,PF02887		PR01050,PR01050,PR01050,PR01050,PR01050,PR01050,PR01050		G3DSA:2.40.33.10,G3DSA:3.20.20.60,G3DSA:3.20.20.60,G3DSA:3.40.1380.20	SSF50800,SSF52935,SSF51621,SSF51621		00230+2.7.1.40,00010+2.7.1.40,00620+2.7.1.40	REACT_474	PWY-1042,PWY-2221,PWY-6901,PWY-7218,PWY-7383,PWY-6886,PWY-5723,PWY-6142,PWY-5484,PWY-7003	UPA00109				
aly425.9	Protein AAR2 homolog		CG12320-PA						PF05282														
aly4250.1	Plasminogen receptor (KT)	GO:0005887,GO:0005739,GO:0006935,GO:0006954,GO:0010756	CG13404-PB						PF10166														
aly4250.10	E3 ubiquitin-protein ligase MARCH2	GO:0006897,GO:0005783,GO:0016567,GO:0031410,GO:0016021,GO:0005789,GO:0005765,GO:0004842,GO:0008270,GO:0016874,GO:0010008	CG2991-PB				SM00744		PF12906	PS51292			G3DSA:3.30.40.10,G3DSA:2.10.25.10	SSF57850					UPA00143				
aly4250.2	Flap endonuclease 1	GO:0005730,GO:0006284,GO:0008409,GO:0006281,GO:0004519,GO:0005634,GO:0017108,GO:0016788,GO:0005654,GO:0005739,GO:0043137,GO:0048256,GO:0003677,GO:0000287,GO:0022008	CG8648-PA	MF_00614			SM00485,SM00279,SM00484		PF00867,PF00752		PR00853,PR00853,PR00853,PR00853,PR00853	PS00841,PS00842	G3DSA:1.10.150.20,G3DSA:3.40.50.1010	SSF47807,SSF88723	94~124								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4250.3	Glucose-6-phosphate isomerase	GO:0005737,GO:0004347,GO:0005811,GO:0004616,GO:0006096,GO:0006094	CG8251-PC	MF_00473					PF00342	PS51463	PR00662,PR00662,PR00662	PS00765	G3DSA:3.40.50.10490,G3DSA:3.40.50.10490,G3DSA:3.40.50.10490	SSF53697		00030+5.3.1.9,00520+5.3.1.9,00500+5.3.1.9,00010+5.3.1.9		PWY-7238,PWY-5384,PWY-3801,PWY-622,PWY-7347,PWY-5054,PWY-6142,PWY-5659,PWY-6992,PWY-621,PWY-	UPA00109				
aly4250.4	Heparan-alpha glucosaminide N-acetyltransferase	GO:0051259,GO:0030203,GO:0016021,GO:0005765,GO:0016746,GO:0044281,GO:0007041,GO:0005975,GO:0015019,GO:0006027	CG6903-PA						PF16401														
aly4250.5	Dolichol-phosphate mannosyltransferase subunit 1	GO:0006486,GO:0005634,GO:0004169,GO:0005789,GO:0033185,GO:0006506,GO:0035268,GO:0035269,GO:0004582,GO:0019348	CG10166-PA						PF00535				G3DSA:3.90.550.10	SSF53448									
aly4250.6	NF-kappa-B inhibitor-interacting Ras like protein	GO:0016020,GO:0005622,GO:0005515,GO:0043124,GO:0006184,GO:0007264,GO:0005525	CG1669-PA				SM00175,SM00173		PF00071,PF00071	PS51419	PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540									
aly4250.7	Sodium-dependent neutral amino acid transporter SLC6A17	GO:0008021,GO:0005328,GO:0007420,GO:0005215,GO:0016021,GO:0006836,GO:0015816,GO:0015804,GO:0015820,GO:0015824,GO:0005887,GO:0005886,GO:0030672,GO:0032328,GO:0005326,GO:0030054	CG43066-PC						PF00209	PS50267	PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176	PS00610		SSF161070,SSF161070									
aly4250.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4250.9	Unknown		n/a												175~195								
aly4260.1	Scavenger receptor class B member 1	GO:0034375,GO:0006898,GO:0015914,GO:0001935,GO:0030301,GO:0048102,GO:0051000,GO:0070328,GO:0032497,GO:0010867,GO:0005737,GO:0070062,GO:0010886,GO:0016021,GO:0016020,GO:0043654,GO:0001530,GO:0010899,GO:0035461,GO:0006702,GO:0008035,GO:0006707,GO:0035071,GO:0015920,GO:0009986,GO:0006952,GO:0043534,GO:0005887,GO:0005886,GO:0007155,GO:0042632,GO:0043691,GO:0034185,GO:0034186,GO:0030169,GO:0031528,GO:0005901,GO:0005044,GO:0034383,GO:0034384,GO:0005764,GO:0005765,GO:0033344,GO:0070508,GO:0031663,GO:0001875,GO:0070506,GO:0044406	CG2727-PB						PF01130		PR01609,PR01609,PR01609												
aly4265.1	Phosphatidylethanolamine-binding protein homolog F40A3.3	GO:0005575,GO:0008150,GO:0003674,GO:0008289,GO:0005739	CG10298-PA						PF01161				G3DSA:3.90.280.10	SSF49777									
aly4265.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4265.3	Mediator of RNA polymerase II transcription subunit 21	GO:0005634,GO:0003713,GO:0001104,GO:0006355,GO:0006357,GO:0006351,GO:0006367,GO:0016592,GO:0016591	CG17397-PB						PF11221					SSF140718	84~122								
aly4265.4	Solute carrier family 35 member G1	GO:0051480,GO:0005829,GO:0016020,GO:0005789,GO:0005886,GO:1990034,GO:0016021	CG5281-PA						PF00892					SSF103481,SSF103481									
aly4265.5	Zinc finger protein 658	GO:0005737,GO:0005819,GO:0003700,GO:0005634,GO:0042254,GO:0071294,GO:0045892,GO:0008270,GO:0003676,GO:0000976,GO:0046872,GO:0005876,GO:0006351	CG8474-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12874,PF13912,PF13912,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57716									
aly4265.6	Unknown		n/a																				
aly4265.7	DnaJ homolog subfamily B member 13	GO:0009408,GO:0006457,GO:0051082	CG5001-PB				SM00271		PF00226,PF01556	PS50076	PR00625,PR00625,PR00625,PR00625	PS00636	G3DSA:1.10.287.110,G3DSA:2.60.260.20,G3DSA:2.60.260.20	SSF49493,SSF46565,SSF49493									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4266.1	Protein lev-9	GO:0005615,GO:0016020,GO:0005576,GO:0045202,GO:0030414,GO:0030054	CG10186-PG				SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032,SM00032		PF00084,PF00084,PF00084,PF00084,PF00084,PF00084,PF00084,PF00084,PF00084	PS50923,PS50835,PS50923,PS50923,PS50923,PS50923,PS50923,PS50923,PS50923,PS50923,PS50923,PS50923,PS50923,PS50923,PS50923,PS50923,PS50923,PS50923			G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.60.40.10	SSF57535,SSF57535,SSF57535,SSF57535,SSF57535,SSF48726,SSF57535,SSF57535,SSF57535,SSF57535,SSF57535,SSF57535,SSF57535,SSF57535,SSF57535								
aly4266.2	Unknown		n/a																				
aly42732.1	Unknown		n/a																				
aly4280.1	Protein Skeletor, isoforms B/C	GO:0005737,GO:0006997,GO:0005819,GO:0051321,GO:0004500,GO:0005874,GO:0005634,GO:0005730,GO:0006584,GO:0005700,GO:0005198,GO:0055114,GO:0005652,GO:0007067,GO:0016363,GO:0005694,GO:0051225,GO:0051301	CG43161-PE				SM00664		PF03351	PS50836					509~529								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4280.2	Ankyrin-1	GO:0045199,GO:0005200,GO:0072661,GO:0019899,GO:0007165,GO:0007411,GO:0030018,GO:0030507,GO:0005856,GO:0031430,GO:0006888,GO:0005634,GO:0006887,GO:0005198,GO:0042383,GO:0051117,GO:0016323,GO:0014731,GO:0045211,GO:0005886,GO:0022008,GO:0007010,GO:0030673,GO:0008093,GO:0005829,GO:0010638,GO:0016529	CG9766-PC				SM00248,SM00248,SM00248,SM00248		PF12796,PF12796	PS50088,PS50088,PS50088,PS50297	PR01415,PR01415		G3DSA:1.25.40.20	SSF48403									
aly4280.3	Unknown		n/a												56~76								
aly4280.4	Unknown		n/a																				
aly4280.5	Unknown		n/a																				
aly4280.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4282.1	Unknown		n/a												36~60								
aly4282.2	Unknown		n/a																				
aly4282.3	Copper-transporting ATPase 2	GO:0016020,GO:0048085,GO:0007595,GO:0051208,GO:0005886,GO:0048066,GO:0002164,GO:0005739,GO:0006825,GO:0005737,GO:0016021,GO:0005770,GO:0006882,GO:0000166,GO:0046688,GO:0015677,GO:0005375,GO:0005507,GO:0005524,GO:0004008,GO:0006878,GO:0034220,GO:0005887,GO:0055065,GO:0055085,GO:0005802,GO:0000139,GO:0015680	CG1886-PB						PF00702				G3DSA:3.40.50.1000	SSF56784,SSF56784									
aly43.1	Secernin-3	GO:0005575,GO:0008150,GO:0016805,GO:0003674	CG10098-PA												296~316								
aly43.10	Unknown		n/a												77~97								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly43.11	Male-specific lethal 1-like 1	GO:0072487,GO:0031936,GO:0007549,GO:0005515,GO:0005694,GO:0005634,GO:0000805,GO:0043984,GO:0046536,GO:0003677,GO:0003682,GO:0016456,GO:0016457,GO:0009047	CG10385-PA						PF15275														
aly43.12	Unknown		n/a												4~24								
aly43.2	ER degradation-enhancing alpha-mannosidase-like protein 3	GO:0044267,GO:0006986,GO:0006457,GO:0030968,GO:0043161,GO:0005788,GO:0016020,GO:0051082,GO:0005789,GO:0018279,GO:0004571,GO:0006516,GO:0005509,GO:0030433,GO:0004569,GO:0043687	CG5682-PA						PF02225,PF01532		PR00747,PR00747,PR00747,PR00747,PR00747,PR00747,PR00747,PR00747		G3DSA:3.50.30.30,G3DSA:1.50.10.50	SSF48225									
aly43.3	MOG interacting and ectopic P-granules protein 1	GO:0007506,GO:0048599,GO:0003682,GO:0070615,GO:0000122,GO:0040025,GO:0008134,GO:0005634,GO:0002119,GO:0008406,GO:0005700,GO:0048813,GO:0042802,GO:0003723,GO:0005515,GO:0017151,GO:0046872,GO:0042826,GO:0010468,GO:0040035,GO:0016581	CG1244-PC				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157		PS00028,PS00028,PS00028,PS00028,PS00028			474~494,438~470									
aly43.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly43.5	Sodium/potassium/calcium exchanger 5	GO:0048021,GO:0015293,GO:0050896,GO:0005802,GO:0055085,GO:0008273,GO:0016021	CG12061-PD					TIGR00367	PF01699,PF01699								REACT_15518						
aly43.6	Sodium/potassium/calcium exchanger 4	GO:0005737,GO:0097186,GO:0015293,GO:0050896,GO:0016021,GO:0016020,GO:0006811,GO:0008273,GO:0005886,GO:0005887,GO:0055085,GO:0007608	CG2893-PF					TIGR00367	PF01699,PF01699								REACT_15518						
aly43.7	Sodium-coupled monocarboxylate transporter 1	GO:0006810,GO:0008507,GO:0015293,GO:0005215,GO:0016021,GO:0016020,GO:0006814,GO:0055085	CG9657-PA					TIGR00813	PF00474	PS50283													
aly43.8	Voltage-gated potassium channel subunit beta-3	GO:0005737,GO:0051259,GO:0006813,GO:0050802,GO:0015459,GO:0008076,GO:0007629,GO:0005249,GO:0016021	CG43388-PM					TIGR01293	PF00248		PR01577,PR01577		G3DSA:3.20.20.100	SSF51430									
aly43.9	Unknown		n/a												25~52								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly430.1	Homeobox protein SIX2	GO:0001656,GO:0090189,GO:0001077,GO:0003677,GO:0001746,GO:0048701,GO:0001744,GO:0001745,GO:0005737,GO:0043565,GO:0097168,GO:0009948,GO:0007455,GO:0005634,GO:0001822,GO:0005654,GO:0032330,GO:0006366,GO:0002062,GO:0016477,GO:0048749,GO:0048704,GO:0048557,GO:0007623,GO:1902732,GO:0008283,GO:0006606,GO:0008134,GO:0031965,GO:0035271,GO:0072161,GO:0007283,GO:0009649,GO:0005886,GO:0030278,GO:0072006,GO:0008347,GO:0042474,GO:0007501,GO:0003700,GO:0072028,GO:0003705,GO:0003337,GO:0032403,GO:0006355,GO:0045944,GO:0005515,GO:0000978,GO:0072038,GO:0045596	CG11121-PA						PF05920,PF16878				G3DSA:1.10.10.60	SSF46689										
aly430.2	Regulator of chromosome condensation	GO:0005737,GO:0050767,GO:0007346,GO:0043547,GO:0005634,GO:0006607,GO:0005087,GO:0030261,GO:0000793,GO:0046822,GO:0007076,GO:0022008,GO:0003682,GO:0007067,GO:0051301,GO:0007417	CG10480-PA						PF00415	PS50012	PR00633,PR00633		G3DSA:2.130.10.30	SSF50985									
aly430.3	Regulator of chromosome condensation	GO:0042393,GO:0000082,GO:0005087,GO:0030261,GO:0031492,GO:0007067,GO:0051225,GO:0051301,GO:0007417,GO:0005737,GO:0050767,GO:0007346,GO:0043547,GO:0005634,GO:0005654,GO:0007088,GO:0031965,GO:0006607,GO:0000793,GO:0000790,GO:0000794,GO:0007076,GO:0007059,GO:0022008,GO:0007052,GO:0046822,GO:0016032,GO:0003682	CG10480-PA						PF00415	PS50012	PR00633,PR00633		G3DSA:2.130.10.30	SSF50985									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly430.4	Methylosome subunit pICln	GO:0005856,GO:0000387,GO:0006884,GO:0005829,GO:0005225,GO:0034715,GO:0006821,GO:0005886,GO:0005634,GO:0034709	CG4924-PA						PF03517						166~189								
aly430.5	Regulation of enolase protein 1	GO:0005737	n/a			PIRSF022704			PF07081				G3DSA:2.60.120.200	SSF49899									
aly430.6	Unknown	GO:0003677	CG8359-PA				SM00595		PF02944,PF10545	PS51029,PS51031													
aly430.7	rRNA 2'-O-methyltransferase fibrillarin	GO:0008649,GO:0032040,GO:0008033,GO:0005732,GO:0005730,GO:1990258,GO:0003723,GO:0051297,GO:0030532,GO:0031167,GO:0001651,GO:1990259,GO:0006364,GO:0009267,GO:0008168,GO:0015030,GO:0031428,GO:0000494,GO:0006396,GO:0003729	CG9888-PA						PF01269,PF01269		PR00052,PR00052,PR00052		G3DSA:3.40.50.150,G3DSA:3.40.50.150,G3DSA:3.30.200.20	SSF53335									
aly430.8	WD repeat-containing protein 43	GO:0044822,GO:0005730	CG30349-PA						PF04003	PS50082,PS50082,PS50294,PS50294			G3DSA:2.130.10.10	SSF50978									
aly430.9	Unknown		CG42671-PK												65~85								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4301.1	Nucleolar protein 58	GO:0005737,GO:0006608,GO:0032040,GO:0031428,GO:0005732,GO:0005730,GO:0000154,GO:0005634,GO:0016020,GO:0016049,GO:0003674,GO:0006364,GO:0015030,GO:0030515,GO:0044822,GO:0070761	CG10206-PA				SM00931		PF08156,PF01798	PS51358				SSF89124	493~513,163~183									
aly4301.2	Carbonyl reductase [NADPH] 3	GO:0005737,GO:0000253,GO:0005615,GO:0006635,GO:0008670,GO:0005829,GO:0050890,GO:0042376,GO:0005654,GO:0004090,GO:0008152,GO:0070402,GO:0016614	CG3699-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly4301.3	Carbonyl reductase [NADPH] 3	GO:0005737,GO:0000253,GO:0005615,GO:0050890,GO:0005829,GO:0005777,GO:0042376,GO:0005654,GO:0004090,GO:0008152,GO:0070402,GO:0016614	CG10672-PA						PF00106,PF00106		PR00081,PR00081,PR00081,PR00081,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									
aly4301.4	Carbonyl reductase [NADPH] 3	GO:0005737,GO:0000253,GO:0005615,GO:0042376,GO:0005829,GO:0050890,GO:0005654,GO:0004090,GO:0008152,GO:0070402,GO:0016491	CG31549-PA						PF00106,PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly4301.5	Neuroligin-1	GO:0050808,GO:0048065,GO:0030425,GO:0030424,GO:0051124,GO:0004872,GO:0002121,GO:0007274,GO:0007416,GO:0016021,GO:0042043,GO:0035176,GO:0009986,GO:0052689,GO:0007628,GO:0046929,GO:0060074,GO:0005887,GO:0005886,GO:0007155,GO:0045433,GO:0045202	CG13772-PA						PF00135			PS00941	G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474	567~567								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4301.6	Unknown		n/a																				
aly4305.1	DnaJ homolog subfamily C member 10	GO:0015035,GO:0005788,GO:0016671,GO:0030433,GO:0045454,GO:0034975	CG40178-PB				SM00271		PF00085,PF00226	PS51352,PS50076	PR00625,PR00625,PR00625,PR00625	PS00194	G3DSA:1.10.287.110,G3DSA:3.40.30.10	SSF52833,SSF46565									
aly4305.10	Protein SCO1 homolog, mitochondrial	GO:0004129,GO:0031987,GO:0046872,GO:0006878,GO:0060361,GO:0005739,GO:0008535,GO:0030016,GO:0005743,GO:0016531,GO:0017004,GO:0006825,GO:0007308,GO:0005507,GO:0048477,GO:0002168	CG8885-PA			PIRSF037736			PF02630	PS51352			G3DSA:3.40.30.10	SSF52833									
aly4305.11	Pro-resilin	GO:0040003,GO:0032992,GO:0005214,GO:0030023,GO:0008010,GO:0031012,GO:0005576,GO:0008061,GO:0042302	CG9036-PA						PF00379	PS51155		PS00233											
aly4305.12	Unknown	GO:0016021,GO:0000902	CG17111-PB				SM00473,SM00473		PF00024	PS50948,PS50948,PS50948				SSF57414									
aly4305.13	Leucine-rich repeat-containing protein 40	GO:0007265	CG9611-PF				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364		PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4305.14	Uncharacterized protein C3orf17 homolog	GO:0022008,GO:0016021	CG14174-PA						PF14780						364~384								
aly4305.15	Protein cappuccino	GO:0005737,GO:0007015,GO:0045010,GO:0030029,GO:0030659,GO:0008017,GO:0003779,GO:0007316,GO:0007315,GO:0007304,GO:0005938,GO:0015031,GO:0045451,GO:0048477,GO:0005829,GO:0005884	CG3399-PF				SM00498		PF02181	PS51444				SSF101447	470~504,1266~1287,1205~1225									
aly4305.16	Hemicentin-2	GO:0030038,GO:0035147,GO:0016337,GO:0005886,GO:0042059,GO:0002121,GO:0035330,GO:0035331,GO:0030054,GO:0002009,GO:0005938,GO:0016021,GO:0007476,GO:0050768,GO:0005576,GO:0005509,GO:0048644,GO:0016319,GO:0035157,GO:0046621,GO:0042060,GO:0090138,GO:0008360,GO:0007173,GO:0005912,GO:0032956,GO:0007156,GO:0005604,GO:0007423,GO:0050896,GO:0007391,GO:0046331,GO:0005515,GO:0005913,GO:0046843	CG12676-PA				SM00060,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409		PF07679,PF07679,PF13895,PF13895,PF13895,PF08205,PF00041	PS50835,PS50835,PS50853,PS50835,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726									
aly4305.17	Esterase B1	GO:0052689	CG6018-PA						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474										
aly4305.18	Splicing factor U2af 38 kDa subunit	GO:0000381,GO:0071011,GO:0005634,GO:0000398,GO:0000166,GO:0007052,GO:0008187,GO:0005686,GO:0046872,GO:0008380,GO:0005681,GO:0003729	CG3582-PA				SM00361,SM00356,SM00356,SM00360		PF13893,PF00642,PF00642	PS50103,PS50103,PS50102	PR01848,PR01848,PR01848,PR01848,PR01848,PR01848		G3DSA:3.30.70.330	SSF54928										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4305.19	Multidrug resistance-associated protein 1	GO:0042626,GO:0016021,GO:0031427,GO:0055085,GO:0008559,GO:0005886,GO:0043492,GO:0005524	CG6214-PA				SM00382		PF00664,PF00664,PF00005,PF00005	PS50929,PS50893,PS50893,PS50929		PS00211,PS00211	G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF90123,SSF90123,SSF52540										
aly4305.2	RNA polymerase II transcriptional coactivator	GO:0005634,GO:0003713,GO:0006355,GO:0006357,GO:0045892,GO:0006351,GO:0005667,GO:0003677,GO:0003697	CG8396-PA						PF02229				G3DSA:2.30.31.10	SSF54447									
aly4305.20	Unknown		n/a						PF07258														
aly4305.21	Unknown		n/a												460~480								
aly4305.22	Transcription factor AP-4	GO:0017022,GO:0001077,GO:0003677,GO:0070888,GO:0043565,GO:0005634,GO:0043065,GO:0042826,GO:2001269,GO:0071157,GO:0008285,GO:0017053,GO:0006461,GO:0045892,GO:0045893,GO:0043922,GO:0043923,GO:0006978,GO:0000978,GO:0044212,GO:0071549,GO:0003705,GO:0006357,GO:0045736,GO:0046983,GO:0042803,GO:0043392	CG7664-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459	98~118,181~201								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4305.23	Plasminogen activator inhibitor 1	GO:1990090,GO:0071248,GO:0071333,GO:0071260,GO:0008585,GO:0044344,GO:0042593,GO:0010629,GO:0035690,GO:0010628,GO:0042594,GO:0032869,GO:0048260,GO:0035009,GO:0048146,GO:0032496,GO:0071372,GO:0005615,GO:0071377,GO:0050820,GO:0051549,GO:0036120,GO:0009611,GO:0046697,GO:0071316,GO:0002020,GO:0071456,GO:0071318,GO:0071559,GO:0030336,GO:0070301,GO:0034097,GO:0071258,GO:0000302,GO:0034616,GO:0055093,GO:0042583,GO:0030162,GO:0042060,GO:0004867,GO:0010951,GO:0070849,GO:0031012,GO:0071404,GO:0090280,GO:0071549,GO:0071363,GO:0071409,GO:0071407,GO:0071321,GO:0071320,GO:0042246,GO:0035865,GO:0071560,GO:0005576,GO:0043627,GO:0045861,GO:0071347,GO:0045576	CG7219-PA				SM00093		PF00079			PS00284	G3DSA:2.30.39.10,G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574,SSF56574										
aly4305.24	Unknown	GO:0007283	CG14341-PB						PF06910														
aly4305.25	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	GO:0005737,GO:0030091,GO:0042742,GO:0006464,GO:0004719	CG2152-PA					TIGR00080	PF01135			PS01279	G3DSA:3.40.50.150	SSF53335									
aly4305.26	DNA repair endonuclease XPF	GO:0006296,GO:0006298,GO:0007143,GO:0006302,GO:0000724,GO:0005634,GO:0045132,GO:0004520,GO:0003697,GO:0006310,GO:0016321,GO:0006289,GO:0006974,GO:0000110,GO:0007131,GO:0043234,GO:0000014,GO:1901255,GO:0000712,GO:0000710,GO:0005515,GO:0007095,GO:0046982,GO:0003684	CG3697-PA				SM00891	TIGR00596	PF02732				G3DSA:3.40.50.10130	SSF47781,SSF52980			REACT_216						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4305.27	Hrp65 protein	GO:0005737,GO:0005856,GO:0006406,GO:0005634,GO:0000398,GO:0000166,GO:0003723,GO:0003676,GO:0008187,GO:0005681,GO:0003729	CG10328-PA				SM00360,SM00360		PF00076,PF00076,PF08075	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928	590~610,352~372,512~560								
aly4305.28	Lipase member H-B	GO:0006909,GO:0016020,GO:0052689,GO:0016042,GO:0005575,GO:0005576,GO:0016298	CG7367-PC						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly4305.29	Inactive pancreatic lipase-related protein 1	GO:0006909,GO:0006629,GO:0016042,GO:0005575,GO:0005576,GO:0005509,GO:0004806,GO:0016298	CG7367-PC						PF00151		PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly4305.3	Ethanolaminephosphotransferase 1	GO:0006646,GO:0006644,GO:0006909,GO:0008654,GO:0016021,GO:0016020,GO:0005789,GO:1903955,GO:0044281,GO:0004307,GO:0046474,GO:0046872,GO:0004142	CG7149-PA																				
aly4305.30	Protein turtle	GO:0045467,GO:0030537,GO:0008039,GO:0098632,GO:0007422,GO:0007638,GO:0007629,GO:0005575,GO:0098609,GO:0046331,GO:0003674,GO:0016199,GO:0005887,GO:0070593,GO:0007411,GO:0007414,GO:0008344,GO:0048814	CG15427-PH				SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408,SM00408,SM00060,SM00060		PF07679,PF07679,PF07679,PF07686,PF13895,PF00041,PF00041	PS50835,PS50853,PS50835,PS50853,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4305.31	Polyphosphoinositide phosphatase	GO:0048666,GO:0007626,GO:0006644,GO:0005783,GO:0007033,GO:0043473,GO:0055037,GO:0032288,GO:0031642,GO:0000139,GO:0042578,GO:0010976,GO:0036092,GO:0043813,GO:0006661,GO:0043812,GO:0004438,GO:0044281,GO:0031902,GO:0031901,GO:0010008	CG17840-PA						PF02383	PS50275													
aly4305.32	Synaptojanin-1	GO:0034595,GO:0016311,GO:0030117,GO:0004439,GO:0043647,GO:0048488,GO:0048489,GO:0000166,GO:0050803,GO:0046856,GO:0046855,GO:0004445,GO:0006661,GO:0044281,GO:0012506,GO:0006644,GO:0016082,GO:0046030,GO:0046488,GO:0007269,GO:0006836,GO:0043195,GO:0016191,GO:0005829,GO:0048790,GO:0006796,GO:0003723,GO:1901632,GO:1903390	CG6562-PB				SM00128		PF02383,PF03372,PF08952	PS50275			G3DSA:3.60.10.10,G3DSA:3.30.70.330	SSF56219	737~757	00562+3.1.3.36		PWY-6368					
aly4305.33	Cytochrome c oxidase subunit 7A1, mitochondrial	GO:0004129,GO:1902600,GO:0016021,GO:0005739,GO:0005746,GO:0006091,GO:0009055	CG34172-PA										G3DSA:4.10.91.10	SSF81419									
aly4305.34	Unknown		n/a																				
aly4305.35	WD repeat-containing and planar cell polarity effector protein fritz	GO:0005737,GO:0005856,GO:0005929,GO:0035320,GO:0005886,GO:0001736	CG17657-PA						PF11768,PF11768						527~527								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4305.36	Unknown	GO:0016021,GO:0000902	CG17111-PB							PS51034													
aly4305.4	Ethanolaminephosphotransferase 1	GO:0006646,GO:0006644,GO:0006909,GO:0016780,GO:0008654,GO:0016021,GO:0016020,GO:0005789,GO:1903955,GO:0044281,GO:0004307,GO:0046474,GO:0046872,GO:0004142	CG7149-PA						PF01066			PS00379											
aly4305.5	Alpha-aminoadipic semialdehyde synthase, mitochondrial	GO:0033512,GO:0005739,GO:0047130,GO:0034969,GO:0031060,GO:0055114,GO:0047131,GO:0004754	CG7144-PA				SM01002,SM01003		PF05222,PF16653,PF03435				G3DSA:3.30.360.10,G3DSA:3.30.360.10,G3DSA:1.10.1870.10,G3DSA:3.40.50.720,G3DSA:3.40.50.1770	SSF51735,SSF52283,SSF55347										
aly4305.6	Kelch-like protein 10	GO:0005737,GO:0048873,GO:0000902,GO:0006919,GO:0009566,GO:0008584,GO:0016567,GO:0007291,GO:0007286,GO:0048808,GO:0031463	CG12423-PA			PIRSF037037	SM00225,SM00612,SM00612,SM00612,SM00612,SM00612,SM00612,SM00875		PF07707,PF01344,PF01344,PF01344,PF01344,PF01344,PF00651	PS50097	PR00501,PR00501,PR00501		G3DSA:2.130.10.80,G3DSA:3.30.710.10	SSF54695,SSF117281										
aly4305.7	Mitochondrial basic amino acids transporter	GO:0015227,GO:0016021,GO:0022857,GO:0005743,GO:0005740,GO:0055085	CG4995-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920	PR00926,PR00926,PR00926		G3DSA:1.50.40.10	SSF103506										
aly4305.8	Zinc finger protein 180	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG3407-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4305.9	Unknown		n/a																				
aly4310.1	Tyrosine-protein kinase RYK	GO:0022038,GO:0031175,GO:0016201,GO:0008045,GO:0007411,GO:0005737,GO:0007435,GO:0016021,GO:0016020,GO:0048843,GO:0004716,GO:0004713,GO:0004672,GO:0005524,GO:0048705,GO:0006468,GO:0030182,GO:0043410,GO:0007409,GO:0005886,GO:0050919,GO:0016055,GO:0042813,GO:0005109,GO:0004888,GO:0017147,GO:0071679,GO:0005634	CG3915-PB				SM00469		PF02019,PF07714	PS50814,PS50011	PR00109,PR00109,PR00109,PR00109	PS00109	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly43107.1	Fasciclin-1	GO:0050839,GO:0016338,GO:0008038,GO:0007158,GO:0005886,GO:0007155,GO:0007411,GO:0007156,GO:0031225	CG6588-PD						PF02469	PS50213			G3DSA:2.30.180.10	SSF82153									
aly4325.1	Unknown		n/a																				
aly4325.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly43253.1	Unknown		n/a																				
aly43259.1	Unknown		n/a																				
aly4333.1	Unknown		n/a																				
aly4333.10	Mitochondrial-processing peptidase subunit beta	GO:0044267,GO:0004222,GO:0005743,GO:0006626,GO:0005811,GO:0008121,GO:0006122,GO:0005739,GO:0031122,GO:0005750,GO:0005759,GO:0017087,GO:0016485,GO:0006508,GO:0046872,GO:0005875	CG3731-PB						PF05193,PF00675			PS00143	G3DSA:3.30.830.10,G3DSA:3.30.830.10	SSF63411,SSF63411									
aly4333.11	Mitochondrial folate transporter/carrier	GO:0006767,GO:0006766,GO:0015884,GO:0016021,GO:0008517,GO:0022857,GO:0005743,GO:0005740,GO:0044281,GO:0006839,GO:0046655,GO:0055085	CG8026-PD						PF00153	PS50920			G3DSA:1.50.40.10	SSF103506									
aly4333.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4333.3	Transcription factor Ken	GO:0007486,GO:0007485,GO:0006909,GO:0007620,GO:0003700,GO:0030539,GO:0005634,GO:0046425,GO:0030540,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046426,GO:0046872,GO:0045496,GO:0045497,GO:0007320	CG5575-PA				SM00225,SM00355,SM00355,SM00355		PF00651	PS50157,PS50157,PS50097		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.710.10,G3DSA:3.30.160.60	SSF57667,SSF54695									
aly4333.4	Apolipoprotein D	GO:0022626,GO:0005783,GO:0006869,GO:0042246,GO:0048678,GO:0030425,GO:0000302,GO:0001525,GO:0051895,GO:0010642,GO:0005615,GO:0014012,GO:2000405,GO:0048471,GO:0043025,GO:0005319,GO:0007420,GO:0048662,GO:0006629,GO:2000098,GO:0009267,GO:0042308,GO:0008340,GO:0034599,GO:0060588,GO:0070062,GO:1900016,GO:0007568,GO:0015485,GO:0042493,GO:0071638,GO:0005576,GO:0006006	CG4604-PA						PF00061		PR01273,PR01273,PR01273	PS00213	G3DSA:2.40.128.20	SSF50814	256~276								
aly4333.5	Apolipoprotein D	GO:0022626,GO:0005783,GO:0006869,GO:0042246,GO:0048678,GO:0030425,GO:0000302,GO:0048662,GO:0001525,GO:0051895,GO:0010642,GO:0005615,GO:0014012,GO:0033500,GO:0060588,GO:2000405,GO:0048471,GO:0043025,GO:0005319,GO:0007420,GO:0070328,GO:0006629,GO:0032504,GO:2000098,GO:0008289,GO:0042308,GO:0008340,GO:0006979,GO:0070062,GO:1900016,GO:0031409,GO:0007568,GO:0015485,GO:0042493,GO:0071638,GO:0005576,GO:0006006	CG33126-PB			PIRSF036893			PF00061		PR01219,PR01219,PR01219,PR01219	PS00213	G3DSA:2.40.128.20	SSF50814									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4333.6	Major facilitator superfamily domain-containing protein 6-A	GO:0016021,GO:0055085	CG31663-PA						PF12832,PF01306				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly4333.7	Protein bunched, class 2/F/G isoform	GO:0016319,GO:0048749,GO:0009996,GO:0008101,GO:0030307,GO:0048102,GO:0007304,GO:0007297,GO:0035282,GO:0005737,GO:0006355,GO:0005634,GO:0001709,GO:0007476,GO:0030707,GO:0045746,GO:0043066,GO:0048477,GO:0042803,GO:0008284,GO:0035071,GO:0008340,GO:0001751,GO:0007422,GO:0003700,GO:0005829,GO:0042246,GO:0002052,GO:0006351,GO:0046843	CG42281-PG																				
aly4333.8	Protein bunched, class 1/class 3/D/E isoforms	GO:0016319,GO:0048749,GO:0009996,GO:0008101,GO:0030307,GO:0048102,GO:0007304,GO:0007297,GO:0035282,GO:0005737,GO:0006355,GO:0005634,GO:0001709,GO:0007476,GO:0030707,GO:0045746,GO:0043066,GO:0048477,GO:0042803,GO:0008284,GO:0035071,GO:0008340,GO:0001751,GO:0007422,GO:0003700,GO:0005829,GO:0042246,GO:0002052,GO:0006351,GO:0046843	CG42281-PG						PF01166			PS01289	G3DSA:1.20.5.490	SSF58026	149~183								
aly4333.9	Conserved oligomeric Golgi complex subunit 3	GO:0008565,GO:0006891,GO:0033227,GO:0006888,GO:0017119,GO:0005801,GO:0006886,GO:0016020,GO:0000139,GO:0007112,GO:0022008	CG3248-PA						PF04136						90~131								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4339.1	NADH dehydrogenase [ubiqui] 1 subunit C2	GO:0008137,GO:0016021,GO:0006120,GO:0005743,GO:0005747,GO:0003954	CG12400-PA			PIRSF017834			PF06374														
aly4339.2	Zinc finger protein 32	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG17328-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776,PF12874,PF12874,PF00096,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667,SSF57667,SSF57667										
aly4339.3	Ell-associated factor Eaf	GO:0006351,GO:0032783,GO:0042060,GO:0005654,GO:0045893,GO:0007275,GO:0043620	CG11166-PC						PF09816														
aly4339.4	Unknown		n/a																				
aly4339.5	Unknown		CG42231-PA						PF15311														
aly4339.6	39S ribosomal protein L4, mitochondrial	GO:0005840,GO:0044822,GO:0005739,GO:0003735,GO:0003723,GO:0005762,GO:0006412	CG5818-PA	MF_01328_B				TIGR03953	PF00573				G3DSA:3.40.1370.10	SSF52166									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4339.7	Aminoacylase-1	GO:0004046,GO:0005737,GO:0070062,GO:0006520,GO:0046872,GO:0008237	CG6726-PB			PIRSF036696		TIGR01880	PF07687,PF01546			PS00759,PS00758	G3DSA:3.30.70.360,G3DSA:3.40.630.10,G3DSA:3.40.630.10	SSF53187,SSF53187,SSF55031		00330+3.5.1.14							
aly4339.8	PIH1 domain-containing protein 1	GO:0006355,GO:0006351	n/a						PF08190,PF08190														
aly4339.9	DnaJ homolog subfamily C member 10	GO:0016020,GO:0005783,GO:0034663,GO:0070059,GO:0034975,GO:0005811,GO:0005788,GO:0001933,GO:0016671,GO:0003756,GO:0030433,GO:2000427,GO:0045454,GO:0015035,GO:0006662,GO:0001671	CG5809-PA						PF00085				G3DSA:3.40.30.10	SSF52833									
aly4341.1	Putative fatty acyl-CoA reductase CG8306	GO:0080019,GO:0006629,GO:0016021,GO:0005777,GO:0012505,GO:0050062,GO:0010025,GO:0035336	CG8306-PA						PF07993,PF03015				G3DSA:3.40.50.720	SSF51735,SSF51735			REACT_22258						
aly4341.2	MAP kinase-activated protein kinase 2	GO:0005737,GO:0006468,GO:0018105,GO:0004871,GO:0051019,GO:0004683,GO:0000165,GO:0009651,GO:0045793,GO:0009931,GO:0004674,GO:0008360,GO:0005516,GO:0007166,GO:0004672,GO:0007155,GO:0046328,GO:0046777,GO:0005524	CG3086-PB				SM00220		PF00069	PS50011		PS00108	G3DSA:1.10.510.10,G3DSA:4.10.1170.10	SSF56112									
aly4341.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4355.1	Unknown	GO:0006508,GO:0004190	n/a									PS00141											
aly4355.2	Unknown		n/a						PF05585														
aly437.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG1213-PA						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171,PR00171		G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473			REACT_15518						
aly437.10	Spermatogenesis-defective protein 39 homolog	GO:0016197,GO:0030897,GO:0005770,GO:0061008,GO:0016023,GO:0090385,GO:0055037,GO:0030154,GO:0090382,GO:0005737,GO:0006355,GO:0035542,GO:0007283,GO:0033263,GO:0006351,GO:0005515,GO:0006955,GO:0015031,GO:0005769	CG18112-PA						PF09787,PF09787														
aly437.11	Attractin	GO:0005737,GO:0043473,GO:0042552,GO:0070062,GO:0016021,GO:0016020,GO:0030246,GO:0008039,GO:0006979,GO:0005575,GO:0003674,GO:0004872,GO:0006954,GO:0005886,GO:0021549,GO:0040014,GO:0005615	CG5634-PB				SM00423,SM00423,SM00423,SM00423		PF01437														
aly437.12	Attractin-like protein 1	GO:0016021,GO:0016020,GO:0030246,GO:0008039,GO:0005575,GO:0003674,GO:0004872,GO:0007186	CG5634-PB				SM00042,SM00181,SM00181		PF00431,PF13854	PS01180			G3DSA:2.60.120.290,G3DSA:2.10.25.10,G3DSA:2.120.10.80	SSF49854,SSF117281,SSF57196									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly437.13	Mushroom body large-type Kenyon cell-specific protein 1	GO:0043565,GO:0006351,GO:0048102,GO:0035071,GO:0006919,GO:0003700,GO:0006914,GO:0071456,GO:0007613,GO:0005700,GO:0006911,GO:0006355,GO:0035327,GO:0008628,GO:0042803,GO:0003677,GO:0045944,GO:0005634,GO:0071390,GO:0045893	CG18389-PC						PF05225,PF05225	PS50960,PS50960				SSF46689,SSF46689	12~32									
aly437.2	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG1213-PA						PF00083	PS50850		PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly437.3	Unknown	GO:0005355,GO:0016021,GO:0055085	CG1213-PA											SSF103473									
aly437.4	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG1213-PA					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171,PR00171,PR00171	PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						
aly437.5	Unknown		n/a										G3DSA:3.30.40.10										
aly437.6	Probable 28S ribosomal protein S25, mitochondrial	GO:0003735,GO:0006412,GO:0005763	CG14413-PA				SM00916		PF05047				G3DSA:3.40.30.10	SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly437.7	Ornithine carbamoyltransferase, mitochondrial	GO:0000050,GO:0006520,GO:0006526,GO:0016743,GO:0005759,GO:0004585,GO:0016597	n/a										G3DSA:3.40.50.1370,G3DSA:3.40.50.1370	SSF53671									
aly437.8	Facilitated trehalose transporter Tret1	GO:0005355,GO:0004252,GO:0004175,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0006508,GO:0055085	CG6484-PA						PF00083	PS50850,PS50096			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473	176~203								
aly437.9	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0046427,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG10960-PB						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00216,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						
aly4371.1	Mitochondrial coenzyme A transporter SLC25A42	GO:0005347,GO:0045089,GO:0015228,GO:0015866,GO:0015867,GO:0016021,GO:0080121,GO:0005740,GO:0005739,GO:0080122,GO:0005743,GO:0022857,GO:0043262,GO:0008152,GO:0050829,GO:0035349,GO:0055085,GO:0015217	CG4241-PA						PF00153	PS50920	PR00926,PR00926		G3DSA:1.50.40.10	SSF103506									
aly4371.2	ETS translocation variant 4	GO:0043565,GO:0048863,GO:0033600,GO:0005730,GO:0003700,GO:0005634,GO:0030154,GO:0006366,GO:0045944,GO:0006355,GO:0001077,GO:0060444,GO:0003677,GO:0008045,GO:0000978,GO:0060762,GO:0000981	CG6892-PB						PF00178	PS50061		PS00345	G3DSA:1.10.10.10	SSF46785									
aly43719.1	Unknown		n/a							PS50948													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4374.1	Ejaculatory bulb-specific protein 3	GO:0007362,GO:0006468,GO:0007552,GO:0019992,GO:0009615,GO:0009617,GO:0045297,GO:0004674,GO:0005576,GO:0004672	CG9358-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly4374.10	Unknown		n/a												28~84								
aly4374.11	Unknown		n/a																				
aly4374.2	Ejaculatory bulb-specific protein 3	GO:0007362,GO:0006468,GO:0007552,GO:0019992,GO:0009615,GO:0009617,GO:0045297,GO:0004674,GO:0005576,GO:0004672	CG9358-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly4374.3	Ejaculatory bulb-specific protein 3	GO:0007362,GO:0006468,GO:0007552,GO:0019992,GO:0009615,GO:0009617,GO:0045297,GO:0004674,GO:0005576,GO:0004672	CG9358-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly4374.4	Ejaculatory bulb-specific protein 3	GO:0007362,GO:0006468,GO:0007552,GO:0019992,GO:0009615,GO:0009617,GO:0045297,GO:0004674,GO:0005576,GO:0004672	CG9358-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4374.5	Unknown		n/a																				
aly4374.6	Unknown		n/a																				
aly4374.7	Unknown		n/a																				
aly4374.8	Unknown		n/a																				
aly4374.9	Unknown		n/a																				
aly43788.1	Adenylyltransferase and sulfurtransferase MOCS3	GO:0006777,GO:0016779,GO:0046872,GO:0070733,GO:0016783,GO:0061605,GO:0005829,GO:0018117,GO:0042292,GO:0032447,GO:0008265,GO:0002143,GO:0034227,GO:0018192,GO:0004792,GO:0061604,GO:0005524,GO:0002098	CG13090-PC						PF00899				G3DSA:3.40.50.720	SSF69572									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly43789.1	Unknown		n/a																				
aly43789.2	Unknown		n/a																				
aly4389.1	Isoleucine--tRNA ligase, mitochondrial (Fragment)	GO:0005737,GO:0004822,GO:0006428,GO:0000166,GO:0002161,GO:0006418,GO:0005759,GO:0005524	CG5414-PB					TIGR00392	PF08264,PF00133		PR00984,PR00984,PR00984,PR00984	PS00178	G3DSA:1.10.730.10,G3DSA:3.90.740.10,G3DSA:3.40.50.620,G3DSA:3.40.50.620	SSF52374,SSF52374,SSF47323,SSF50677		00970+6.1.1.5	REACT_71						
aly4389.2	Protein LTV1 homolog	GO:0005575,GO:0008150,GO:0003674	CG7686-PA						PF04180,PF04180						200~227								
aly4389.3	Vacuolar protein sorting associated protein 35	GO:0008565,GO:0016021,GO:0006897,GO:0016192,GO:1990126,GO:0097422,GO:0005829,GO:0005770,GO:0045056,GO:0006624,GO:0030904,GO:0005765,GO:1902823,GO:0042147,GO:0006886,GO:0015031,GO:0097481,GO:0005768,GO:0005769,GO:0070062	CG5625-PB						PF03635,PF03635						737~757								
aly4389.4	Trafficking protein particle complex subunit 12	GO:0006508,GO:0004175,GO:0005793,GO:0005515,GO:0016192	CG11396-PA				SM00028,SM00028		PF14559	PS50293,PS50005,PS50005			G3DSA:1.25.40.10	SSF48452									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4389.5	Histone-arginine methyltransferase CARMER	GO:0005737,GO:0016274,GO:0042054,GO:0006338,GO:0006355,GO:0005634,GO:0035097,GO:0008469,GO:0034969,GO:0016571,GO:0035241,GO:0035242,GO:0019919,GO:0006351	CG5358-PA						PF05185,PF11531	PS51678			G3DSA:2.70.160.11,G3DSA:3.40.50.150	SSF53335									
aly4389.6	ATP-dependent RNA helicase DDX24	GO:0005730,GO:0044822,GO:0016020,GO:0004004,GO:0004386,GO:0005524,GO:0003729	CG9143-PA				SM00487		PF00270,PF00270	PS51195,PS51192			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									
aly4389.7	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly4389.8	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly439.1	Unknown	GO:0004252,GO:0006508	CG11842-PA						PF00089				G3DSA:2.40.10.10	SSF50494									
aly4392.1	SID1 transmembrane family member 1	GO:0016021,GO:0033227,GO:0051033	n/a						PF13965														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4392.2	SID1 transmembrane family member 1	GO:0016021,GO:0033227,GO:0051033	n/a						PF13965														
aly4395.1	Unknown		n/a						PF03564														
aly4395.2	Alpha-tocopherol transfer protein-like	GO:0016020,GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG2663-PA						PF00650	PS50191	PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087									
aly4395.3	Unknown	GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG2663-PA											SSF46938									
aly4395.4	Alpha-tocopherol transfer protein-like	GO:0016020,GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG2663-PA						PF00650	PS50191	PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087									
aly4395.5	Alpha-tocopherol transfer protein	GO:0032502,GO:0008431,GO:0005770,GO:0051180,GO:0046909,GO:0005215,GO:0005829,GO:0006810,GO:0090212,GO:0019842,GO:0005546,GO:0005622,GO:0043325,GO:0042360,GO:0060548,GO:0051452,GO:0009268,GO:0009636,GO:0001892,GO:0007584	CG2663-PA						PF00650	PS50191	PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4395.6	Unknown		n/a																				
aly43989.1	ATP-dependent DNA helicase PIF1	GO:0000723,GO:0006310,GO:0000002,GO:0006281,GO:0005634,GO:0003677,GO:0005739,GO:0043141,GO:0003678,GO:0005524	CG3238-PA						PF05970				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									
aly43989.2	PiggyBac transposable element-derived protein 3		n/a						PF13843														
aly44.1	Unknown		CG4269-PA																				
aly44.2	Hemicentin-1	GO:0005604,GO:0070062,GO:0050896,GO:0007601,GO:0008039,GO:0003674,GO:0005509,GO:0005886,GO:0007155,GO:0030054,GO:0005938	CG43079-PE				SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408		PF13927,PF13927,PF13895,PF07679,PF07679	PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726									
aly44.3	Synaptogenesis protein syg-2	GO:0007155,GO:0003674,GO:0008039,GO:0005515,GO:0005886	CG43079-PE				SM00409,SM00409,SM00409,SM00406		PF08205,PF07686	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly44.4	Unknown		n/a																				
aly44.5	Unknown		n/a																				
aly44.6	Unknown		n/a																				
aly440.1	Unknown		n/a																				
aly440.2	Unknown		n/a																				
aly4420.1	KiSS-1 receptor	GO:0004930,GO:0016021,GO:0008261,GO:0007218,GO:0031989,GO:0004946,GO:0005887,GO:0008188,GO:0005886,GO:0007186,GO:0009986	CG30106-PA						PF00001	PS50262	PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4420.2	Unknown		n/a																				
aly4420.3	Unknown		n/a																				
aly4428.1	Acidic fibroblast growth factor intracellular-binding protein	GO:0070062,GO:0005634,GO:0016020,GO:0017134,GO:0005622,GO:0005654,GO:0012505,GO:0070527	CG8660-PB						PF05427														
aly443.1	Calcium and integrin-binding family member 3	GO:0008597,GO:0055074,GO:0005509,GO:0007602	CG9236-PB				SM00054,SM00054,SM00054		PF13499	PS50222,PS50222,PS50222		PS00018	G3DSA:1.10.238.10	SSF47473										
aly443.10	Unknown		n/a																				
aly443.11	Unknown		CG7924-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly443.12	Unknown		n/a																				
aly443.13	Unknown		n/a																				
aly443.14	Unknown		n/a																				
aly443.15	Unknown		n/a																				
aly443.16	Unknown		CG11370-PA																				
aly443.17	Unknown		n/a								PR01228,PR01228,PR01228,PR01228,PR01228												

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly443.18	Unknown		n/a																				
aly443.19	Unknown		n/a																				
aly443.2	Ubiquitin-conjugating enzyme E2 N	GO:0007630,GO:0051124,GO:0035370,GO:0016881,GO:0010942,GO:0007412,GO:0000209,GO:0005737,GO:0006301,GO:0004842,GO:0005634,GO:1902916,GO:0006979,GO:0045977,GO:0070534,GO:0005524,GO:0007625,GO:0007629,GO:0008594,GO:0046330,GO:0031625,GO:0060074,GO:0007409,GO:0016874,GO:0048471,GO:0031624,GO:0072347,GO:0016567	CG18319-PA				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				
aly443.20	Unknown		n/a								PR01228,PR01228,PR01228,PR01228												
aly443.21	Solute carrier organic anion transporter family member 3A1	GO:0006857,GO:0006810,GO:0015198,GO:0008514,GO:0009986,GO:0016020,GO:0015347,GO:0015711,GO:0016324,GO:0005887,GO:0009925	CG7571-PA						PF03137,PF03137				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly443.22	Deoxynucleosi de kinase	GO:0005737,GO:0006230,GO:0016773,GO:0016310,GO:0019136,GO:0016301,GO:0046939,GO:0005739,GO:0009157,GO:0071897,GO:0006165,GO:0004797,GO:0005524	CG5452-PA			PIRSF000705			PF01712				G3DSA:3.40.50.300	SSF52540	199~219								
aly443.23	Protein disulfide-isomerase A6	GO:0042470,GO:0006457,GO:0016853,GO:0005811,GO:0005788,GO:0070527,GO:0003756,GO:0005886,GO:2000427,GO:0045454,GO:0015035,GO:0006662,GO:0030168,GO:0005783	CG5809-PA					TIGR01126	PF00085	PS51352	PR00421,PR00421,PR00421	PS00194	G3DSA:3.40.30.10	SSF52833									
aly443.24	Protein disulfide-isomerase A6	GO:0042470,GO:0005790,GO:0006457,GO:0005783,GO:0005793,GO:0005811,GO:0005788,GO:0070527,GO:0003756,GO:0005886,GO:2000427,GO:0045454,GO:0034976,GO:0015035,GO:0006662,GO:0030168,GO:0005509	CG5809-PA																				
aly443.25	Unknown		CG4455-PA																				
aly443.26	Dolichyl-diphosphoolig osaccharide--protein glycosyltransfe rase subunit 1	GO:0042470,GO:0005783,GO:0006486,GO:0016021,GO:0005789,GO:0004579,GO:0008250	CG33303-PA						PF04597							00513+2.4.99.18,00510+2.4.99.18			UPA00378				
aly443.27	Translation initiation factor eIF-2B subunit delta	GO:0005737,GO:0043547,GO:0051716,GO:0019509,GO:0001541,GO:0005851,GO:0006446,GO:0005085,GO:0046523,GO:0045947,GO:0014003,GO:0042552,GO:0022008,GO:0006413,GO:0005829,GO:0003743	CG10315-PA						PF01008				G3DSA:3.40.50.10470	SSF100950		00270+5.3.1.23		PWY-7174,PWY-4361	UPA00904				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly443.28	Translation initiation factor eIF-2B subunit delta	GO:0005737,GO:0043547,GO:0051716,GO:0019509,GO:0001541,GO:0005851,GO:0006446,GO:0005085,GO:0044237,GO:0046523,GO:0045947,GO:0014003,GO:0042552,GO:0022008,GO:0006413,GO:0005829,GO:0003743	CG10315-PA						PF01008					SSF100950	421~441	00270+5.3.1.23		PWY-7174,PWY-4361	UPA00904				
aly443.29	N-acetylgalactosamine kinase	GO:0005737,GO:0006012,GO:0033858,GO:0046835,GO:0004335,GO:0005524	CG5288-PD			PIRSF000530		TIGR00131	PF00288,PF10509,PF08544		PR00959,PR00959,PR00959,PR00959,PR00473,PR00473,PR00473,PR00473	PS00106,PS00627	G3DSA:3.30.230.10,G3DSA:3.30.70.890,G3DSA:3.30.70.890	SSF54211,SSF55060,SSF55060		00520+2.7.1.6,00052+2.7.1.6		PWY-6317,PWY-6527,PWY-3821	UPA00214				
aly443.3	Protein lin-10	GO:0008105,GO:0030425,GO:0003674,GO:0045202,GO:0007270,GO:0030054,GO:0005737,GO:0040026,GO:0001540,GO:0005615,GO:0097120,GO:0043005,GO:0043025,GO:0005794,GO:0050975,GO:1903361,GO:0032504,GO:0030140,GO:0006810,GO:0005886,GO:0032580,GO:0007399,GO:0000138,GO:0005515	CG32677-PA				SM00228,SM00228,SM00462		PF00595,PF00595,PF00640,PF00640	PS01179,PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.29.30,G3DSA:2.30.29.30	SSF50729,SSF50156,SSF50729,SSF50156									
aly443.30	Zinc finger protein 510	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868,SM00868		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57716									
aly443.31	Zinc finger protein 677	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG6654-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57716,SSF57667,SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly443.32	Probable peroxisomal acyl-coenzyme A oxidase 1	GO:0050660,GO:0006629,GO:0006635,GO:0005777,GO:0033540,GO:0006693,GO:0003995,GO:0019395,GO:0003997,GO:0006091,GO:0055114	CG5009-PA			PIRSF000168			PF01756,PF02770,PF14749				G3DSA:1.20.140.10,G3DSA:1.20.140.10,G3DSA:1.10.540.10,G3DSA:2.40.110.10	SSF56645,SSF47203,SSF47203		00071+1.3.3.6,00592+1.3.3.6		PWY-6920,PWY-7291,PWY-7340,PWY-7606,PWY-7338,PWY-6837,PWY-735,PWY-5136,PWY-7007,PWY-7337,PWY-						
aly443.33	60S ribosomal protein L19	GO:0005840,GO:0022625,GO:0005622,GO:0003735,GO:0000022,GO:0006412,GO:0051298	CG2746-PA	MF_01475					PF01280			PS00526	G3DSA:1.10.1650.10,G3DSA:1.10.1200.60	SSF48140	156~183								
aly443.34	Probable peroxisomal acyl-coenzyme A oxidase 1	GO:0050660,GO:0006629,GO:0006635,GO:0005777,GO:0033540,GO:0006693,GO:0003995,GO:0019395,GO:0003997,GO:0006091,GO:0055114	CG5009-PA			PIRSF000168			PF02770,PF14749,PF01756				G3DSA:1.20.140.10,G3DSA:1.20.140.10,G3DSA:2.40.110.10,G3DSA:1.10.540.10	SSF56645,SSF47203,SSF47203	19~39	00071+1.3.3.6,00592+1.3.3.6		PWY-6920,PWY-7291,PWY-7340,PWY-7606,PWY-7338,PWY-6837,PWY-735,PWY-5136,PWY-7007,PWY-7337,PWY-						
aly443.35	Probable peroxisomal acyl-coenzyme A oxidase 1	GO:0050660,GO:0006629,GO:0006635,GO:0005777,GO:0033540,GO:0006693,GO:0003995,GO:0019395,GO:0003997,GO:0006091	CG5009-PA			PIRSF000168			PF14749,PF01756				G3DSA:2.40.110.10,G3DSA:1.10.540.10,G3DSA:1.20.140.10,G3DSA:1.20.140.10	SSF47203,SSF56645,SSF47203		00071+1.3.3.6,00592+1.3.3.6		PWY-6920,PWY-7291,PWY-7340,PWY-7606,PWY-7338,PWY-6837,PWY-735,PWY-5136,PWY-7007,PWY-7337,PWY-7288						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly443.36	Probable peroxisomal acyl-coenzyme A oxidase 1	GO:0050660,GO:0006629,GO:0006635,GO:0005777,GO:0033540,GO:0006693,GO:0003995,GO:0019395,GO:0003997,GO:0006091	CG5009-PA						PF14749				G3DSA:1.10.540.10		32~52	00071+1.3.3.6,00592+1.3.3.6		PWY-6920,PWY-7291,PWY-7340,PWY-7606,PWY-7338,PWY-6837,PWY-735,PWY-5136,PWY-7007,PWY-7337,PWY-7288					
aly443.37	Probable peroxisomal acyl-coenzyme A oxidase 1	GO:0050660,GO:0006629,GO:0006635,GO:0005777,GO:0033540,GO:0006693,GO:0003995,GO:0019395,GO:0003997,GO:0006091	CG5009-PA			PIRSF000168			PF02770,PF14749,PF01756				G3DSA:2.40.110.10,G3DSA:1.20.140.10,G3DSA:1.10.540.10,G3DSA:1.20.140.10	SSF56645,SSF47203,SSF47203		00071+1.3.3.6,00592+1.3.3.6		PWY-6920,PWY-7291,PWY-7340,PWY-7606,PWY-7338,PWY-6837,PWY-735,PWY-5136,PWY-7007,PWY-7337,PWY-7288					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly443.38	Probable peroxisomal acyl-coenzyme A oxidase 1	GO:0050660,GO:0006629,GO:0006635,GO:0016627,GO:0005777,GO:0033540,GO:0006693,GO:0008152,GO:0003995,GO:0019395,GO:0003997,GO:0006091,GO:0055114	CG5009-PA			PIRSF000168			PF02770,PF01756,PF14749				G3DSA:1.10.540.10,G3DSA:1.20.140.10,G3DSA:2.40.110.10,G3DSA:1.20.140.10	SSF56645,SSF47203,SSF47203		00071+1.3.3.6,00592+1.3.3.6		PWY-6920,PWY-7291,PWY-7340,PWY-7606,PWY-7338,PWY-6837,PWY-735,PWY-5136,PWY-7007,PWY-7337,PWY-7288					
aly443.39	Probable peroxisomal acyl-coenzyme A oxidase 1	GO:0050660,GO:0006629,GO:0006635,GO:0005777,GO:0033540,GO:0006693,GO:0003995,GO:0019395,GO:0003997,GO:0006091,GO:0055114	CG5009-PA						PF02770,PF14749,PF01756				G3DSA:1.20.140.10,G3DSA:1.10.540.10,G3DSA:2.40.110.10,G3DSA:1.20.140.10	SSF47203,SSF56645,SSF47203	445~465	00071+1.3.3.6,00592+1.3.3.6		PWY-6920,PWY-7291,PWY-7340,PWY-7606,PWY-7338,PWY-6837,PWY-735,PWY-5136,PWY-7007,PWY-7337,PWY-7288					
aly443.4	Unknown		n/a						PF00078														
aly443.40	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly443.41	Syndecan	GO:0007427,GO:0005925,GO:0098595,GO:0021782,GO:0008092,GO:0009986,GO:0005886,GO:0004888,GO:0031594,GO:0045887,GO:0005576,GO:0045202,GO:0007517,GO:0008045,GO:0007411,GO:0050908,GO:0097009,GO:2000637,GO:0016021,GO:0044246	CG10497-PJ				SM00294		PF01034			PS00964											
aly443.42	Unknown		n/a																				
aly443.43	Solute carrier organic anion transporter family member 1B3	GO:0005887,GO:0008514,GO:0016021,GO:0031427,GO:0015347,GO:0015711,GO:0016323,GO:0015721,GO:0044281,GO:0005515,GO:0005886,GO:0008206,GO:0043252,GO:0055085	CG3380-PA						PF07648	PS51465			G3DSA:3.30.60.30	SSF100895									
aly443.44	Probable peroxisomal acyl-coenzyme A oxidase 1	GO:0050660,GO:0006629,GO:0006635,GO:0005777,GO:0033540,GO:0006693,GO:0003995,GO:0019395,GO:0003997,GO:0006091	CG5009-PA						PF01756				G3DSA:1.20.140.10	SSF47203		00071+1.3.3.6,00592+1.3.3.6		PWY-6920,PWY-7291,PWY-7340,PWY-7606,PWY-7338,PWY-6837,PWY-735,PWY-5136,PWY-7007,PWY-7337,PWY-						
aly443.5	Epidermal retinol dehydrogenase 2	GO:0043616,GO:0004745,GO:0016021,GO:0005811,GO:0005789,GO:0008152,GO:0050908,GO:0042574,GO:0042572,GO:0016491	CG2254-PA						PF00106		PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly443.6	Protein MEF2BNB homolog	GO:0005575,GO:0008150,GO:0003674	CG32590-PA						PF10167														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly443.7	ATP-binding cassette sub-family A member 2	GO:0043190,GO:0042626,GO:0008152,GO:0006869,GO:0016023,GO:0005215,GO:0016021,GO:0006810,GO:0005815,GO:0005764,GO:0005765,GO:0006357,GO:0048545,GO:0016887,GO:0042632,GO:0032383,GO:0005768,GO:0055085,GO:0005524,GO:0010008	CG1718-PB						PF00005	PS50893			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	323~343								
aly443.8	ATP-binding cassette sub-family A member 10	GO:0042626,GO:0043231,GO:0006869,GO:0016021,GO:0016887,GO:0055085,GO:0005524	CG42816-PB										G3DSA:3.40.50.300	SSF52540									
aly443.9	Unknown		n/a																				
aly444.1	Protein argonaute-2	GO:0003676,GO:0030423,GO:0030422,GO:0030154,GO:0019899,GO:0000340,GO:0031054,GO:0007294,GO:0007416,GO:0005737,GO:0007367,GO:0005850,GO:0006342,GO:0005634,GO:0030727,GO:0070551,GO:0030529,GO:0035068,GO:1900153,GO:0016246,GO:0006402,GO:0046872,GO:0070578,GO:0005845,GO:0048471,GO:0045947,GO:0060213,GO:0031047,GO:0035279,GO:0035278,GO:0036099,GO:0090502,GO:0005844,GO:0035198,GO:0035195,GO:0035196,GO:0035197,GO:0000932,GO:0006355,GO:0006351,GO:0005515,GO:0017148,GO:0016442,GO:0003743	CG6671-PC				SM00949,SM00950		PF02171,PF16486,PF08699,PF16488,PF02170,PF16487	PS50822,PS50821			G3DSA:3.30.420.10,G3DSA:3.40.50.2300,G3DSA:2.170.260.10	SSF53098,SSF101690	731~751		REACT_12472						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly444.10	Outer dense fiber protein 3-like protein 2	GO:0005643,GO:0007605,GO:0022008,GO:0005881	CG8086-PI						PF07004,PF07004,PF07004														
aly444.2	Eukaryotic translation initiation factor 3 subunit E	GO:0005852,GO:0043231,GO:0051726,GO:0016282,GO:0005829,GO:0048812,GO:0005515,GO:0033290,GO:0006909,GO:0001731,GO:0006413,GO:0006446,GO:0003743	CG9677-PA	MF_03004		PIRSF016255	SM00088		PF01399,PF09440				G3DSA:1.10.10.10	SSF46785										
aly444.3	39S ribosomal protein L53, mitochondrial	GO:0070126,GO:0006996,GO:0070124,GO:0070125,GO:0005840,GO:0003735,GO:0005743,GO:0005762,GO:0032543	CG30481-PA						PF10780														
aly444.4	Mitochondrial ribonuclease P protein 1 homolog	GO:0008033,GO:0005739,GO:0005575,GO:0008150,GO:0008168,GO:0003674	CG5190-PA						PF01746	PS51675					50~70			PWY-7286,PWY-7285,PWY-6829					
aly444.5	Death-inducer obliterator 1	GO:0005737,GO:0005819,GO:0000381,GO:0030532,GO:0003700,GO:0005634,GO:0097190,GO:0016817,GO:0006355,GO:0000790,GO:0006351,GO:0005515,GO:0044822,GO:0008270	CG6525-PB				SM00510,SM00249,SM00592		PF00628,PF07500,PF07744,PF07533	PS51321,PS50016		PS01359	G3DSA:3.30.40.10,G3DSA:1.10.472.30	SSF57903,SSF160481,SSF46942	1731~1758								
aly444.6	Peptidyl-prolyl cis-trans isomerase	GO:0005737,GO:0000413,GO:0008024,GO:0035071,GO:0016538,GO:0005829,GO:0042277,GO:0048102,GO:0003755,GO:0019908,GO:0006457,GO:0005875	CG9916-PA			PIRSF001467			PF00160	PS50072	PR00153,PR00153,PR00153,PR00153,PR00153	PS00170	G3DSA:2.40.100.10	SSF50891									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly444.7	Solute carrier organic anion transporter family member 5A1	GO:0008514,GO:0005215,GO:0016021,GO:0015711,GO:0005886	CG3811-PA						PF07648,PF03137,PF03137	PS51465			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:3.30.60.30	SSF103473,SSF103473,SSF103473,SSF100895	478~483,446~447								
aly444.8	Unknown		n/a																				
aly444.9	Xanthine dehydrogenase 1	GO:0042554,GO:0050660,GO:0016614,GO:0008762,GO:0009115,GO:0005829,GO:0051537,GO:0046110,GO:0000302,GO:0016903,GO:0009414,GO:0004855,GO:0004854,GO:0005506,GO:0009055,GO:0006145,GO:0043546,GO:0055114,GO:0016491	CG6045-PA				SM01092,SM01008		PF01315,PF03450,PF00941,PF01799,PF02738,PF02738,PF00111			PS00197	G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:1.10.150.120,G3DSA:3.90.1170.50,G3DSA:3.10.20.30,G3DSA:3.30.390.50,G3DSA:3.30.365.10,G3DSA:3.30.365.10	SSF56003,SSF54292,SSF54665,SSF55447,SSF47741,SSF56176									
aly44400.1	Lethal(3)malignant brain tumor-like protein 3	GO:0030225,GO:0010629,GO:0043249,GO:0005737,GO:0043565,GO:0007517,GO:0007347,GO:0000122,GO:0005634,GO:0030851,GO:0008285,GO:0007405,GO:0003700,GO:0031523,GO:0035190,GO:0005700,GO:0006355,GO:0048813,GO:0006351,GO:0005515,GO:0016568,GO:0043035	CG5954-PB				SM00561,SM00561,SM00561		PF02820,PF02820,PF02820	PS51079,PS51079,PS51079			G3DSA:2.30.30.160,G3DSA:2.30.30.160,G3DSA:2.30.30.160	SSF63748,SSF63748,SSF63748	833~853								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly44400.2	Pre-mRNA-processing factor 19	GO:0016020,GO:0000244,GO:0000245,GO:0048711,GO:0071006,GO:0000349,GO:0048026,GO:0061630,GO:0005875,GO:0005737,GO:0005654,GO:0005819,GO:0006303,GO:0072422,GO:0004842,GO:0005634,GO:0005811,GO:0000209,GO:0045665,GO:0010467,GO:0008380,GO:0042802,GO:0016607,GO:0034450,GO:0005515,GO:0071011,GO:0071013,GO:0034613,GO:0016874,GO:0008610,GO:0035861,GO:0001833,GO:0010498,GO:0000151,GO:0000398,GO:0070534,GO:0016567,GO:0000974,GO:0005681	CG5519-PA				SM00504,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF08606	PS50294,PS50082,PS50082,PS50082,PS50082,PS51698	PR00320,PR00320,PR00320	PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:3.30.40.10	SSF57850,SSF50978					UPA00143				
aly44400.3	E3 ubiquitin-protein ligase RNF185	GO:0006914,GO:0005789,GO:0016567,GO:0005741,GO:0008270,GO:0016874,GO:0016021	CG8974-PC				SM00184		PF13920	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850									
aly44400.4	Protein-L-isoaspartate O-methyltransferase domain-containing protein 1	GO:0005737,GO:0030091,GO:0042742,GO:0006464,GO:0004719	CG2152-PA						PF01135				G3DSA:3.40.50.150	SSF53335									
aly44400.5	Unknown		n/a												153~187								
aly44400.6	Unknown	GO:0016023,GO:0016328,GO:0031252,GO:0007508	CG30023-PA												96~116,64~84,157~181								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly44400.7	Unknown		n/a										G3DSA:3.10.10.10	SSF56672									
aly445.1	Unknown	GO:0005044,GO:0030247,GO:0006955	CG42339-PB																				
aly445.2	Somatomedin-B and thrombospondin type-1 domain-containing protein	GO:0005044,GO:0030247,GO:0005578,GO:0006955	CG42339-PB				SM00209		PF01033,PF00090	PS50958,PS50092		PS00524	G3DSA:2.20.100.10	SSF82895,SSF90188									
aly445.3	Unknown		n/a																				
aly4455.1	Unknown		n/a																				
aly4455.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4455.3	Unknown		n/a																				
aly4455.4	Unknown		n/a						PF00078	PS50878				SSF56672									
aly4456.1	Myosin heavy chain, muscle	GO:0031033,GO:0030241,GO:0060361,GO:0050821,GO:0030017,GO:0007298,GO:0007517,GO:0032982,GO:0000146,GO:0042623,GO:0031672,GO:0071689,GO:0005859,GO:0016459,GO:0003774,GO:0005524,GO:0042803,GO:0006936,GO:0030239,GO:0030898,GO:0008307,GO:0045214,GO:0008152,GO:0007527,GO:0040011,GO:0007427,GO:0005703,GO:0042692	CG17927-PR				SM00242,SM00015		PF02736,PF01576,PF00063	PS50096,PS51456	PR00193,PR00193,PR00193,PR00193,PR00193		G3DSA:1.20.5.340,G3DSA:4.10.270.10	SSF90257,SSF90257,SSF90257,SSF90257,SSF90257,SSF52540	1530~1607,1812~1930,1615~1810,1010~1163,1171~1227,1242~1318,849~1002,1460~1522,1333~1381,1390~1452									
aly4456.10	Unknown	GO:0005575,GO:0008150,GO:0003674	CG2206-PA						PF16061														
aly4456.11	Unknown	GO:0005575,GO:0008150,GO:0003674	CG2206-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4456.12	E3 ubiquitin-protein ligase UBR3	GO:0005737,GO:0001701,GO:0007608,GO:0016567,GO:0042048,GO:0016874,GO:0016021,GO:0061630,GO:0000151,GO:0009790,GO:0006511,GO:0008270,GO:0001967,GO:0004842,GO:0071596	CG42593-PB										G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57850	303~336								
aly4456.13	Forkhead box protein J3	GO:0030154,GO:0001158,GO:0009792,GO:0009653,GO:0043565,GO:0007346,GO:0001707,GO:0060914,GO:0000122,GO:0007380,GO:0005634,GO:0045665,GO:0003690,GO:0010468,GO:0000981,GO:0048665,GO:0035058,GO:0008134,GO:0002052,GO:0009888,GO:0008595,GO:0008301,GO:0007379,GO:0042305,GO:0007350,GO:0045787,GO:0007507,GO:0051090,GO:0009953,GO:0003700,GO:0003705,GO:0016199,GO:0006355,GO:0006357,GO:0045944,GO:0006351,GO:0005667	CG16738-PA				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053		G3DSA:1.10.10.10	SSF46785									
aly4456.14	Myosin-IA	GO:0005737,GO:0042623,GO:0007498,GO:0007368,GO:0003779,GO:0048803,GO:0016459,GO:0005938,GO:0008152,GO:0071907,GO:0003774,GO:0005524	CG7438-PA				SM00242,SM00015,SM00015		PF06017,PF00063	PS50096,PS51456	PR00193,PR00193,PR00193,PR00193,PR00193,PR00193		G3DSA:3.40.50.300	SSF52540									
aly4456.15	Cationic amino acid transporter 2	GO:1903352,GO:0042116,GO:0006865,GO:0015189,GO:0015181,GO:0006809,GO:0002537,GO:0097639,GO:0097638,GO:0016020,GO:0050727,GO:0005292,GO:1903401,GO:0015297,GO:0097640,GO:0005887,GO:0005886,GO:0015809,GO:0005289,GO:0097626,GO:0097627,GO:0003333,GO:0015326,GO:0000064,GO:0043030,GO:0015171	CG5535-PC			PIRSF006060			PF13520														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4456.16	High affinity cationic amino acid transporter 1	GO:1903401,GO:0015297,GO:0016020,GO:0016021,GO:0000064,GO:0097638,GO:0003333,GO:0006865,GO:1903352,GO:0015809,GO:0015326,GO:0015189,GO:0005887,GO:0015181,GO:0015171	CG5535-PC						PF13906														
aly4456.17	Gastric triacylglycerol lipase	GO:0004806,GO:0006629,GO:0007586,GO:0016788,GO:0016042,GO:0005576,GO:0005739,GO:0016298,GO:0006108,GO:0055114,GO:0016615	CG7329-PA			PIRSF000862			PF04083				G3DSA:3.40.50.1820	SSF53474									
aly4456.18	Lipase 1	GO:0004806,GO:0006629,GO:0007586,GO:0016788,GO:0016042,GO:0048812,GO:0005576	CG31871-PA			PIRSF000862			PF00561				G3DSA:3.40.50.1820	SSF53474									
aly4456.19	Lipase 3	GO:0006629,GO:0016788,GO:0016042	CG18301-PA			PIRSF000862			PF04083				G3DSA:3.40.50.1820	SSF53474									
aly4456.2	Multiple inositol polyphosphate phosphatase 1	GO:0034417,GO:0005788,GO:0004721,GO:0003993,GO:0052826	CG4123-PB			PIRSF000894			PF00328				G3DSA:3.40.50.1240	SSF53254									
aly4456.20	Lipase 3	GO:0004806,GO:0006629,GO:0016788,GO:0016042	CG6113-PC			PIRSF000862			PF00561				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4456.21	Lipase member K	GO:0005576,GO:0006629,GO:0016788,GO:0016042	CG18301-PA						PF04083				G3DSA:3.40.50.1820	SSF53474									
aly4456.22	Myosin heavy chain, muscle	GO:0031033,GO:0030241,GO:0060361,GO:0050821,GO:0030017,GO:0007298,GO:0007517,GO:0032982,GO:0000146,GO:0042623,GO:0031672,GO:0071689,GO:0005859,GO:0016459,GO:0003774,GO:0005524,GO:0042803,GO:0006936,GO:0030239,GO:0030898,GO:0008307,GO:0045214,GO:0008152,GO:0007527,GO:0040011,GO:0007427,GO:0005703,GO:0042692	CG17927-PR																				
aly4456.23	Myosin-7 (Fragment)	GO:0031033,GO:0030241,GO:0060361,GO:0050821,GO:0030017,GO:0007298,GO:0007517,GO:0032982,GO:0000146,GO:0042623,GO:0031672,GO:0005859,GO:0016459,GO:0003774,GO:0005524,GO:0042803,GO:0006936,GO:0030239,GO:0030898,GO:0008307,GO:0045214,GO:0007527,GO:0040011,GO:0030016,GO:0007427,GO:0005703,GO:0042692	CG17927-PR						PF00063,PF00063	PS51456	PR00193,PR00193			SSF52540,SSF52540										
aly4456.24	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4456.3	Unknown		n/a																				
aly4456.4	Multiple inositol polyphosphate phosphatase 1	GO:0070062,GO:0016311,GO:0052826,GO:0005788,GO:0004721,GO:0005886,GO:0034417,GO:0003993	CG4123-PB						PF00328				G3DSA:3.40.50.1240	SSF53254									
aly4456.5	Odorant receptor Or1	GO:0005549,GO:0007608,GO:0042048,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG9969-PA						PF02949,PF02949														
aly4456.6	Sodium-dependent serotonin transporter	GO:0051610,GO:0015222,GO:0015844,GO:0006837,GO:0008504,GO:0016021,GO:0005886,GO:0005261,GO:0030424,GO:0005887,GO:0006836,GO:0005328,GO:0098655,GO:0006909,GO:0043679	CG4545-PA						PF00209	PS50267	PR00176,PR00176,PR00176,PR00176			SSF161070									
aly4456.7	Unknown		n/a																				
aly4456.8	Probable ATP-dependent RNA helicase DDX56	GO:0005730,GO:0044822,GO:0016020,GO:0004004,GO:0006364,GO:0003676,GO:0022008,GO:0010501,GO:0005524	CG1666-PB				SM00487		PF00271,PF00270	PS51195,PS51192			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4456.9	E3 ubiquitin-protein ligase UBR3	GO:0005737,GO:0001701,GO:0007608,GO:0016567,GO:0042048,GO:0016874,GO:0016021,GO:0061630,GO:0000151,GO:0009790,GO:0006511,GO:0008270,GO:0001967,GO:0004842,GO:0071596	CG42593-PB				SM00396		PF02207	PS51157													
aly44667.1	Protein phosphatase 1 regulatory subunit 3B	GO:0048149,GO:0005977,GO:0019888,GO:0005981,GO:0000164,GO:0004721,GO:0005979,GO:0008157,GO:0005515,GO:0042587,GO:0008599,GO:0043231	CG9238-PB						PF03370	PS51159													
aly4467.1	Unknown		n/a												6~34								
aly4467.2	Unknown		n/a																				
aly4472.1	RNA-binding protein fusilli	GO:0005634,GO:0043484,GO:0000166,GO:0007173,GO:0003676,GO:0003729,GO:0008380,GO:0006397	CG8205-PE																				
aly4472.2	N-acetyltransferase eco	GO:0008080,GO:0016407,GO:0007052,GO:0000790,GO:0008152,GO:0007064,GO:0046872	CG8598-PA						PF13878						618~638								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4472.3	Guanine nucleotide-binding protein G(s) subunit alpha	GO:0007632,GO:0048148,GO:0005886,GO:0035220,GO:0007611,GO:0002165,GO:0004871,GO:0001664,GO:0010353,GO:0005834,GO:0007476,GO:0046872,GO:0007186,GO:0005525,GO:0031683,GO:0007608,GO:2000253,GO:0003924,GO:0007528,GO:0022416,GO:0007268,GO:0006184,GO:0031234,GO:0005604,GO:0050916,GO:0007191,GO:0007190	CG2835-PB				SM00275		PF00503		PR00443,PR00443,PR00443,PR00443,PR00443,PR00443,PR00318,PR00318,PR00318,PR00318,PR00318,PR00318		G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.400.10	SSF52540,SSF52540,SSF47895			REACT_14797						
aly4472.4	Origin recognition complex subunit 6	GO:0031105,GO:0032185,GO:0043547,GO:0000808,GO:0000087,GO:0006270,GO:0005096,GO:0032156,GO:0006260,GO:0006261,GO:0005886,GO:0006342,GO:0007067,GO:0042803,GO:0003677,GO:0005664	CG1584-PA												202~222								
aly4472.5	Sodium/hydrogen exchanger 8	GO:0055085,GO:0006885,GO:0016021,GO:0015299,GO:0006814,GO:0005886,GO:0015385,GO:0010352	CG12178-PB						PF00999				G3DSA:1.20.120.350										
aly4472.6	Sodium/hydrogen exchanger 10	GO:0055085,GO:0031514,GO:0016021,GO:0030154,GO:0015299,GO:0006814,GO:0034220,GO:0007283,GO:0005886,GO:0030317,GO:0007275	n/a						PF00027	PS50042			G3DSA:2.60.120.10	SSF51206									
aly4472.7	Death-associated protein 1	GO:0006919,GO:0006914,GO:0097190,GO:0032088,GO:0034198,GO:0010507	CG12384-PA						PF15228														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4472.8	Protein tyrosine phosphatase domain-containing protein 1	GO:0005654,GO:0004725,GO:0008138,GO:0060271,GO:0007224	n/a												17~44								
aly4472.9	Retinol dehydrogenase 13	GO:0042462,GO:0016614,GO:0010842,GO:0005743,GO:0008152,GO:0009644,GO:0016491	CG7675-PB						PF00106		PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly4479.1	Unknown		n/a																				
aly44821.1	Unknown	GO:0046872	n/a							PS50157		PS00028		SSF57667									
aly44898.1	Myocilin	GO:0005783,GO:0038031,GO:0005929,GO:0030335,GO:0060348,GO:0035024,GO:0008045,GO:0051897,GO:0001649,GO:0051894,GO:0005615,GO:0016023,GO:0031410,GO:0051497,GO:0005758,GO:0043408,GO:0031175,GO:0005794,GO:0016201,GO:0005791,GO:0014734,GO:0038133,GO:0014068,GO:0031012,GO:0070062,GO:0022011,GO:0045162,GO:0001953,GO:0005743,GO:0005741,GO:0051901,GO:0051496,GO:0033268,GO:0005578,GO:1900026	CG6867-PA						PF02191	PS51132													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4502.1	Unknown		n/a																				
aly45030.1	Unknown		n/a												184~225								
aly45036.1	Unknown	GO:0007424,GO:0035151,GO:0008045,GO:0035159	CG8561-PB						PF13855				G3DSA:3.80.10.10	SSF52058									
aly4505.1	5-hydroxytryptamine receptor	GO:0007208,GO:0004930,GO:0016021,GO:0007615,GO:0001586,GO:0007210,GO:0007198,GO:0045187,GO:0005887,GO:0005886,GO:0008227,GO:0004993	CG16720-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly4505.2	Unknown		n/a																				
aly4506.1	Protein trapped in endoderm-1	GO:0004930,GO:0043005,GO:0035234,GO:0016021,GO:0042923,GO:0007218,GO:0007281,GO:0007280,GO:0005938,GO:0005887,GO:0007186,GO:0007187,GO:0008354	CG3171-PC						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4506.10	Protocadherin Fat 1	GO:0016337,GO:0005911,GO:0030175,GO:0007155,GO:0007163,GO:0003015,GO:0005925,GO:0007219,GO:0070062,GO:0009653,GO:0005634,GO:0005509,GO:0048471,GO:0016477,GO:0005112,GO:0030027,GO:0009986,GO:0005887,GO:0005886,GO:0007267,GO:0007156,GO:0007015	CG31665-PB				SM00179,SM00042,SM00042,SM00042,SM00034,SM00181,SM00181,SM00181		PF00008,PF00431,PF00431,PF00059,PF00059	PS50041,PS50041,PS01180,PS50026,PS01180,PS50026,PS01180		PS00022,PS00022,PS01186,PS00022	G3DSA:2.10.25.10,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.10.25.10,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:3.10.100.10,G3DSA:3.10.100.10,G3DSA:2.10.25.10	SSF57196,SSF49854,SSF49854,SSF49854,SSF49854,SSF56436,SSF56436,SSF57196										
aly4506.11	Unknown		n/a																				
aly4506.2	ATP synthase subunit d, mitochondrial	GO:0005811,GO:0015992,GO:0051881,GO:0046034,GO:0000276,GO:0005739,GO:0015078,GO:0015986,GO:0006979,GO:0032007,GO:0008340,GO:0008553,GO:0070373,GO:0005875	CG6030-PB			PIRSF005514			PF05873					SSF161065	105~125								
aly4506.3	Probable ATP-dependent RNA helicase DDX5	GO:0008026,GO:0050681,GO:0003676,GO:2001014,GO:0005875,GO:0072332,GO:0000381,GO:0000122,GO:0003713,GO:0048511,GO:0045667,GO:0008380,GO:0005524,GO:0006351,GO:0030331,GO:0043517,GO:0060765,GO:0005730,GO:0003724,GO:0045944,GO:0003723,GO:0005681,GO:0006397	CG10077-PA				SM00487,SM00490		PF00270,PF00271	PS51192,PS51194,PS51195		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									
aly4506.4	Tektin-B1	GO:0005737,GO:0000226,GO:0005874	CG3085-PA						PF03148		PR00511,PR00511,PR00511,PR00511				225~252,279~306								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4506.5	Serine palmitoyltransferase 1	GO:0016021,GO:0017059,GO:0004758,GO:0009058,GO:0006686,GO:0035339,GO:0046511,GO:0046512,GO:0046513,GO:0030170	CG4016-PC						PF00155				G3DSA:3.40.640.10	SSF53383									
aly4506.6	Unknown		n/a																				
aly4506.7	Ubiquitin-conjugating enzyme E2 W	GO:0006281,GO:0004842,GO:0005634,GO:0006515,GO:0006513,GO:0071218,GO:0006508,GO:0016874,GO:0043161,GO:0005524	CG7220-PB				SM00212		PF00179	PS50127			G3DSA:3.10.110.10	SSF54495									
aly4506.8	Putative inositol monophosphatase 3	GO:0005737,GO:0008934,GO:0046872,GO:0008441,GO:0016311,GO:0016021,GO:0052833,GO:0006796,GO:0007165,GO:0052832,GO:0046854,GO:0006661,GO:0006021	CG15743-PA						PF00459				G3DSA:3.30.540.10,G3DSA:3.40.190.80	SSF56655									
aly4506.9	CAS1 domain-containing protein 1	GO:0016021,GO:0046331	CG2938-PB						PF07779,PF13839														
aly45061.1	Transposable element Tc3 transposase	GO:0015074,GO:0005634,GO:0004803,GO:0006313,GO:0003677	n/a						PF13358														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4509.1	ATP-dependent RNA helicase MAK5	GO:0005730,GO:0004004,GO:0004386,GO:0006364,GO:0003723,GO:0005524,GO:0003729	CG9143-PA				SM00490		PF00271	PS51194			G3DSA:3.40.50.300	SSF52540									
aly451.1	Gustatory and odorant receptor 24	GO:0007608,GO:0016021,GO:0004984,GO:0008527,GO:0050911,GO:0050912,GO:0007610,GO:0005886,GO:0010037,GO:0008340,GO:0050909,GO:0003031	CG14979-PB						PF08395														
aly451.10	Microtubule-associated proteins 1A/1B light chain 3C	GO:0006995,GO:0000421,GO:0000422,GO:0031410,GO:0005829,GO:0016236,GO:0005776,GO:0000045,GO:0061025,GO:0044804,GO:0012505,GO:0000407,GO:0019898,GO:0005874,GO:0008017,GO:0031090	CG12334-PA						PF02991,PF02991				G3DSA:3.10.20.90,G3DSA:3.10.20.90	SSF54236,SSF54236									
aly451.11	Mediator of RNA polymerase II transcription subunit 29	GO:0007548,GO:0018993,GO:0019101,GO:0008134,GO:0001104,GO:0006355,GO:0006357,GO:0006351,GO:0016592,GO:0007530	CG13201-PA						PF11568														
aly451.12	DNA repair protein RAD51 homolog 3	GO:0033063,GO:0009994,GO:0007294,GO:0003677,GO:0007066,GO:0007141,GO:0005737,GO:0000724,GO:0009949,GO:0005634,GO:0033065,GO:0030720,GO:0005739,GO:0005657,GO:0048471,GO:0048477,GO:0048476,GO:0005524,GO:0031023,GO:0006281,GO:0010971,GO:0007131,GO:0006310,GO:0008094,GO:0000400,GO:0009951,GO:0007283,GO:0030717,GO:0008298,GO:0006259,GO:0008821,GO:0046843	CG31069-PA						PF08423	PS50162			G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly451.13	Annexin B9	GO:0003779,GO:0012505,GO:0005543,GO:0048190,GO:0061467,GO:0032509,GO:0005544,GO:0010797,GO:0005509,GO:0005515,GO:0030011,GO:0030507,GO:0005938	CG5730-PD				SM00335,SM00335,SM00335,SM00335		PF00191,PF00191,PF00191,PF00191		PR00196,PR00196,PR00196,PR00196,PR00196,PR00196,PR00196,PR01808,PR01808,PR01808	PS00223,PS00223,PS00223	G3DSA:1.10.220.10,G3DSA:1.10.220.10,G3DSA:1.10.220.10,G3DSA:1.10.220.10	SSF47874									
aly451.14	ATP-binding cassette sub-family E member 1	GO:0005737,GO:0016071,GO:0005852,GO:0040007,GO:0051536,GO:0016020,GO:0005739,GO:0006412,GO:0016049,GO:0043524,GO:0016887,GO:0008428,GO:0006413,GO:0043024,GO:0005524	CG5651-PA				SM00382,SM00382		PF04068,PF00005,PF00005,PF00037	PS50893,PS51379,PS50893,PS51379	PR01868,PR01868,PR01868,PR01868,PR01868	PS00198,PS00211	G3DSA:3.30.70.20,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF54862,SSF52540									
aly451.15	Copper homeostasis protein cutC homolog	GO:0005737,GO:0034220,GO:0005634,GO:0005730,GO:0051262,GO:0005654,GO:0055070,GO:0006825,GO:0005507,GO:0055085	CG6136-PB						PF03932				G3DSA:3.20.20.380	SSF110395									
aly451.16	Unknown		n/a									PS00018	G3DSA:1.10.238.10	SSF47473									
aly451.17	Unknown		CG7330-PA																				
aly451.18	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly451.19	Atrial natriuretic peptide receptor 2	GO:0017046,GO:0060348,GO:0001503,GO:0008217,GO:0004872,GO:0007166,GO:0007168,GO:0035556,GO:1900194,GO:0016021,GO:0016849,GO:0004672,GO:0009190,GO:0005524,GO:0005525,GO:0006468,GO:0004383,GO:0044702,GO:0005886,GO:0042562,GO:0006182,GO:0051447,GO:0016941,GO:0005622,GO:0097011,GO:0004888,GO:0007165	CG31183-PA				SM00044		PF00211,PF07701	PS50125		PS00452	G3DSA:3.30.70.1230	SSF55073	102~122	00230+4.6.1.2							
aly451.2	Hsp90 co-chaperone Cdc37	GO:0005737,GO:0051087,GO:0051082,GO:0019901,GO:0007169,GO:0035556,GO:0022008,GO:0030296	CG12019-PA				SM01070,SM01069,SM01071		PF08565,PF08564,PF03234					SSF101391	140~160,37~67,263~287,78~108								
aly451.20	Semaphorin-5B	GO:0031987,GO:0001700,GO:0007399,GO:0042048,GO:0048854,GO:0016021,GO:0030154,GO:0001964,GO:0004872,GO:0005886,GO:0007411,GO:0048036	CG5661-PA				SM00630,SM00209,SM00209,SM00209,SM00209,SM00423		PF01403,PF01437,PF00090,PF00090,PF00090,PF00090	PS50092,PS50092,PS51004,PS50092,PS50092	PR01705,PR01705,PR01705		G3DSA:3.30.1680.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.130.10.10	SSF103575,SSF82895,SSF82895,SSF82895,SSF101912,SSF82895									
aly451.21	Proclotting enzyme	GO:0004252,GO:0042381,GO:0048812,GO:0006508,GO:0005576,GO:0008236	CG9372-PA				SM00680,SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly451.22	Acidic amino acid decarboxylase GADL1 (Fragment)	GO:0005737,GO:0004068,GO:0019752,GO:0008239,GO:0030170,GO:0006508,GO:0004782	CG5618-PA						PF00282				G3DSA:3.40.640.10,G3DSA:3.90.1150.10	SSF53383									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly451.23	Guanine deaminase	GO:0051067,GO:0008892,GO:0006726,GO:0008270,GO:0046098,GO:0004153,GO:0006147	CG18143-PA					TIGR02967	PF01979,PF13191,PF00211,PF00211	PS50125,PS50125			G3DSA:3.40.50.300,G3DSA:3.30.70.1230,G3DSA:3.30.70.1230,G3DSA:3.20.20.140	SSF52540,SSF51556,SSF55073,SSF55073	1699~1719,1628~1655,300~320	00230+3.5.4.3		PWY-6608,PWY-7442,PWY-5497,PWY-6606	UPA00603				
aly451.24	Rho GTPase-activating protein 20	GO:0051056,GO:0007480,GO:0005829,GO:0005096,GO:0005622,GO:0005575,GO:0007165,GO:0005100,GO:0007266,GO:0007264	CG32149-PD				SM00324		PF00620	PS51257			G3DSA:1.10.555.10,G3DSA:1.10.555.10	SSF48350			REACT_11044						
aly451.25	Probable ATP-dependent RNA helicase DDX43	GO:0004004,GO:0005622,GO:0003723,GO:0004386,GO:0010501,GO:0005524	CG7878-PA				SM00490,SM00322,SM00487		PF00270,PF00013,PF00271	PS50084,PS51195,PS51192,PS51194		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.30.1370.10	SSF54791,SSF52540									
aly451.26	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	GO:0006099,GO:0005739,GO:0003824,GO:0003878,GO:0048037,GO:0008152,GO:0004775,GO:0004776,GO:0005525,GO:0022008,GO:0045244	CG1065-PB			PIRSF001553	SM00881	TIGR01019	PF02629,PF00549		PR01798,PR01798,PR01798,PR01798	PS00399,PS01216	G3DSA:3.40.50.261,G3DSA:3.40.50.720	SSF52210,SSF51735		00640+6.2.1.5,00660+6.2.1.5,00020+6.2.1.5,00720+6.2.1.5		PWY-5913,PWY-7384,PWY-5392,PWY-6969,PWY-5537,PWY-6728,PWY-5538,PWY-5690	UPA00223				
aly451.27	Mannose-1-phosphate guanyltransferase beta	GO:0009298,GO:0004475,GO:0005575,GO:0009058,GO:0008150,GO:0005525	CG1129-PE						PF00483,PF00132				G3DSA:2.160.10.10,G3DSA:3.90.550.10	SSF53448			REACT_17015						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly451.28	Probable DNA mismatch repair protein Msh6	GO:0008094,GO:0000400,GO:0045910,GO:0008630,GO:0006301,GO:0006281,GO:0005215,GO:0016021,GO:0003684,GO:0009411,GO:0000710,GO:0000228,GO:0032138,GO:0032137,GO:0007131,GO:0043570,GO:0055085,GO:0005524,GO:0032301	CG7003-PA				SM00533,SM00534		PF01624,PF05190,PF05192,PF05188,PF00488,PF00083	PS50850		PS00216,PS00486	G3DSA:3.30.420.110,G3DSA:1.10.1420.10,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:3.40.50.300,G3DSA:3.40.1170.10	SSF55271,SSF48334,SSF53150,SSF52540,SSF103473	5~25,1192~1212								
aly451.29	Unknown		n/a																				
aly451.3	CCR4-NOT transcription complex subunit 2	GO:0030014,GO:0005737,GO:0000288,GO:0000289,GO:0001829,GO:0000122,GO:0005634,GO:0016020,GO:0010467,GO:2000036,GO:0006402,GO:0033147,GO:0001104,GO:0046331,GO:0031047,GO:0090503,GO:0001226,GO:0005829,GO:0010606,GO:0006355,GO:0006357,GO:0006351,GO:0005515,GO:0017148,GO:0006417,GO:0007095	CG2161-PA						PF04153								REACT_21257						
aly451.30	Palmitoyltransferase ZDHHC2	GO:0005794,GO:0018345,GO:0055038,GO:0008270,GO:0005887,GO:0005886,GO:0019706,GO:0016409,GO:0005783	CG1407-PG						PF01529	PS50216													
aly451.31	Dynein light chain Tctex-type 1	GO:0019060,GO:0007286,GO:0043657,GO:0008277,GO:2001019,GO:0030286,GO:0007067,GO:0005874,GO:0005875,GO:0051301,GO:0005819,GO:0042623,GO:0043087,GO:0006886,GO:0051493,GO:0045505,GO:0050768,GO:0003774,GO:0042803,GO:0005794,GO:0005868,GO:0008340,GO:0000132,GO:0007018,GO:0048812	CG12363-PA						PF03645														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly451.32	Protein capicua homolog	GO:0007362,GO:0043565,GO:0001700,GO:0003682,GO:0048190,GO:0030308,GO:0000122,GO:0003700,GO:0005634,GO:0003712,GO:0007474,GO:0006355,GO:0045892,GO:0006351,GO:0048286,GO:0003677,GO:0070491,GO:0048592,GO:0046843	CG43122-PG				SM00398		PF16090,PF00505	PS50118			G3DSA:1.10.30.10	SSF47095										
aly451.33	ATP synthase subunit s-like protein	GO:0005739	CG4042-PA										G3DSA:3.80.10.10	SSF52047									
aly451.34	Regucalcin	GO:0019853,GO:0005737,GO:0005829,GO:0009631,GO:0004341,GO:0090256,GO:0005509,GO:0044720,GO:0030234,GO:0008270	CG7390-PC						PF08450		PR01790,PR01790,PR01790,PR01790,PR01790,PR01791,PR01791,PR01791,PR01791,PR01791		G3DSA:2.120.10.30	SSF63829		00030+3.1.1.17,00053+3.1.1.17,00930+3.1.1.17		PWY-2221,PWY-5530,PWY-7165					
aly451.35	Proclotting enzyme	GO:0004252,GO:0042381,GO:0005576,GO:0048812,GO:0006508,GO:0008236	CG9372-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly451.4	V-type proton ATPase subunit E	GO:0033178,GO:0015992,GO:0015991,GO:0033181,GO:0000221,GO:0046961,GO:0005886	CG1088-PB	MF_00311					PF01991					SSF160527	16~36								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly451.5	Pseudouridine-5'-phosphatase	GO:0016787,GO:0070062,GO:1990738,GO:0042060,GO:0009117,GO:0008152,GO:0046872	CG15441-PA					TIGR01509	PF13419				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF56784									
aly451.6	Glutamate [NMDA] receptor subunit 1	GO:0042391,GO:0007616,GO:0055074,GO:0004972,GO:0030054,GO:0008355,GO:0072375,GO:0042331,GO:0016021,GO:0016020,GO:0007476,GO:0004970,GO:0050975,GO:0008328,GO:0035235,GO:0006811,GO:0005234,GO:0045211,GO:0008306,GO:0014069,GO:0007268,GO:0017146	CG2902-PA				SM00918,SM00079		PF00060,PF10562,PF10613,PF01094,PF01094		PR00177,PR00177,PR00177,PR00177,PR00177		G3DSA:3.40.50.2300,G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:1.10.287.70	SSF53822,SSF53850,SSF53850,SSF81324									
aly451.7	Mitochondrial glutamate carrier 1	GO:0089711,GO:0016021,GO:0015293,GO:0015813,GO:0005313,GO:0005740,GO:0005739,GO:0005314,GO:0005654,GO:0005743,GO:0022857,GO:0055085	CG18347-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920	PR00926,PR00926,PR00926,PR00926,PR00926		G3DSA:1.50.40.10	SSF103506	136~156								
aly451.8	SWI/SNF complex subunit SMARCC2	GO:0035060,GO:0008587,GO:0008586,GO:0021882,GO:0003677,GO:0090544,GO:2000134,GO:0000122,GO:0005634,GO:0043044,GO:0003713,GO:0007474,GO:0005654,GO:0016514,GO:0048477,GO:0000980,GO:0017053,GO:0007480,GO:0000790,GO:0045892,GO:0045893,GO:0022008,GO:0043234,GO:0006351,GO:0006338,GO:0006337,GO:0071565,GO:0071564,GO:0005515,GO:0000978,GO:0003682	CG18740-PA				SM00717		PF00249,PF04433,PF16496,PF16495	PS51293,PS50934			G3DSA:3.40.50.10190,G3DSA:3.40.50.10190,G3DSA:1.10.10.60,G3DSA:1.10.10.10	SSF46689,SSF46689,SSF52113,SSF52113	682~716								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly451.9	Biotin--protein ligase	GO:0019899,GO:0009374,GO:0000785,GO:0044281,GO:0005737,GO:0070781,GO:0005739,GO:0004080,GO:0016570,GO:0005652,GO:0016363,GO:0005524,GO:0018271,GO:0006767,GO:0006766,GO:0008283,GO:0018054,GO:0009305,GO:0071110,GO:0006768,GO:0006464,GO:0009408,GO:0005829,GO:0005700,GO:0004079,GO:0004078,GO:0004077	CG14670-PC						PF03099	PS51733			G3DSA:3.30.930.10	SSF55681		00785+2.3.1.181		PWY-6987,PWY-7381					
aly4523.1	Probable tRNA methyltransferase 9-like protein	GO:0008168,GO:0008033,GO:0008152	CG42261-PB						PF08241				G3DSA:3.40.50.150,G3DSA:3.40.50.150	SSF53335	761~781,1082~1102								
aly4523.2	DNA topoisomerase 3-beta-1	GO:0000793,GO:0005634,GO:0005654,GO:0006265,GO:0003917,GO:0003677,GO:0007059,GO:0044822	n/a																				
aly4523.3	DNA topoisomerase 3-beta-1	GO:0000793,GO:0005634,GO:0000737,GO:0004520,GO:0005654,GO:0006265,GO:0003917,GO:0003916,GO:0051965,GO:0003677,GO:0007059,GO:0005694,GO:0044822	CG3458-PA				SM00493,SM00436,SM00437		PF01131,PF01131,PF01751	PS50880	PR00417,PR00417,PR00417		G3DSA:1.10.460.10,G3DSA:1.10.460.10,G3DSA:3.40.50.140	SSF56712,SSF56712									
aly4523.4	NEDD4 family-interacting protein 1	GO:0050699,GO:0016021,GO:0005770,GO:0000151,GO:0035220,GO:0000139,GO:0008593	CG32177-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4523.5	Unknown		n/a																				
aly45289.1	Alpha-2-macroglobulin receptor-associated protein	GO:0032091,GO:0031982,GO:0016021,GO:0006457,GO:0005783,GO:0009986,GO:0006898,GO:0010916,GO:0051082,GO:0008201,GO:0048019,GO:0048237,GO:0005576,GO:0004873,GO:1900222,GO:0005886,GO:0070326,GO:0016192,GO:1900116,GO:0005875,GO:0050750	CG8507-PA						PF06400,PF06401				G3DSA:1.20.81.10,G3DSA:1.20.81.10	SSF47045,SSF47045									
aly4529.1	Cytoplasmic aconitate hydratase	GO:0005783,GO:0009791,GO:0006099,GO:0010040,GO:0005737,GO:0070062,GO:0005739,GO:0005506,GO:0046872,GO:0005794,GO:0006879,GO:0006447,GO:0030350,GO:0008152,GO:0051539,GO:0005829,GO:0050892,GO:0006101,GO:0003723,GO:0006417,GO:0003994,GO:0003729	CG6342-PA						PF00330		PR00415,PR00415,PR00415,PR00415		G3DSA:3.30.499.10	SSF53732		00290+4.2.1.33			UPA00048				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4533.1	5-hydroxytryptamine receptor 2A	GO:0045907,GO:0050965,GO:0050966,GO:0048148,GO:0014832,GO:0007613,GO:0030424,GO:0043267,GO:0005901,GO:0043025,GO:0001659,GO:0014059,GO:0008219,GO:0004930,GO:0007186,GO:0016023,GO:0007210,GO:0033674,GO:0051209,GO:0045600,GO:0071886,GO:0004993,GO:0008284,GO:0006874,GO:0014824,GO:0050795,GO:0044380,GO:0046883,GO:0030431,GO:0005887,GO:0005886,GO:0014065,GO:0070852,GO:0008144,GO:0008227,GO:0007208,GO:0051378,GO:0007568,GO:0043406,GO:0050731,GO:0043198,GO:0005829,GO:0007202,GO:0042493,GO:0051967,GO:0045821,GO:0010513,GO:0070374,GO:0016021	CG42796-PE						PF00001	PS50262	PR00237,PR00237,PR00237		G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly4533.2	Acetylcholinesterase	GO:0005737,GO:0004104,GO:0042135,GO:0042331,GO:0006581,GO:0016020,GO:0052689,GO:0003990,GO:0045202,GO:0007268,GO:0001507,GO:0042426,GO:0007271,GO:0005886,GO:0042803,GO:0046683,GO:0030054,GO:0046681	CG17907-PA						PF00135		PR00878,PR00878,PR00878,PR00878		G3DSA:3.40.50.1820	SSF53474									
aly4533.3	Acetylcholinesterase	GO:0042135,GO:0005811,GO:0052689,GO:0045202,GO:0003990,GO:0030054	CG2505-PA						PF00135			PS00122,PS00941	G3DSA:3.40.50.1820	SSF53474									
aly4533.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4533.5	Unknown		n/a																				
aly45390.1	Alpha-N-acetylgalactosaminidase	GO:0005737,GO:0008456,GO:0005975,GO:0016139,GO:0009311,GO:0005764,GO:0004557,GO:0046477	CG5731-PA						PF16499				G3DSA:3.20.20.70	SSF51445									
aly45450.1	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG1441-PA						PF07993				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly4547.1	Unknown		n/a																				
aly4547.2	Protein LSM12 homolog		CG15735-PA				SM00995		PF09793														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4547.3	Intersectin-1	GO:0005737,GO:0008021,GO:0008104,GO:0006897,GO:0007269,GO:0042734,GO:0030027,GO:0030054,GO:0006887,GO:0045179,GO:0045746,GO:0002052,GO:0051124,GO:0005509,GO:0005515,GO:0005886,GO:0043195,GO:0045860,GO:0048488,GO:0005905	CG1099-PD				SM00326,SM00326		PF14604,PF14604	PS50002,PS50002	PR00452,PR00452,PR00452,PR00452,PR00499,PR00499,PR00499		G3DSA:2.30.30.40,G3DSA:2.30.30.40	SSF50044,SSF50044	235~240								
aly45470.1	Unknown		n/a																				
aly455.1	Dopamine receptor 1	GO:0007612,GO:0007613,GO:0004952,GO:0035240,GO:0042594,GO:0090328,GO:0008542,GO:0060158,GO:0008355,GO:0001588,GO:0004930,GO:0007212,GO:0016021,GO:0040040,GO:0007186,GO:0001963,GO:0007606,GO:0071329,GO:0008306,GO:0005887,GO:0008227,GO:0009744,GO:0010579,GO:0043052,GO:0007191	CG9652-PE						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly4550.1	Unknown		n/a												434~454								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4550.2	Gamma-aminobutyric acid receptor subunit beta	GO:0005886,GO:0030425,GO:0030424,GO:0034707,GO:0009612,GO:0030285,GO:0090328,GO:0030054,GO:0008503,GO:0016021,GO:0007214,GO:0042749,GO:0004890,GO:0005254,GO:0005230,GO:0006811,GO:0001505,GO:0045211,GO:0050805,GO:0007268,GO:0006836,GO:0046682,GO:0042493,GO:0030431	CG10537-PG						PF02932,PF02931		PR01160,PR01160,PR01160,PR00252,PR00252,PR00252,PR00252,PR00253,PR00253,PR00253	PS00236	G3DSA:1.20.58.390,G3DSA:1.20.58.390,G3DSA:2.70.170.10,G3DSA:2.70.170.10	SSF63712,SSF90112										
aly4550.3	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	GO:0032922,GO:0035220,GO:0046972,GO:0035020,GO:0008047,GO:0051571,GO:0008375,GO:0005815,GO:0006486,GO:0043995,GO:0043996,GO:0032868,GO:0030854,GO:0070688,GO:0031397,GO:0080182,GO:0016757,GO:0016262,GO:0006915,GO:0046626,GO:0045475,GO:0005886,GO:0005547,GO:0048015,GO:0006110,GO:0090526,GO:0006493,GO:0000123,GO:0043982,GO:0005829,GO:0043981,GO:0097363,GO:0043984,GO:0061087,GO:0071300,GO:0045944,GO:0005515,GO:0045862	CG10392-PC				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF13414,PF13414,PF13424,PF13844	PS50005,PS50005,PS50005,PS50293,PS50005,PS50005,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452					UPA00378					
aly4550.4	Tryptophan 5-hydroxylase 1	GO:0004510,GO:0005737,GO:0004505,GO:0016714,GO:0045600,GO:0006568,GO:0045187,GO:0009072,GO:0042427,GO:0005506,GO:0016597,GO:0055114,GO:0046849	CG9122-PA						PF00351	PS51410	PR00372,PR00372,PR00372,PR00372,PR00372	PS00367	G3DSA:1.10.800.10	SSF56534									
aly4556.1	Unknown	GO:0000723,GO:0003678,GO:0006281	n/a						PF05970														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly456.1	TBC1 domain family member 4	GO:0005737,GO:0005178,GO:0070062,GO:0032313,GO:0009986,GO:0005096,GO:0005097,GO:0030659,GO:0032869,GO:0016192,GO:0033627	CG1093-PA						PF00566	PS50086				SSF47923	250~270,135~176								
aly4567.1	Unknown		n/a																				
aly4567.2	5-formyltetrahydrofolate cyclo-ligase	GO:0005737,GO:0009396,GO:0005829,GO:0005739,GO:0030272,GO:0046653,GO:0046872,GO:0005542,GO:0005524	CG34424-PB			PIRSF006806		TIGR02727	PF01812				G3DSA:3.40.50.10420	SSF100950									
aly4567.3	Unknown		CG30377-PA																				
aly4568.1	Protein white	GO:0006856,GO:0042626,GO:0031409,GO:0042332,GO:0042441,GO:0070731,GO:0043190,GO:0031410,GO:0016021,GO:0016887,GO:0048072,GO:0006727,GO:0006726,GO:0042401,GO:0004888,GO:0005395,GO:0005887,GO:0006810,GO:0008049,GO:0007613,GO:0005524	CG2759-PA						PF01061,PF00005				G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4568.2	Protein scarlet	GO:0006856,GO:0042626,GO:0006810,GO:0016887,GO:0043190,GO:0016021,GO:0016020,GO:0006727,GO:0006726,GO:0031409,GO:0005395,GO:0005887,GO:0005524	CG4314-PA						PF01061														
aly4568.3	Unknown	GO:0006856,GO:0042626,GO:0043190,GO:0006728,GO:0007605,GO:0006810,GO:0006727,GO:0006726,GO:0005395,GO:0005887,GO:0005524	CG17632-PA										G3DSA:3.40.50.300										
aly4568.4	Protein brown	GO:0006856,GO:0042626,GO:0043190,GO:0016887,GO:0006728,GO:0007605,GO:0016021,GO:0006810,GO:0006727,GO:0006726,GO:0031409,GO:0005395,GO:0005887,GO:0005524	CG17632-PA						PF00005				G3DSA:3.40.50.300	SSF52540									
aly4568.5	ATPase inhibitor mai-2, mitochondrial	GO:0032780,GO:0005739,GO:0042030,GO:0050830,GO:0004857,GO:0045980	CG13551-PA						PF13873,PF04568				G3DSA:1.20.5.500	SSF64602	270~290,368~395								
aly4568.6	Protein brown	GO:0006856,GO:0042626,GO:0043190,GO:0005887,GO:0016887,GO:0006728,GO:0007605,GO:0016021,GO:0016020,GO:0006727,GO:0006726,GO:0031409,GO:0005395,GO:0006810,GO:0005524	CG17632-PA						PF01061														
aly4573.1	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0046331,GO:0046693,GO:0008364,GO:0005576,GO:0006006,GO:0045455,GO:0055114,GO:0016491	CG9518-PA						PF00732,PF05199			PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4573.2	Unknown		n/a																				
aly4573.3	Glucose dehydrogenase [FAD, qui]	GO:0005575,GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG45065-PA			PIRSF000137			PF05199,PF00732			PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly4576.1	Ran GTPase-activating protein 1	GO:0044614,GO:0006611,GO:0048678,GO:0030425,GO:0007165,GO:0005737,GO:0072686,GO:0043547,GO:0045132,GO:0000922,GO:0048471,GO:0000777,GO:0005098,GO:0000278,GO:0031965,GO:0005096,GO:0006913,GO:0032853,GO:0022008,GO:0007264,GO:0071375,GO:0005643,GO:0005829,GO:0046826	CG9999-PA				SM00368,SM00368,SM00368		PF13516,PF13516				G3DSA:3.80.10.10	SSF52047									
aly458.1	Pantothenate kinase 3	GO:0000910,GO:0005737,GO:0007126,GO:0005819,GO:0070328,GO:0071480,GO:0015937,GO:0004594,GO:0007476,GO:0061024,GO:0007283,GO:0040011,GO:0005886,GO:0007059,GO:0007067,GO:0048477,GO:0006979,GO:0005524,GO:0045475	CG5725-PE					TIGR00555	PF03630					SSF53067,SSF53067,SSF53067		00770+2.7.1.33	REACT_11193	PWY-3961	UPA00241				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly458.2	Adrenodoxin, mitochondrial	GO:0042446,GO:0051537,GO:0006694,GO:0009055,GO:0005759,GO:0046872,GO:0055114,GO:0008203	CG1319-PB						PF00111	PS51085	PR00355,PR00355,PR00355	PS00814	G3DSA:3.10.20.30	SSF54292									
aly458.3	Tetratricopeptide repeat protein 1	GO:0005737,GO:0005778,GO:0006457,GO:0051082,GO:0005515	CG14894-PA				SM00028,SM00028,SM00028		PF00515,PF13414	PS50005,PS50005,PS50293,PS50005			G3DSA:1.25.40.10	SSF48452									
aly458.4	Charged multivesicular body protein 7	GO:0008565,GO:0006997,GO:0007034,GO:0000815,GO:0000920,GO:0007080,GO:0045324,GO:0015031	CG5498-PB						PF03357														
aly4592.1	Calmodulin	GO:0005509	CG11638-PA				SM00054,SM00054,SM00054,SM00054		PF13499,PF13499	PS50222,PS50222,PS50222,PS50222		PS00018,PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly4592.2	Serine/threonine-protein phosphatase Pgam5, mitochondrial	GO:0072347,GO:0035970,GO:0006470,GO:0016021,GO:0090141,GO:0005739,GO:0005741,GO:0010821,GO:0004721,GO:0005515,GO:0009408,GO:0043539	CG14816-PA				SM00855		PF00300,PF00300				G3DSA:3.40.50.1240	SSF53254									
aly4592.3	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463		G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4592.4	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG3466-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463		G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly4599.1	GS homeobox 1	GO:0007419,GO:0010629,GO:0001077,GO:0021984,GO:0007417,GO:0007389,GO:0000122,GO:0005634,GO:0043565,GO:0021854,GO:0048663,GO:0021527,GO:0008134,GO:0007400,GO:0009953,GO:0007420,GO:0007398,GO:0003700,GO:0006355,GO:0006357,GO:0045944,GO:0000978	CG11551-PB				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly4600.1	Unknown		n/a																				
aly4600.2	Unknown		n/a																				
aly4600.3	Membrane metallo-endopeptidase-like 1	GO:0005794,GO:0004175,GO:0004222,GO:0005615,GO:0016021,GO:0008270,GO:0006508,GO:0008237,GO:0005783	CG9761-PB						PF01431,PF05649		PR00786,PR00786,PR00786,PR00786		G3DSA:3.40.390.10,G3DSA:3.40.390.10	SSF55486									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4600.4	Neuralized-like protein 4	GO:0007317,GO:0008104,GO:0008103,GO:0005814,GO:0045451	CG6451-PA				SM00588,SM00588,SM00588,SM00588		PF07177,PF07177,PF07177,PF07177,PF07177,PF07177	PS51065,PS51065,PS51065,PS51065,PS51065,PS51065				SSF49899										
aly4600.5	Unknown		n/a																				
aly4600.6	Unknown		n/a																				
aly4600.7	Unknown		n/a																				
aly461.1	Upstream stimulatory factor 2	GO:0005654,GO:0000430,GO:0043565,GO:0003700,GO:0005634,GO:0006366,GO:0003705,GO:0019086,GO:0055088,GO:0007595,GO:0045944,GO:0006351,GO:0000432,GO:0043425,GO:0070888,GO:0046983,GO:0046982,GO:0042803	CG17592-PB				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459	187~228								
aly461.10	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly461.11	Unknown	GO:0005737,GO:0032958,GO:0005516,GO:0008440,GO:0048306	CG45017-PF																				
aly461.12	Unknown		n/a																				
aly461.13	Nuclear RNA export factor 1	GO:0005737,GO:0030534,GO:0016973,GO:0051168,GO:0047485,GO:0007616,GO:0005635,GO:0031965,GO:0000166,GO:0005654,GO:0003723,GO:0006378,GO:0006406	CG1664-PA				SM00804		PF09162,PF03943,PF02136	PS50177,PS51450,PS51281,PS51450			G3DSA:3.30.70.330,G3DSA:3.10.450.50,G3DSA:3.80.10.10,G3DSA:1.10.8.10	SSF54427,SSF46934,SSF52058,SSF54928										
aly461.14	Serine/threonine-protein kinase minibrain	GO:0007632,GO:1900244,GO:0007623,GO:0007420,GO:0007399,GO:2000253,GO:0030154,GO:0006468,GO:0007611,GO:0004674,GO:0045887,GO:0004712,GO:0005524,GO:0004672,GO:0043195,GO:0008355,GO:0005634,GO:0035332,GO:0045927	CG42273-PH																				
aly461.15	Serine/threonine-protein kinase minibrain	GO:0006468,GO:1900244,GO:0007623,GO:0007420,GO:0007399,GO:2000253,GO:0030154,GO:0007632,GO:0007611,GO:0004674,GO:0045887,GO:0004712,GO:0035332,GO:0004672,GO:0043195,GO:0008355,GO:0005634,GO:0005524,GO:0045927	CG42273-PH				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112										
aly461.16	Unknown	GO:0005575,GO:0005856,GO:0003674,GO:0008150	CG43867-PK																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly461.17	Unknown		n/a																				
aly461.2	Myoneurin	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872,GO:0008270	CG7372-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667,SSF57667										
aly461.3	Protein FAM177A1		CG8300-PA						PF14774						96~116								
aly461.4	Unknown		n/a										G3DSA:2.10.60.10	SSF57302									
aly461.5	B-cell lymphoma/leukemia 11A	GO:0003714,GO:0048671,GO:0048672,GO:0003676,GO:0001078,GO:0005737,GO:0000122,GO:0005634,GO:0030183,GO:0005654,GO:2000171,GO:0046872,GO:0032463,GO:0042803,GO:0030217,GO:0010977,GO:0010976,GO:0030517,GO:0016925,GO:0050773,GO:0045944,GO:0006351,GO:0000978,GO:0046982	CG9650-PG				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667	575~595										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly461.6	Unknown		n/a																				
aly461.7	Putative ATP-dependent RNA helicase DHX57	GO:0005737,GO:0008026,GO:0044822,GO:0004004,GO:0004386,GO:0005739,GO:0006396,GO:0003676,GO:0046872,GO:0005524	CG1582-PA				SM00487,SM00847,SM00356,SM00490		PF05773,PF00642,PF07717,PF04408,PF00270,PF00271	PS50103,PS51192,PS51194			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:4.10.1000.10	SSF52540,SSF52540,SSF90229	135~155								
aly461.8	Open rectifier potassium channel protein 1	GO:0005267,GO:0071805,GO:0006813,GO:0016021,GO:0005886,GO:0030322,GO:0002027,GO:0034705,GO:0045475,GO:0005887,GO:0022841,GO:0042803	CG1615-PC						PF07885,PF07885	PS01124	PR01333,PR01333		G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324,SSF81324	737~757,35~55								
aly461.9	Inositol-trisphosphate 3-kinase B	GO:0005737,GO:0045059,GO:0008440,GO:0048306,GO:0005829,GO:0046638,GO:0000165,GO:0046579,GO:0043647,GO:0005516,GO:0007166,GO:0032958,GO:0044281,GO:0005524,GO:0007165	CG45017-PF						PF03770					SSF56104,SSF56104									
aly4613.1	Neuroglobin	GO:0005506,GO:0019825,GO:0005344,GO:0020037,GO:0043204	n/a						PF00042	PS01033			G3DSA:1.10.490.10	SSF46458									
aly4613.2	Neuroglobin	GO:0005506,GO:0005344,GO:0020037,GO:0043204	n/a						PF00042	PS01033			G3DSA:1.10.490.10	SSF46458									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly46162.1	Unknown		n/a																				
aly462.1	Unknown		n/a																				
aly46231.1	Ethanolamine-phosphate cytidylyltransferase	GO:0006646,GO:0009058,GO:0042439,GO:0004306	CG5547-PB																				
aly46405.1	Glyoxylate reductase/hydroxypyruvate reductase	GO:0005737,GO:0043648,GO:0005782,GO:0070062,GO:0007588,GO:0016618,GO:0051287,GO:0005829,GO:0031406,GO:0008152,GO:0051259,GO:0034641,GO:0004617,GO:0044281,GO:0030267,GO:0070402,GO:0046487,GO:0008465,GO:0055114,GO:0042803	CG1236-PA						PF02826,PF00389				G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735,SSF52283									
aly46405.10	Unknown		CG45011-PA				SM00280		PF00050	PS51465		PS00282	G3DSA:3.30.60.30	SSF100895									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly46405.11	Nudix hydrolase 3	GO:0016787,GO:0016818,GO:0000287,GO:0030145,GO:0009132	CG11095-PA						PF00293	PS51462		PS00893	G3DSA:3.90.79.10	SSF55811									
aly46405.12	Nucleoside diphosphate-linked moiety X motif 8, mitochondrial	GO:0016787,GO:0046872,GO:0005739	CG11095-PA						PF00293	PS51462		PS00893	G3DSA:3.90.79.10	SSF55811									
aly46405.13	Chloride intracellular channel exc-4	GO:0035150,GO:0005764,GO:0034707,GO:0048060,GO:0005254,GO:0008289,GO:0043296,GO:0016324,GO:0006821,GO:0005509,GO:0005887,GO:0008340,GO:0005244,GO:0097305,GO:0006979,GO:0002064	CG10997-PA										G3DSA:3.40.30.10,G3DSA:1.20.1050.10	SSF52833,SSF47616									
aly46405.14	Pre-mRNA-splicing factor Syf2	GO:0071011,GO:0071013,GO:0022008,GO:0000398	CG12343-PA						PF08231														
aly46405.15	TGF-beta-activated kinase 1 and MAP3K7-binding protein 2	GO:0007507,GO:0061057,GO:0045433,GO:0003700,GO:0043123,GO:0005634,GO:0009617,GO:0006964,GO:0005654,GO:0006355,GO:0048813,GO:0046331,GO:0045860,GO:0008270,GO:0070530,GO:0002230,GO:0005829,GO:0033160	CG7417-PA				SM00547			PS50199		PS01358		SSF90209	255~282,502~529,461~488									
aly46405.16	Ragulator complex protein LAMTOR3 homolog	GO:0005070,GO:0071230,GO:0016310,GO:0034613,GO:0071986,GO:0032008,GO:0032006,GO:0043547	CG5110-PA						PF08923				G3DSA:3.30.450.30	SSF103196									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly46405.17	Glyoxylate reductase/hydroxypyruvate reductase	GO:0005737,GO:0043648,GO:0005782,GO:0007588,GO:0016616,GO:0016618,GO:0051287,GO:0005829,GO:0031406,GO:0008152,GO:0042803,GO:0034641,GO:0005576,GO:0051259,GO:0030267,GO:0070402,GO:0046487,GO:0044281,GO:0008465,GO:0055114,GO:0070062	CG9331-PC						PF00389,PF02826			PS00671	G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF52283,SSF51735									
aly46405.18	Glyoxylate reductase/hydroxypyruvate reductase	GO:0005737,GO:0043648,GO:0005782,GO:0070062,GO:0007588,GO:0016618,GO:0051287,GO:0005829,GO:0031406,GO:0008152,GO:0051259,GO:0034641,GO:0044281,GO:0030267,GO:0070402,GO:0046487,GO:0008465,GO:0055114,GO:0042803	CG31674-PA						PF02826,PF00389			PS00671	G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF52283,SSF51735									
aly46405.2	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1	GO:0008094,GO:0036292,GO:0005634,GO:0005705,GO:0004386,GO:1990163,GO:0006357,GO:0005524,GO:0003677,GO:0006259,GO:0000733,GO:0032508,GO:0016568,GO:0036310	CG3753-PA				SM00487,SM00490		PF07443,PF00271,PF00176	PS51194,PS51192,PS51467			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540									
aly46405.3	Congested-like trachea protein	GO:0015879,GO:0005215,GO:0016021,GO:0035002,GO:0005743,GO:0005740,GO:0003382,GO:0006839,GO:0006844,GO:0005476,GO:0006909	CG3057-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly46405.4	G patch domain and ankyrin repeat-containing protein 1 homolog	GO:0005575,GO:0008150,GO:0003674,GO:0003676	CG8152-PA				SM00248,SM00248,SM00443		PF13857,PF01585	PS50174,PS50088,PS50297			G3DSA:1.25.40.20	SSF48403									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly46405.5	Sarcoplasmic calcium-binding protein 1	GO:0016529,GO:0005509	CG15848-PA				SM00054,SM00054		PF13499	PS50222,PS50222,PS50222		PS00018,PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									
aly46405.6	Niemann-Pick C1 protein	GO:0046718,GO:0005635,GO:0005783,GO:0071383,GO:0007591,GO:0030301,GO:0007291,GO:0007041,GO:0070062,GO:0006486,GO:0032374,GO:0016021,GO:0016020,GO:0031579,GO:0005576,GO:0046686,GO:0048471,GO:0031902,GO:0005794,GO:0016125,GO:0060548,GO:0006914,GO:0031982,GO:0007628,GO:0005887,GO:0005886,GO:0045456,GO:0042632,GO:0008206,GO:0008158,GO:0008203,GO:0006897,GO:0015485,GO:0090150,GO:0071404,GO:0045121,GO:0042493,GO:0016242,GO:0005764,GO:0005765,GO:0033344,GO:2000189,GO:0005768	CG5722-PA					TIGR00917	PF16414,PF02460	PS50156			G3DSA:1.20.1640.10,G3DSA:1.20.1640.10	SSF82866,SSF82866									
aly46405.7	Unknown		n/a																				
aly46405.8	Thioredoxin domain-containing protein 15	GO:0045454,GO:0016021,GO:0005623	CG8297-PA						PF00085	PS51352			G3DSA:3.40.30.10	SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly46405.9	Serine protease inhibitor dipetalogastin (Fragment)	GO:0005515,GO:0005576,GO:0004866,GO:0004867,GO:0010951,GO:0050819	CG32354-PA				SM00280,SM00280,SM00280,SM00280,SM00280,SM00280,SM00280		PF07648,PF00050,PF00050,PF00050,PF00050,PF00050	PS51465,PS51465,PS51465,PS51465,PS51465,PS51465		PS00282,PS00282,PS00282,PS00282,PS00282	G3DSA:3.30.60.30,G3DSA:1.10.1890.10,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30	SSF100895,SSF100895,SSF100895,SSF100895,SSF100895,SSF100895										
aly46443.1	Retrovirus-related Pol polyprotein from transposon 412	GO:0003964,GO:0015074,GO:0004190,GO:0003676,GO:0004519	n/a																				
aly4645.1	Unknown		n/a						PF14214														
aly4645.10	Pentatricopeptide repeat-containing protein 1, mitochondrial	GO:0005759,GO:0000049,GO:0042780	CG4611-PA					TIGR00756,TIGR00756	PF13041,PF13041	PS51375,PS51375,PS51375,PS51375,PS51375,PS51375					556~583								
aly4645.11	Glutamate-rich WD repeat-containing protein 1	GO:0005737,GO:0005730,GO:0044822,GO:0005575,GO:0003674,GO:0005515,GO:0008150	CG12792-PB				SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF12265	PS50294,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678	G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4645.12	Mismatch repair endonuclease PMS2	GO:0032389,GO:0006298,GO:0030983,GO:0016887,GO:0003677,GO:0005875,GO:0005737,GO:0007126,GO:0005634,GO:0005654,GO:0032138,GO:0032407,GO:0003697,GO:0005524,GO:0015630,GO:0006281,GO:0006974,GO:0007131,GO:0004519,GO:0032300,GO:0016447,GO:0016446	CG8169-PA				SM00853	TIGR00585	PF08676,PF01119,PF13589			PS00058	G3DSA:3.30.230.10,G3DSA:3.30.230.10,G3DSA:3.30.565.10	SSF54211,SSF54211,SSF55874,SSF118116										
aly4645.13	WW domain-binding protein 2	GO:0005737,GO:0005634,GO:0045572,GO:0035329,GO:0045893	CG11009-PE						PF02893,PF10349					SSF50729									
aly4645.14	Unknown		n/a				SM00211,SM00211		PF00086	PS51162,PS51162			G3DSA:4.10.800.10,G3DSA:4.10.800.10	SSF57610,SSF57610,SSF57610									
aly4645.15	Unknown		n/a						PF00086	PS51162			G3DSA:4.10.800.10	SSF57610									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4645.16	Neurabin-1	GO:0008022,GO:0015629,GO:0030426,GO:0050805,GO:0030175,GO:0051020,GO:1900454,GO:0045202,GO:0031175,GO:0002121,GO:0030054,GO:0005856,GO:0051497,GO:0030027,GO:0060999,GO:0031594,GO:0032403,GO:0043025,GO:0042803,GO:0048666,GO:0043005,GO:0019722,GO:0042048,GO:0051015,GO:0019901,GO:0008157,GO:0030425,GO:0007015,GO:1900272,GO:0043197,GO:0051489,GO:0097237,GO:0019904,GO:0030864,GO:0005515,GO:0045860,GO:0005829,GO:0010976	CG16757-PJ				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156										
aly4645.17	Sterile alpha motif domain-containing protein 14	GO:0042048,GO:0002121,GO:0008157,GO:0005515	CG16757-PJ						PF00536	PS50105			G3DSA:1.10.150.50	SSF47769	295~322								
aly4645.18	p21-activated protein kinase-interacting protein 1-like	GO:0009968,GO:0005515,GO:0005730	CG12608-PA				SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50082,PS50294,PS50082,PS50082,PS50294		PS00678	G3DSA:2.130.10.10	SSF50978									
aly4645.19	Unknown	GO:0022008,GO:0009987	CG5466-PA						PF12540														
aly4645.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4645.20	Methyltransferase-like protein 9		CG5339-PA						PF05219				G3DSA:3.40.50.150	SSF53335									
aly4645.3	ATP-dependent DNA helicase pfh1	GO:0000723,GO:0006310,GO:0006281,GO:0035861,GO:0032508,GO:0003677,GO:0005739,GO:0017116,GO:0000790,GO:1902983,GO:1903469,GO:0016887,GO:0043141,GO:0003678,GO:0043504,GO:0005634,GO:0005730,GO:0005524	CG3238-PA				SM00382		PF05970				G3DSA:3.40.50.300,G3DSA:3.60.10.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF56219,SSF52540,SSF52540,SSF52540,SSF52540	36~56								
aly4645.4	Unknown		CG13251-PA						PF15236						291~368								
aly4645.5	Unknown		CG6216-PB																				
aly4645.6	Unknown		n/a												213~233,250~273								
aly4645.7	Unknown		n/a												91~111								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4645.8	Thioredoxin, mitochondrial	GO:0034599,GO:0005737,GO:0006457,GO:0005730,GO:0001103,GO:0005739,GO:0006974,GO:0016671,GO:0006662,GO:0015035,GO:0045454,GO:0055114,GO:0015036	CG8993-PA					TIGR01068	PF00085	PS51352	PR00421,PR00421,PR00421		G3DSA:3.40.30.10	SSF52833									
aly4645.9	Eukaryotic translation initiation factor 3 subunit L	GO:0005737,GO:0005852,GO:0016282,GO:0006446,GO:0048812,GO:0033290,GO:0001731,GO:0006413,GO:0003743	CG5642-PA	MF_03011					PF10255					SSF48452									
aly4646.1	Unknown	GO:0008411,GO:0006084,GO:0022008,GO:0005811	CG7920-PA										G3DSA:3.40.1080.10										
aly4646.2	Cytosolic beta-glucosidase	GO:0005975,GO:0005829,GO:0016139,GO:0008422,GO:0004565,GO:0006687,GO:0004553,GO:0017042,GO:0046477,GO:0006665,GO:0044281	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly4646.3	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653	G3DSA:3.20.20.80	SSF51445									
aly4646.4	V-type proton ATPase subunit B	GO:0033181,GO:0016820,GO:0015992,GO:0007035,GO:0046034,GO:0015991,GO:0033178,GO:0033180,GO:0000221,GO:0046961,GO:0005886,GO:0005903,GO:0048471,GO:0005769,GO:0005524	CG17369-PC	MF_00310					PF00306,PF00006,PF00006,PF02874			PS00152	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540		00195+3.6.3.14,00190+3.6.3.14		PWY-7219					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4646.5	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	GO:0000184,GO:0006909,GO:0030308,GO:0000086,GO:0006470,GO:0030155,GO:0000188,GO:0030111,GO:0015630,GO:0051754,GO:0005739,GO:0019932,GO:0051306,GO:0045595,GO:0008601,GO:0008543,GO:0051225,GO:0006461,GO:0000278,GO:0005737,GO:0042518,GO:0070062,GO:0005634,GO:0016020,GO:0005814,GO:0007143,GO:0010467,GO:0007084,GO:2001241,GO:0008380,GO:0010033,GO:0051232,GO:0008287,GO:0051298,GO:0034047,GO:0070262,GO:0006914,GO:0006915,GO:0007052,GO:1903538,GO:0003823,GO:0007059,GO:0022008,GO:0000775,GO:0006996,GO:0000159,GO:0005829,GO:0051297,GO:0004722,GO:0006275,GO:0040008,GO:0006355,GO:0007098,GO:0007099,GO:0046982,GO:0006672	CG17291-PC						PF13646,PF13646	PS50077,PS50077,PS50077,PS50077,PS50077,PS50077,PS50077,PS50077,PS50077,PS50077			G3DSA:1.25.10.10	SSF48371										
aly4646.6	Unknown		n/a						PF16039														
aly4646.7	Unknown		n/a																				
aly46465.1	Adenylate cyclase	GO:0050808,GO:0005622,GO:0004674,GO:1900242,GO:0000287,GO:0032418,GO:0017137,GO:0004016,GO:0005765,GO:0018105,GO:0004672,GO:0035556,GO:0007264,GO:0031902,GO:0005524,GO:0005525	CG5483-PD				SM00369,SM00369,SM00364,SM00364,SM00364		PF13855	PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52075										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4674.1	T-cell leukemia homeobox protein 3	GO:0043234,GO:0043565,GO:0001707,GO:0045747,GO:0003700,GO:0005634,GO:0007501,GO:0005737,GO:0035218,GO:0006355,GO:0048800,GO:0022416,GO:0035015,GO:0045893,GO:0048484,GO:0045892,GO:0051726,GO:0007480,GO:0050774	CG7937-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689	248~268								
aly4674.10	Hexosaminidase D	GO:0005737,GO:0004563,GO:0005975,GO:0005634,GO:0004553	CG7985-PA																				
aly4674.2	Chymotrypsin	GO:0004252,GO:0005615,GO:0007586,GO:0045087,GO:0030574,GO:0006952,GO:0050830,GO:0005576,GO:0045752,GO:0006508	CG5896-PB				SM00020,SM00020,SM00020		PF00089,PF00089,PF00089,PF00089	PS50240,PS50240,PS50240,PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494,SSF50494,SSF50494,SSF50494,SSF50494,SSF50494,SSF50494,SSF50494									
aly4674.3	Unknown		n/a												18~38								
aly4674.4	MethenyltetraHydrofolate synthase domain-containing protein	GO:0005737,GO:0009396,GO:0009952,GO:0071011,GO:0000166,GO:0071013,GO:0019094,GO:0000398,GO:0030529,GO:0030272,GO:0008298,GO:0003723,GO:0007310,GO:0007277,GO:0044822,GO:0005524,GO:0045451	CG14648-PA						PF01812				G3DSA:3.40.50.10420	SSF100950									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4674.5	BTB/POZ domain-containing protein KCTD9	GO:0051260	CG14647-PB				SM00225		PF00805,PF00805,PF02214,PF11834	PS50097			G3DSA:3.30.710.10	SSF54695,SSF141571									
aly4674.6	Unknown	GO:0005252,GO:0016021,GO:0005267,GO:0071805	CG34396-PC																				
aly4674.7	Unknown		n/a												52~72								
aly4674.8	TWiK family of potassium channels protein 18	GO:0040011,GO:0005267,GO:0006936,GO:0071805,GO:0006813,GO:0016021,GO:0016020,GO:0005252,GO:0015271	CG15655-PA						PF07885,PF07885		PR01333,PR01333		G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324,SSF81324	559~579								
aly4674.9	Hexosaminidase D	GO:0005737,GO:0004563,GO:0005975,GO:0005634,GO:0004553	CG7985-PA										G3DSA:3.20.20.80	SSF51445									
aly4675.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4675.2	Unknown		n/a																				
aly4683.1	Unknown	GO:0005515	n/a				SM00228			PS50106			G3DSA:2.30.42.10	SSF50156	451~471								
aly4683.2	Cysteine-rich PDZ-binding protein	GO:0005737,GO:0043197,GO:0005730,GO:0043198,GO:0008017,GO:0030425,GO:0031122,GO:0045184,GO:0030165,GO:0014069,GO:0032403,GO:1902897,GO:0043025,GO:0035372,GO:0030054	CG4537-PB						PF10235														
aly4683.3	Serologically defined colon cancer antigen 8 homolog	GO:0005814,GO:0030054	CG45105-PC						PF15964,PF15964						353~387,575~627,163~190,306~333,261~295,407~540								
aly4683.4	Unknown		n/a																				
aly4683.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4683.6	Unknown		n/a												130~150								
aly4698.1	Unknown		n/a																				
aly4698.2	Collagen alpha chain CG42342	GO:0005581,GO:0016021,GO:0005575,GO:0008150,GO:0005886,GO:0003674	CG42342-PH						PF01391,PF01391,PF01391,PF01391,PF01391														
aly4698.3	Protein toll	GO:0009897,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0007165,GO:0008063,GO:0006955,GO:0007416,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0002229,GO:0006952,GO:0042802,GO:0016201,GO:0009880,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005887,GO:0005886,GO:0007155,GO:0007352,GO:0043234,GO:0007507,GO:0009950,GO:0009620,GO:0004888,GO:0045944,GO:0005515,GO:0030097,GO:0045610,GO:0005769,GO:0035007	CG5490-PC				SM00369,SM00369,SM00369,SM00369,SM00369,SM00255		PF01582	PS51450,PS51450,PS51450,PS51450,PS51450,PS50104,PS51450	PR01537,PR01537		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.40.50.10140	SSF52047,SSF52047,SSF52047,SSF52200									
aly4698.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly47029.1	MORN repeat-containing protein 4	GO:0043652,GO:0016028	CG10233-PA				SM00698,SM00698,SM00698,SM00698		PF02493,PF02493,PF02493,PF02493				G3DSA:2.20.110.10	SSF82185									
aly47029.2	Elongation of very long chain fatty acids protein 4	GO:0005575,GO:0005783,GO:0016021,GO:0030497,GO:0005789,GO:0009922,GO:0042811,GO:0030176,GO:0019368,GO:0016740,GO:0042759,GO:0019367,GO:0042761	CG32072-PA						PF01151			PS01188				00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					
aly47176.1	Unknown		n/a												70~110								
aly47226.1	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0005534,GO:0030246	CG3410-PA				SM00034,SM00034		PF00059,PF00059	PS50041,PS50041		PS00615	G3DSA:3.10.100.10,G3DSA:3.10.100.10	SSF56436,SSF56436									
aly47226.2	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246	n/a				SM00034		PF00059	PS50041,PS50041		PS00615	G3DSA:3.10.100.10,G3DSA:3.10.100.10	SSF56436,SSF56436									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly47226.3	Unknown		n/a																				
aly47395.1	Unknown		CG8861-PC																				
aly4740.1	Unknown		n/a												375~395								
aly476.1	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG12268-PA						PF03015														
aly476.2	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG12268-PA						PF07993				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly476.3	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG12268-PA						PF03015,PF07993				G3DSA:3.40.50.720	SSF51735,SSF51735			REACT_22258						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly476.4	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG12268-PA						PF03015,PF07993				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly4775.1	G protein-activated inward rectifier potassium channel 4	GO:0042391,GO:0034765,GO:0009897,GO:0006813,GO:0090099,GO:0016021,GO:0007268,GO:0015467,GO:0035220,GO:0008076,GO:0030315,GO:0048812,GO:0005887,GO:0005886,GO:0010107,GO:0005242	CG4370-PD						PF01007		PR01320,PR01320,PR01320,PR01320,PR01320,PR01320		G3DSA:1.10.287.70,G3DSA:2.60.40.1400	SSF81296,SSF81324									
aly4775.2	Nephrin	GO:0043234,GO:0007517,GO:0051393,GO:0030507,GO:0016021,GO:0016020,GO:0003094,GO:0019904,GO:0005886,GO:0008045,GO:0007155,GO:0036057,GO:0045121	CG31062-PC				SM00409,SM00409,SM00409,SM00408,SM00408		PF13895,PF13895,PF08205	PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726									
aly4775.3	Unknown		n/a																				
aly4778.1	Leucine-rich repeat and guanylate kinase domain containing protein	GO:0005737,GO:0005654,GO:0016301,GO:0004385,GO:0006163,GO:0005515,GO:0005524	CG11811-PA				SM00365,SM00365,SM00365,SM00072		PF00625	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS50052,PS51450			G3DSA:3.30.63.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.80.10.10	SSF52058,SSF52540									
aly4778.10	Dynein regulatory complex protein 1	GO:0005856,GO:0070286,GO:0005930,GO:0005575,GO:0008150,GO:0003674,GO:0060285,GO:0071973	CG10958-PA						PF14772						318~338,258~292,343~363,145~165,106~133								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4778.11	Unknown	GO:0005575,GO:0008150,GO:0003674	CG10958-PA																				
aly4778.12	Androgen-induced gene 1 protein	GO:0016021	CG3625-PB						PF04750	PS51257													
aly4778.13	Dyslexia-associated protein KIAA0319	GO:0016021,GO:0001764,GO:2000171,GO:0005886,GO:0004568,GO:0005769,GO:0031901	CG7565-PA				SM00089,SM00089,SM00089,SM00089,SM00089			PS50093			G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.60.40.670,G3DSA:2.60.40.670,G3DSA:2.60.40.670	SSF49299,SSF49299,SSF49299,SSF49299									
aly4778.14	Unknown		n/a										G3DSA:2.40.10.10	SSF50494									
aly4778.15	Cytochrome P450 4c3	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00465,PR00465,PR00465,PR00465,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly4778.16	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067				G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4778.17	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly4778.18	Protein smoothened	GO:0030425,GO:0048100,GO:0007165,GO:0005929,GO:0001746,GO:0090004,GO:0042981,GO:0002385,GO:0004930,GO:2000134,GO:0007455,GO:0016021,GO:0030707,GO:0045746,GO:0043025,GO:0048099,GO:0048592,GO:0007346,GO:0005887,GO:0005886,GO:0035019,GO:0007350,GO:0007224,GO:0005113,GO:0004888,GO:0048812,GO:0005515,GO:0017147,GO:0007193,GO:0005768	CG1109-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00063		PF01392,PF01534,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50082,PS50082,PS50082,PS50294,PS50038,PS50261,PS50082	PR00489,PR00489,PR00489,PR00489,PR00489,PR00489,PR00489		G3DSA:2.130.10.10,G3DSA:1.10.2000.10	SSF63501,SSF50978	604~624		REACT_14797						
aly4778.19	Unknown	GO:0000042,GO:0048047,GO:0046331,GO:0008049,GO:0007619	CG14039-PA						PF01465	PS50913					378~405,350~370,178~212,443~463								
aly4778.2	Unknown		n/a																				
aly4778.20	Clavesin-2	GO:0008431,GO:0005802,GO:0080025,GO:0005215,GO:0006810,GO:0005622,GO:0007040,GO:0030136,GO:0005768,GO:0031901,GO:0016918	CG10237-PB				SM01100,SM00516		PF00650	PS50191	PR00180,PR00180,PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF52087,SSF46938									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4778.21	Glutaredoxin-C4	GO:0005794,GO:0005783,GO:0005773,GO:0045454,GO:0009055,GO:0015035,GO:0015036	CG7975-PA					TIGR02180	PF00462	PS51354	PR00160,PR00160,PR00160	PS00195	G3DSA:3.40.30.10	SSF52833									
aly4778.22	Actin-related protein 5	GO:0006310,GO:0006338,GO:0006281,GO:0005634,GO:0031011,GO:0006355,GO:0006351,GO:0043140	CG7940-PA												64~98,12~32								
aly4778.3	26S proteasome non-ATPase regulatory subunit 14	GO:0004175,GO:0005838,GO:0000502,GO:0043161,GO:0009987,GO:0004843,GO:0008237,GO:0006508,GO:0032436,GO:0046872,GO:0016579,GO:0005875,GO:0008541	CG18174-PA				SM00232		PF13012,PF01398				G3DSA:3.40.140.10	SSF102712									
aly4778.4	COX assembly mitochondrial protein homolog	GO:0046872,GO:0005739	CG17996-PA						PF08583														
aly4778.5	tRNA-splicing endonuclease subunit Sen2	GO:0004518,GO:0016829,GO:0000214,GO:0000213,GO:0003676,GO:0006388,GO:0006397	CG31812-PB			PIRSF011789		TIGR00324	PF01974				G3DSA:3.40.1350.10	SSF53032				PWY-6689					
aly4778.6	V-type proton ATPase subunit H	GO:0016820,GO:0015991,GO:0033227,GO:0033181,GO:0000221,GO:0046961,GO:0005886,GO:0008340	CG17332-PB			PIRSF032184			PF11698,PF03224				G3DSA:1.25.40.150,G3DSA:1.25.10.10	SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4778.7	Actin-related protein 5	GO:0006310,GO:0005737,GO:0006302,GO:0006338,GO:0006281,GO:0005634,GO:0031011,GO:0006355,GO:0070914,GO:0006351,GO:0043140	CG7940-PA				SM00268		PF00022,PF00022				G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.90.640.10,G3DSA:3.90.640.10	SSF53067,SSF53067,SSF53067										
aly4778.8	Zinc finger protein 182	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF13912,PF13912,PF13912,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly4778.9	60S ribosomal protein L11	GO:0005737,GO:0005840,GO:0005730,GO:0022625,GO:0005703,GO:0006412,GO:0003735,GO:0007052,GO:0005515,GO:0000228,GO:0019843,GO:0000022,GO:0051298	CG7726-PB			PIRSF002161			PF00673,PF00281			PS00358	G3DSA:3.30.1440.10	SSF55282									
aly4779.1	Polyadenylate-binding protein-interacting protein 2B	GO:0000900,GO:0008143,GO:0017148,GO:0005575,GO:0001558,GO:0005515,GO:0045947	CG12358-PA																				
aly4779.2	Unknown	GO:0046872	CG14962-PA				SM00355,SM00355,SM00355					PS00028			244~270								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly47856.1	Unknown		n/a												54~74								
aly479.1	Unknown		n/a																				
aly479.10	Ras-GEF domain-containing family member 1B	GO:0005088,GO:0005770,GO:0030496,GO:0046579,GO:0005622,GO:0005575,GO:0008360,GO:0007264,GO:0005769	CG7369-PA				SM00147		PF00618,PF00617	PS50212,PS50009			G3DSA:1.20.870.10,G3DSA:1.10.840.10,G3DSA:1.10.840.10	SSF48366,SSF48366									
aly479.11	S-antigen protein	GO:0002009,GO:0005605,GO:0007507,GO:0020003,GO:0035088,GO:0007508,GO:0061343,GO:0016477,GO:0005578	CG5700-PB																				
aly479.12	General receptor for phosphoinositides 1-associated scaffold protein	GO:0008104,GO:0005515,GO:0097107,GO:0045211,GO:0014069,GO:0007165,GO:0030160,GO:0048471,GO:0030054	CG30483-PA				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156	166~186								
aly479.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly479.14	Unknown		n/a												82~102								
aly479.15	Unknown		n/a																				
aly479.16	Dynein heavy chain 6, axonemal	GO:0016887,GO:0007018,GO:0005858,GO:0001539,GO:0003777,GO:0008152,GO:0005874,GO:0005524	n/a												30~57								
aly479.2	Unknown		n/a																				
aly479.3	Ras-specific guanine nucleotide-releasing factor RalGPS2	GO:0005737,GO:0005085,GO:0008321,GO:0005622,GO:0005575,GO:0032485,GO:0005886,GO:0007264	CG5522-PA				SM00147,SM00233		PF00617,PF00169	PS50009,PS50003			G3DSA:1.10.840.10,G3DSA:2.30.29.30	SSF48366,SSF50729									
aly479.4	Cat eye syndrome critical region protein 2	GO:0000910,GO:0005719,GO:0090102,GO:0016192,GO:0060122,GO:0007616,GO:0005634,GO:0043044,GO:0006309,GO:0007611,GO:0005575,GO:0097194,GO:0003674,GO:0007338,GO:0005515,GO:0007010,GO:0001843,GO:0001842,GO:0090537,GO:0008355	CG42799-PF				SM00297		PF00439	PS50014	PR00503,PR00503,PR00503,PR00503		G3DSA:1.20.920.10	SSF47370	916~936								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly479.5	Prefoldin subunit 1	GO:0006457,GO:0016272,GO:0051082	CG13993-PA						PF01920				G3DSA:1.10.287.370	SSF46579	77~125								
aly479.6	WW domain-containing adapter protein with coiled-coil	GO:0016607,GO:0006974,GO:0003682,GO:0032435,GO:0010390,GO:0005575,GO:0016239,GO:0003674,GO:0045893,GO:0005515,GO:0008150,GO:0044783,GO:0000993,GO:0005654,GO:0071894,GO:0005681,GO:0006351	CG8949-PF				SM00456		PF00397	PS50020		PS01159	G3DSA:2.20.70.10	SSF51045									
aly479.7	WW domain-containing adapter protein with coiled-coil	GO:0016607,GO:0006974,GO:0003682,GO:0032435,GO:0010390,GO:0005575,GO:0016239,GO:0003674,GO:0045893,GO:0008150,GO:0044783,GO:0000993,GO:0005654,GO:0071894,GO:0005681,GO:0006351	CG8949-PF																				
aly479.8	Dynein heavy chain 6, axonemal	GO:0008152,GO:0042623,GO:0007018,GO:0005858,GO:0005875,GO:0001539,GO:0005524,GO:0016887,GO:0005874,GO:0003774,GO:0003777	CG7092-PA						PF12781,PF12780,PF12777,PF03028				G3DSA:3.40.50.300		641~664,336~363								
aly479.9	Dynein heavy chain 6, axonemal	GO:0008152,GO:0042623,GO:0007018,GO:0005858,GO:0005875,GO:0001539,GO:0005524,GO:0016887,GO:0005874,GO:0003774,GO:0003777	CG7092-PA						PF12774,PF12775,PF08393,PF07728,PF12780				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540									
aly47987.1	26S proteasome non-ATPase regulatory subunit 13	GO:0004175,GO:0005838,GO:0022624,GO:0043161,GO:0006508,GO:0007096,GO:0008541	CG10230-PA												14~34								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly48.1	Neuroligin-4, X-linked	GO:0050808,GO:0006909,GO:0005887,GO:0005886,GO:0007612,GO:0030425,GO:0045202,GO:0035265,GO:0030054,GO:0050839,GO:0003360,GO:0016021,GO:0097105,GO:0007416,GO:0042803,GO:0042043,GO:0030182,GO:0035176,GO:0009986,GO:0052689,GO:0045211,GO:0014069,GO:0007158,GO:0045216,GO:0060076,GO:0022008,GO:0021549,GO:0030534,GO:0090394,GO:0031404,GO:0097110,GO:0071625,GO:0004872	CG34127-PC						PF00135			PS00941	G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474										
aly48.2	Neuroligin-4, Y-linked	GO:0031594,GO:0051124,GO:0071625,GO:0035176,GO:0009986,GO:0007612,GO:0052689,GO:0007528,GO:0045211,GO:0042043,GO:0030054,GO:0004872,GO:0005887,GO:0050808,GO:0014069,GO:0050839,GO:0097110,GO:0007416,GO:0007158	CG31146-PD						PF00135			PS00941	G3DSA:3.40.50.1820	SSF53474	1460~1461									
aly48053.1	Unknown		n/a																				
aly4806.1	Unknown	GO:0032296,GO:0035074,GO:0006308,GO:0003723,GO:0003677,GO:0004844	CG18410-PB																				
aly4808.1	Regulator of G protein signaling 7	GO:0005737,GO:0031681,GO:0038032,GO:0043547,GO:0005834,GO:0005829,GO:0005096,GO:0008277,GO:0004871,GO:0005886,GO:0043234,GO:0035556,GO:0007186	CG9108-PA				SM00315,SM00049,SM00224		PF00610,PF00615,PF00631	PS50132,PS50186	PR01301,PR01301,PR01301		G3DSA:1.10.167.10,G3DSA:1.10.10.10,G3DSA:1.10.196.10,G3DSA:4.10.260.10	SSF48670,SSF46785,SSF48097	333~360								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly481.1	SAYSvFN domain-containing protein 1	GO:0030659,GO:0016021,GO:0043231	CG13663-PA						PF10260														
aly481.10	Unknown		n/a																				
aly481.11	Metastasis-associated protein MTA1	GO:0032922,GO:0003714,GO:0006909,GO:0005783,GO:0001103,GO:0050727,GO:0008270,GO:0032496,GO:0005874,GO:0005737,GO:0043565,GO:0010212,GO:0006302,GO:0006325,GO:0043161,GO:0005634,GO:0005635,GO:0003713,GO:0040029,GO:0005654,GO:0046872,GO:1902499,GO:1903507,GO:0000118,GO:0045475,GO:0001047,GO:0001046,GO:0043231,GO:0016581,GO:0003700,GO:0007565,GO:0006355,GO:0006351,GO:0043153,GO:0003682,GO:0033363,GO:0007165	CG2244-PD				SM00717,SM00401,SM00439		PF01426,PF00320,PF01448	PS51038,PS50157,PS51293,PS51156		PS00028	G3DSA:3.30.160.60	SSF46689									
aly481.12	Protein hairless	GO:0036335,GO:0044719,GO:0007219,GO:0048190,GO:0005634,GO:0003714,GO:0008587,GO:0008586,GO:0008052,GO:1903507,GO:0045746,GO:0016360,GO:0046331,GO:0005515,GO:0003677,GO:0035019,GO:0010941	CG5460-PA																				
aly481.13	Eukaryotic initiation factor 4A-III	GO:0010501,GO:0071011,GO:0006413,GO:0016281,GO:0045495,GO:0005634,GO:0004004,GO:0046579,GO:0006974,GO:0070374,GO:0000398,GO:0005515,GO:1903040,GO:0010468,GO:0051028,GO:0003743,GO:0071013,GO:0008380,GO:0005524,GO:0045451	CG7483-PA				SM00490,SM00487		PF00270,PF00271	PS51195,PS51192,PS51194		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly481.14	Ubiquitin-conjugating enzyme E2 J1	GO:0005737,GO:0031625,GO:0016567,GO:0042534,GO:0016874,GO:0016021,GO:0007286,GO:0005789,GO:1904153,GO:0030433,GO:0061630,GO:0061631,GO:0004842,GO:0018279,GO:0005524	CG5823-PB				SM00212		PF00179	PS50127			G3DSA:3.10.110.10	SSF54495									
aly481.15	Splicing factor 3B subunit 2	GO:0016032,GO:0071011,GO:0005634,GO:0044822,GO:0000398,GO:0008380,GO:0005654,GO:0010467,GO:0005689,GO:0005686,GO:0071013,GO:0005681,GO:0006397	CG3605-PA				SM00581		PF04037,PF04046														
aly481.16	Electron transfer flavoprotein subunit beta	GO:0070062,GO:0017133,GO:0005811,GO:0005739,GO:0043231,GO:0009055,GO:0005875,GO:0055114,GO:0006119	CG7834-PB			PIRSF000090	SM00893		PF01012			PS01065	G3DSA:3.40.50.620	SSF52402			REACT_6305						
aly481.17	DDB1- and CUL4-associated factor 10 homolog	GO:0005575,GO:0008150,GO:0003674,GO:0005515	CG1523-PA				SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50294,PS50082,PS50082		PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978									
aly481.18	Nucleoporin GLE1	GO:0005643,GO:0015031,GO:0016973,GO:0003674,GO:0005739	CG14749-PA						PF07817						280~309								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly481.19	DNA polymerase epsilon catalytic subunit A	GO:0006297,GO:0035265,GO:0000082,GO:0008270,GO:0003676,GO:0003677,GO:0006283,GO:0005737,GO:0005654,GO:0008408,GO:0001701,GO:0008622,GO:0005634,GO:0000166,GO:0003887,GO:0006260,GO:0006261,GO:0000723,GO:0006287,GO:0000278,GO:0006281,GO:0006289,GO:0006974,GO:0005886,GO:0022008,GO:0000722,GO:0007113,GO:0051539,GO:0006270,GO:0032201,GO:0000731,GO:0003682,GO:0008296	CG6768-PA				SM00486		PF00136,PF03104,PF08490				G3DSA:3.30.420.10	SSF53098,SSF53098,SSF56672,SSF56672,SSF56672,SSF56672		00240+2.7.7.7,00230+2.7.7.7							
aly481.2	FERM domain containing protein 8	GO:0005856,GO:0070201,GO:0003674,GO:0030178,GO:0005886	CG11848-PB				SM00295		PF00373	PS50057			G3DSA:1.20.80.10	SSF47031									
aly481.20	Protein SEC13 homolog	GO:0090114,GO:0070062,GO:0031080,GO:0005789,GO:0035859,GO:0006607,GO:0006900,GO:0008363,GO:0010629,GO:0000776,GO:0005515,GO:0012507,GO:0015031,GO:0051028,GO:0005198,GO:0035293,GO:0030127,GO:0007184,GO:0016192	CG6773-PA				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50294,PS50082			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978									
aly481.21	Unknown		CG30159-PB										G3DSA:2.40.50.90	SSF50199									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly481.22	Ras-related protein Rab-8A	GO:0008021,GO:0055038,GO:0006904,GO:0055037,GO:0030425,GO:0042593,GO:0045202,GO:0046326,GO:0032869,GO:0051223,GO:0048169,GO:0032880,GO:0036064,GO:0030667,GO:0072659,GO:0031982,GO:0005730,GO:0016023,GO:0005813,GO:0006886,GO:0031513,GO:0005654,GO:0030140,GO:0043025,GO:0005525,GO:0042384,GO:0009306,GO:0003924,GO:0048210,GO:0019901,GO:0030659,GO:0045335,GO:0014069,GO:0007409,GO:0005886,GO:0007264,GO:0070062,GO:0016192,GO:0030670,GO:0032482,GO:0016079,GO:0005622,GO:0019003,GO:0015031,GO:0017157,GO:0005768	CG8287-PA				SM00177,SM00174,SM00173,SM00176,SM00175	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly481.23	DNA-directed RNA polymerase II subunit RPB7	GO:0000291,GO:0006367,GO:0005730,GO:0005634,GO:0006915,GO:0000932,GO:0003727,GO:0060213,GO:0005665,GO:0006351,GO:0005515,GO:0006366,GO:0045948,GO:0003899,GO:0031369,GO:0003697,GO:0003723	CG31155-PA						PF03876,PF00575				G3DSA:3.30.1490.120,G3DSA:2.40.50.140	SSF88798,SSF50249										
aly481.24	Unknown		n/a																				
aly481.25	Myosin-I heavy chain	GO:0006909,GO:0030175,GO:0000902,GO:0042623,GO:0016020,GO:0003779,GO:0016459,GO:0009847,GO:0003774,GO:0005524,GO:0031589,GO:0008017,GO:0031252,GO:0051015,GO:0030048,GO:0030898,GO:0008152,GO:0043621,GO:0001891,GO:0005829,GO:0005515,GO:0046847	CG15831-PB				SM00242,SM00139,SM00295		PF00373,PF00063,PF00784,PF00784	PS50096,PS51016,PS51016,PS51456,PS50057	PR00193,PR00193,PR00193,PR00193,PR00193		G3DSA:3.40.50.300,G3DSA:1.20.80.10,G3DSA:2.30.29.30	SSF54236,SSF52540,SSF47031	879~899,799~826									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly481.26	LysM and putative peptidoglycan-binding domain-containing protein 2		CG12207-PB				SM00257		PF01476				G3DSA:3.10.350.10	SSF54106	139~159								
aly481.27	Abnormal pharyngeal pumping eat-20	GO:0004930,GO:0009986,GO:0016020,GO:0030424,GO:0005575,GO:0008150,GO:0005515,GO:0003674,GO:0016021	CG44153-PA				SM00008,SM00181,SM00181,SM00409		PF13895,PF00008	PS50026,PS50227,PS50026,PS50221,PS50835		PS00022,PS01186,PS00022,PS01186	G3DSA:2.60.40.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF48726,SSF57196,SSF111418									
aly481.3	Dynein regulatory complex subunit 7	GO:0005737,GO:0005856,GO:0031514,GO:0030317,GO:0003674,GO:0046693	CG34110-PC												89~116								
aly481.4	Unknown		n/a																				
aly481.5	Unknown		n/a																				
aly481.6	Protein distal antenna	GO:0048749,GO:0007469,GO:0007379,GO:0005634,GO:0021556,GO:0006355,GO:0003700,GO:0005515,GO:0003677,GO:0006351	CG11849-PB						PF04218	PS50960			G3DSA:1.10.10.60	SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly481.7	Coiled-coil domain-containing protein lobo	GO:0005737,GO:0005856,GO:0031514,GO:0030317,GO:0003674,GO:0046693	CG34110-PC												142~145								
aly481.8	Calcineurin B homologous protein 1	GO:0032417,GO:0005783,GO:0048306,GO:0006611,GO:0010923,GO:0031953,GO:0061025,GO:0061024,GO:0006469,GO:0070885,GO:0051453,GO:0051222,GO:0005925,GO:0030133,GO:0005737,GO:0070062,GO:0005634,GO:0005509,GO:0005886,GO:0031397,GO:0017156,GO:0015630,GO:0005793,GO:0019722,GO:0005215,GO:0008017,GO:0060050,GO:0031122,GO:0004860,GO:0019900,GO:0042308,GO:1901214,GO:0090314,GO:0032088,GO:0051259,GO:0022406,GO:0050821,GO:0001578,GO:0005829,GO:0000139,GO:0001933,GO:0071468	CG2185-PA				SM00054,SM00054		PF13499	PS50222,PS50222,PS50222		PS00018,PS00018	G3DSA:1.10.238.10	SSF47473										
aly481.9	Protein transport protein Sec23A	GO:0005795,GO:0048081,GO:0005783,GO:0035149,GO:0005789,GO:0008270,GO:0030011,GO:0030134,GO:0022409,GO:0070971,GO:0040003,GO:0006888,GO:0007029,GO:0006886,GO:0034394,GO:0048812,GO:0048471,GO:0016203,GO:0005096,GO:0008363,GO:0008360,GO:0035293,GO:0030127,GO:0050774,GO:0007030,GO:0030868,GO:0003331,GO:0000139,GO:0032320,GO:0003400,GO:0071711,GO:0005101	CG1250-PH						PF04811,PF04810,PF08033,PF00626,PF04815				G3DSA:3.40.20.10,G3DSA:3.40.50.410	SSF81811,SSF82754,SSF53300,SSF81995,SSF81995,SSF82919			REACT_11123							
aly48150.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly48476.1	Sodium-dependent dopamine transporter	GO:0005328,GO:0005329,GO:0042136,GO:0007595,GO:0005886,GO:0015872,GO:0042745,GO:0035240,GO:0060134,GO:0042053,GO:0042420,GO:0005737,GO:0016600,GO:0016021,GO:0007268,GO:0021984,GO:0043025,GO:0007626,GO:0005330,GO:0015844,GO:0007608,GO:0009986,GO:0042416,GO:0019811,GO:0030431,G	CG8380-PB						PF00209	PS50267				SSF161070									
aly486.1	Aldehyde dehydrogenase, cytosolic 1	GO:0004028,GO:0004029,GO:0051289,GO:0005829,GO:0035106,GO:0005739,GO:0042802,GO:0006068,GO:0008152,GO:0018479,GO:0005759,GO:0001758,GO:0006090,GO:0055114,GO:0016491	CG31075-PB						PF00171			PS00687,PS00070	G3DSA:3.40.309.10,G3DSA:3.40.605.10	SSF53720									
aly486.2	Unknown		n/a										G3DSA:1.10.287.450										
aly486.3	Ras-related protein Rab-8A	GO:0008021,GO:0055038,GO:0006904,GO:0055037,GO:0030425,GO:0042593,GO:0007165,GO:0046326,GO:0032869,GO:0051223,GO:0048169,GO:0032880,GO:0036064,GO:0030667,GO:0031982,GO:0005730,GO:0016023,GO:0005813,GO:0006886,GO:0016020,GO:0031513,GO:0005654,GO:0030140,GO:0043025,GO:0005525,GO:0042384,GO:0009306,GO:0003924,GO:0048210,GO:0019901,GO:0030659,GO:0045335,GO:0014069,GO:0007409,GO:0005886,GO:0072659,GO:0070062,GO:0016192,GO:0030670,GO:0032482,GO:0016079,GO:0019003,GO:0015031,GO:0017157,GO:0005768,GO:0045202	CG31118-PA				SM00173,SM00174,SM00175,SM00176	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly486.4	Ras-related and estrogen-regulated growth inhibitor-like protein	GO:0016020,GO:0003924,GO:0005622,GO:0005575,GO:0008150,GO:0007165,GO:0006184,GO:0007264,GO:0005525	CG8519-PA				SM00173,SM00175		PF00071	PS51421			G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly486.5	Unknown		n/a																				
aly486.6	Ras-related and estrogen-regulated growth inhibitor-like protein	GO:0016020,GO:0003924,GO:0005622,GO:0005575,GO:0008150,GO:0007165,GO:0006184,GO:0007264,GO:0005525	CG8519-PA				SM00173,SM00175		PF00071	PS51421	PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540									
aly4868.1	Putative inorganic phosphate cotransporter	GO:0051938,GO:0015293,GO:0044341,GO:0015319,GO:0016021,GO:0006541,GO:0005314,GO:0005316,GO:0015321,GO:0015114,GO:0005886,GO:0006814,GO:0055085,GO:0007005	CG5304-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly4868.2	Putative inorganic phosphate cotransporter	GO:0051938,GO:0022857,GO:0015293,GO:0044341,GO:0015319,GO:0016021,GO:0006541,GO:0005314,GO:0006814,GO:0005316,GO:0015321,GO:0006820,GO:0005886,GO:0015114,GO:0055085,GO:0007005	CG5304-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly4868.3	Inactive rhomboid protein 1	GO:0004252,GO:0050708,GO:0005783,GO:0016021,GO:0042059,GO:0042058,GO:0010841,GO:0030431,GO:0015031,GO:0006508,GO:0005789,GO:0007165	CG33304-PA						PF01694				G3DSA:1.20.1540.10	SSF144091,SSF144091									
aly4868.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly48720.1	Unknown		n/a																				
aly489.1	Unknown		n/a																				
aly489.10	Muscle-specific homeobox protein tinman	GO:0061320,GO:0048615,GO:0007498,GO:0061101,GO:0010002,GO:0003677,GO:0071907,GO:0008354,GO:0007435,GO:0007510,GO:0005634,GO:0007552,GO:0008406,GO:0000980,GO:0055007,GO:0035051,GO:0035050,GO:0007280,GO:0045892,GO:0045893,GO:0007522,GO:0007525,GO:0007506,GO:0007507,GO:0007501,GO:0003705,GO:0006355,GO:0045944,GO:0048542,GO:0001708	CG7895-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689										
aly489.11	Mpv17-like protein 2	GO:0005743,GO:0016021	CG14777-PB						PF04117														
aly489.12	Odorant receptor 4	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0004984	CG17911-PA						PF02949														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly489.2	Protein BCCIP homolog	GO:0005575,GO:0045859,GO:0019887	CG9286-PA			PIRSF028983			PF13862														
aly489.3	Protein polybromo-1	GO:0031936,GO:0007507,GO:0000228,GO:0006351,GO:0001890,GO:0006338,GO:0007480,GO:0005700,GO:0006355,GO:0007305,GO:0007306,GO:0003677,GO:0090544,GO:0003682,GO:0007067,GO:0000776,GO:0008285	CG11375-PA				SM00439,SM00439,SM00398,SM00297,SM00297,SM00297,SM00297,SM00297		PF00439,PF00439,PF00439,PF00439,PF00439,PF01426,PF01426,PF00505	PS50014,PS51038,PS50014,PS50118,PS50014,PS50014,PS50014,PS51038	PR00503,PR00503,PR00503	PS00633,PS00633,PS00633	G3DSA:1.10.30.10,G3DSA:1.20.920.10,G3DSA:1.20.920.10,G3DSA:1.20.920.10,G3DSA:1.20.920.10,G3DSA:1.20.920.10,G3DSA:1.20.920.10	SSF47370,SSF47095,SSF47370,SSF47370,SSF47370,SSF47370,SSF47370	1064~1091								
aly489.4	Unknown	GO:0046872	n/a							PS50157		PS00028											
aly489.5	Transcription factor LBX1	GO:0030154,GO:0003677,GO:0008544,GO:0007417,GO:0043565,GO:0007517,GO:0051450,GO:1901739,GO:0000122,GO:0005634,GO:0007519,GO:0045664,GO:0016477,GO:0048666,GO:0007483,GO:0007480,GO:0042659,GO:0007520,GO:0007507,GO:0007501,GO:0003700,GO:0003705,GO:0006355,GO:0048813,GO:0000976,GO:0006351,GO:0005667	CG6545-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024,PR00031,PR00031	PS00027	G3DSA:1.10.10.60	SSF46689	71~98								
aly489.6	Unknown	GO:0051450,GO:0007417,GO:0007517,GO:0008544,GO:1901739,GO:0000122,GO:0005634,GO:0007519,GO:0045664,GO:0016477,GO:0048666,GO:0007483,GO:0007480,GO:0042659,GO:0007520,GO:0007507,GO:0007501,GO:0003700,GO:0003705,GO:0006355,GO:0048813,GO:0000976	CG6545-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly489.7	Phosphoacetylglucosamine mutase	GO:0006048,GO:0005975,GO:0001707,GO:0006487,GO:0060438,GO:0005829,GO:0000287,GO:0007283,GO:0004610,GO:0045743,GO:0004614,GO:0019255,GO:0030097,GO:0006493	CG10627-PA			PIRSF016408			PF02878,PF02878,PF00408				G3DSA:3.40.120.10,G3DSA:3.30.310.50,G3DSA:3.40.120.10	SSF53738,SSF53738,SSF55957,SSF53738		00520+5.4.2.3,00520+5.4.2.10		PWY-5514,PWY-6906,PWY-6749	UPA00113				
aly489.8	2-aminoethanethiol dioxygenase	GO:0046872,GO:0016702,GO:0005739,GO:0055114,GO:0047800	CG7550-PA						PF07847				G3DSA:2.60.120.10	SSF51182,SSF51182									
aly489.9	Homeobox protein bagpipe	GO:0043565,GO:0045165,GO:0007494,GO:0007501,GO:0003700,GO:0005634,GO:0003705,GO:0007498,GO:0006357,GO:0045944,GO:0003677,GO:0007507,GO:0007522,GO:0001710	CG7902-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly4893.1	Unknown		n/a																				
aly4893.2	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (Fragment)	GO:0045252,GO:0005811,GO:0033512,GO:0006099,GO:0005739,GO:0009353,GO:0004149,GO:0005875	CG5214-PA					TIGR01347	PF00364,PF00198			PS00189	G3DSA:3.30.559.10,G3DSA:2.40.50.100	SSF51230,SSF52777		00310+2.3.1.61,00020+2.3.1.61		PWY-5084	UPA00868				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4893.3	Ras-related protein Rab-1A	GO:0007015,GO:0005783,GO:0030334,GO:0006888,GO:0031982,GO:0050774,GO:0009306,GO:0006886,GO:0005811,GO:0003924,GO:0006913,GO:0015031,GO:0032482,GO:0008360,GO:0007165,GO:0005794,GO:0007155,GO:0007264,GO:0043025,GO:0016192,GO:0005525	CG3320-PA				SM00176,SM00173,SM00177,SM00175,SM00174,SM00320,SM00320,SM00320	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:2.130.10.10,G3DSA:3.40.50.300	SSF50978,SSF52540	1025~1045		REACT_11044						
aly4893.4	Potassium channel subfamily K member 9	GO:0005267,GO:0046982,GO:0071805,GO:0016021,GO:0005252,GO:0005244	CG9361-PA						PF07885,PF07885		PR01095,PR01095,PR01095,PR01333,PR01333		G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324,SSF81324									
aly4893.5	Bifunctional glutamate/proline--tRNA ligase	GO:0005737,GO:0006424,GO:0004827,GO:0006433,GO:0004818,GO:0017101,GO:0004812,GO:0003723,GO:0006418,GO:0005524	CG5394-PA				SM00991,SM00991,SM00991	TIGR00463	PF00458,PF00458,PF00458,PF00043,PF03950,PF00749	PS51185,PS51185,PS50405,PS51185	PR00987,PR00987,PR00987,PR00987,PR00987	PS00762,PS00178,PS00762	G3DSA:2.40.240.10,G3DSA:3.90.800.10,G3DSA:2.40.240.10,G3DSA:1.10.287.10,G3DSA:1.10.287.10,G3DSA:1.10.287.10,G3DSA:3.40.50.620,G3DSA:3.40.50.620,G3DSA:1.10.1160.10,G3DSA:1.20.1050.10	SSF47060,SSF47060,SSF47060,SSF47616,SSF52374,SSF50715	824~844,947~947	00970+6.1.1.17,00860+6.1.1.17	REACT_71	PWY-5188						
aly4893.6	Unknown		n/a																				
aly490.1	Protein disconnected	GO:0007469,GO:0007479,GO:0007623,GO:0007420,GO:0003700,GO:0050896,GO:0005634,GO:0007601,GO:0001158,GO:0006355,GO:0045944,GO:0045475,GO:0008062,GO:0003677,GO:0046872,GO:0010468,GO:0045494,GO:0045893	CG32577-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028		SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly490.10	Gonadotropin-releasing hormone receptor	GO:0004930,GO:0070328,GO:0097004,GO:0016021,GO:0005886,GO:0033500,GO:0016042,GO:0055088,GO:0097003,GO:0004968,GO:0005887,GO:0008188,GO:0007186	CG11325-PC						PF00001	PS50262	PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly490.11	Actin-binding Rho-activating protein	GO:0030016,GO:0051091,GO:0015629,GO:0030017,GO:0003713,GO:0000060,GO:0003779,GO:0035025,GO:0045944,GO:0045893,GO:0005886,GO:0006351	CG3630-PA						PF14705														
aly490.12	Protein unc-13 homolog B	GO:0008021,GO:0010808,GO:0005886,GO:0031594,GO:0004872,GO:0004871,GO:0035556,GO:0035249,GO:0030054,GO:0005737,GO:0060384,GO:0019992,GO:0048786,GO:0046872,GO:0005794,GO:0016082,GO:0007588,GO:0097151,GO:0016081,GO:0006915,GO:0014047,GO:0045211,GO:0048172,GO:0007269,GO:0007268,GO:0007528,GO:0043195,GO:0016079,GO:0005829,GO:0005516,GO:0005515,GO:0007165	CG2999-PE				SM00109,SM00239,SM00239		PF06292,PF10540,PF00130,PF00168,PF00168	PS51259,PS50081,PS50004,PS50004,PS51258	PR00360,PR00360,PR00360	PS00479	G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:3.30.60.20	SSF49562,SSF57889,SSF49562	953~973,2322~2349,258~278									
aly490.2	Probable ATP-dependent RNA helicase DHX34	GO:0005737,GO:0000184,GO:2000623,GO:0006396,GO:0005634,GO:0016020,GO:0004004,GO:0004386,GO:0000956,GO:0000398,GO:0003676,GO:0044822,GO:0005524	CG32533-PA				SM00487		PF07717	PS51192,PS51194			G3DSA:3.40.50.300	SSF52540	633~653								
aly490.3	Ubiquitin-conjugating enzyme E2 Q2	GO:0005737,GO:0004842,GO:0016881,GO:0070936,GO:0016874,GO:0005524	CG2924-PA				SM00212		PF00179	PS50127			G3DSA:3.10.110.10	SSF54495									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly490.4	Glutathione S-transferase 1	GO:0005737,GO:0004364,GO:0006749,GO:0005515,GO:0009408,GO:0006979	CG5164-PA						PF13417,PF00043	PS50404,PS50405			G3DSA:3.40.30.10,G3DSA:1.20.1050.10	SSF47616,SSF52833									
aly490.5	Ribose-phosphate pyrophosphokinase 1	GO:0043234,GO:0002189,GO:0016208,GO:0043531,GO:0016301,GO:0031100,GO:0009156,GO:0000287,GO:0007476,GO:0030246,GO:0019693,GO:0004749,GO:0009165,GO:0006167,GO:0006015,GO:0019003,GO:0046101,GO:0007399,GO:0034418,GO:0005524,GO:0042803	CG6767-PB					TIGR01251	PF14572,PF13793			PS00114	G3DSA:3.40.50.2020,G3DSA:3.40.50.2020	SSF53271		00030+2.7.6.1,00230+2.7.6.1	REACT_474		UPA00087				
aly490.6	Lysosomal alpha-glucosidase	GO:0017177,GO:0005975,GO:0005980,GO:0030246,GO:0005764,GO:0005765,GO:0005576,GO:0032450,GO:0004558,GO:0005875	CG14476-PB						PF01055				G3DSA:4.10.110.10	SSF51011,SSF51445,SSF74650,SSF57492									
aly490.7	Unknown		n/a																				
aly490.8	Gonadotropin-releasing hormone II receptor	GO:0004930,GO:0070328,GO:0097004,GO:0016021,GO:0005886,GO:0033500,GO:0016042,GO:0055088,GO:0097003,GO:0004968,GO:0005887,GO:0008188,GO:0007186	CG11325-PC						PF00001	PS50262	PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly490.9	Gonadotropin-releasing hormone II receptor	GO:0004930,GO:0070328,GO:0097004,GO:0016500,GO:0016021,GO:0005886,GO:0033500,GO:0016042,GO:0055088,GO:0097003,GO:0005887,GO:0008188,GO:0007186	CG11325-PC						PF00001	PS50262			G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly49012.1	Unknown		n/a																				
aly4903.1	Unknown		n/a																				
aly49097.1	Cytochrome P450 9e2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0035220,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG11466-PA						PF00067		PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly49099.1	Unknown		n/a										G3DSA:3.60.10.10	SSF56219	115~142								
aly491.1	UDP-glucose 6-dehydrogenase	GO:0016319,GO:0007507,GO:0007427,GO:0016055,GO:0007367,GO:0030206,GO:0042048,GO:0051287,GO:0007224,GO:0007476,GO:0007428,GO:0007509,GO:0015012,GO:0006065,GO:0006024,GO:0007166,GO:0015014,GO:0003979,GO:0008543,GO:0002121,GO:0055114	CG10072-PA			PIRSF000124,PIRSF500133	SM00984	TIGR03026	PF03720,PF00984,PF03721				G3DSA:1.20.5.100,G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735,SSF52413,SSF48179		00053+1.1.1.22,00500+1.1.1.22,00040+1.1.1.22,00520+1.1.1.22		PWY-7346	UPA00038				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly491.2	Segment polarity protein dishevelled homolog DVL 3	GO:0048675,GO:0016318,GO:0008104,GO:0030032,GO:0070300,GO:0007275,GO:0008585,GO:0006928,GO:0003136,GO:0007163,GO:0007164,GO:0048106,GO:0004871,GO:0008045,GO:0007411,GO:0035556,GO:0001745,GO:0035317,GO:0005737,GO:0032231,GO:0007435,GO:0060914,GO:0007476,GO:0030707,GO:0090163,GO:0045746,GO:0016055,GO:0035159,GO:0031290,GO:0048477,GO:0005112,GO:0016201,GO:0042384,GO:0005912,GO:0048076,GO:0042067,GO:0016348,GO:0032053,GO:0035309,GO:0045198,GO:0005938,GO:0005886,GO:0035019,GO:0001737,GO:0001736,GO:0007507,GO:0007423,GO:0008013,GO:0007394,GO:0007464,GO:0007391,GO:0007298,GO:0005515,GO:0048730,GO:0046847,GO:0060071,GO:0019904	CG18361-PA				SM00021,SM00228		PF00595,PF02377,PF00778	PS50841,PS50106	PR01760,PR01760		G3DSA:2.30.42.10	SSF54236,SSF50156									
aly491.3	Unknown		n/a												22~69,87~107								
aly491.4	AT-rich interactive domain-containing protein 5B	GO:0030325,GO:0060612,GO:0048468,GO:0008585,GO:0060021,GO:0009791,GO:0048008,GO:0006807,GO:0060325,GO:0035264,GO:0003677,GO:0045444,GO:0000122,GO:0005634,GO:0003713,GO:0001822,GO:0060613,GO:0010761,GO:0048644,GO:0006351,GO:0048705,GO:0001227,GO:0008584,GO:0044212,GO:0051091,G	n/a				SM00501,SM01014		PF01388				G3DSA:1.10.150.60	SSF46774									
aly4912.1	Unknown		n/a												336~356,364~384,445~465								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4912.2	Serine hydrolase-like protein 2	GO:0016787,GO:0017171,GO:0007586,GO:0005777,GO:0009636,GO:0005739,GO:0005575,GO:0016023,GO:0048471	CG3943-PA						PF00561				G3DSA:3.40.50.1820	SSF53474									
aly49163.1	Importin subunit alpha-1	GO:0005737,GO:0000059,GO:0042332,GO:0015629,GO:0008283,GO:0005643,GO:0005634,GO:0005811,GO:0006606,GO:0006607,GO:0008320,GO:0007301,GO:0007291,GO:0048542,GO:0008565,GO:0016482,GO:0007303,GO:0005875,GO:0051298	CG4799-PA				SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185		PF16186,PF00514,PF00514				G3DSA:1.25.10.10	SSF48371									
aly49173.1	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232			PS00653	G3DSA:3.20.20.80	SSF51445									
aly4930.1	Unknown		n/a																				
aly4930.2	Unknown		n/a												185~205								
aly4930.3	Unknown		CG31323-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly49300.1	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6298-PA				SM00020		PF00089,PF00089	PS50240		PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494,SSF50494									
aly4936.1	Multidrug resistance protein homolog 49	GO:0015893,GO:0042626,GO:0031427,GO:0042623,GO:0016021,GO:0006810,GO:0006855,GO:0015238,GO:0008559,GO:0008354,GO:0005887,GO:0005886,GO:0001666,GO:0055085,GO:0005524	CG3879-PA				SM00382,SM00382		PF00664,PF00664,PF00005,PF00005	PS50893,PS50929,PS50929,PS50893		PS00211,PS00211	G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF90123,SSF90123,SSF90123									
aly49398.1	Unknown		n/a						PF04408						50~70								
aly49433.1	N-alpha-acetyltransferase 35, NatC auxiliary subunit	GO:0005737,GO:0005844,GO:0031417,GO:0043066,GO:0003674,GO:0048659,GO:0008150	CG4065-PA																				
aly495.1	Sucrose-6-phosphate hydrolase	GO:0005737,GO:0005985,GO:0004575	n/a				SM00640	TIGR01322	PF08244,PF00251			PS00609	G3DSA:2.60.120.560,G3DSA:2.115.10.20	SSF75005,SSF49899		00500+3.2.1.26,00052+3.2.1.26		PWY-621	UPA00238				
aly495.2	Proton-coupled amino acid transporter 4	GO:0003333,GO:0006865,GO:0016021,GO:0015171,GO:0015293	CG8785-PB						PF01490														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly495.3	Cholecystokinin receptor type A	GO:0007631,GO:0051924,GO:0005783,GO:0006950,GO:0009314,GO:0031016,GO:0009408,GO:0004951,GO:0051384,GO:0042594,GO:0008188,GO:0032496,GO:0030073,GO:0005737,GO:0004930,GO:0038188,GO:0031532,GO:0016021,GO:0030157,GO:0002023,GO:0007186,GO:0031100,GO:0007586,GO:0007584,GO:0007218,GO:0007528,GO:0032870,GO:0046883,GO:0042755,GO:0005887,GO:0005886,GO:0042277,GO:0008345,GO:0008344,GO:0001659,GO:0090274,GO:0043195,GO:0043266,GO:0043025,GO:0005829,GO:0015054,GO:0007204,GO:0005764,GO:1901652,GO:0001696,GO:0005768,GO:0048545	CG42301-PA						PF00001	PS50262	PR00237,PR00237,PR01822,PR01822	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly4956.1	Unknown		n/a																				
aly4956.2	Unknown		n/a						PF15255														
aly4957.1	Unknown		CG15601-PA				SM00595		PF10545	PS51029					161~181,160~80								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4957.2	Unknown		n/a																				
aly4957.3	Unknown		n/a																				
aly49641.1	Protein FAM193B	GO:0005737,GO:0005654,GO:0005634,GO:0005730	n/a												991~1018								
aly49658.1	5'-3' exoribonuclease 1	GO:0071044,GO:0000184,GO:0071028,GO:0005886,GO:0003676,GO:0003677,GO:0005737,GO:0016020,GO:0010603,GO:0008409,GO:0000288,GO:0005634,GO:0007369,GO:0007476,GO:0010467,GO:0006401,GO:0046529,GO:0005794,GO:0044822,GO:0045111,GO:0042060,GO:0007283,GO:0016246,GO:0043928,GO:0016075,GO:0004534,GO:0000932,GO:0007391,GO:0000956,GO:0005829,GO:0034428	CG3291-PB																				
aly4966.1	Unknown	GO:0005737,GO:0010629,GO:0005634,GO:0007165	CG7047-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4966.10	Unknown		n/a																				
aly4966.11	28S ribosomal protein S11, mitochondrial	GO:0070126,GO:0006996,GO:0070124,GO:0070125,GO:0005840,GO:0044822,GO:0005739,GO:0032543,GO:0003735,GO:0005743,GO:0042769,GO:0005763,GO:0006412	CG5184-PA	MF_01310					PF00411				G3DSA:3.30.420.80	SSF53137									
aly4966.12	Proline-rich protein PRCC	GO:0005654,GO:0005634,GO:0043231,GO:0007093	CG17249-PA						PF10253						656~676								
aly4966.13	Coiled-coil domain-containing protein 124	GO:0005737,GO:0030496,GO:0051301,GO:0007049,GO:0005815	CG6013-PA						PF06244						73~105,46~70								
aly4966.14	Diphthamide biosynthesis protein 2	GO:0017183,GO:0005737	CG7265-PA					TIGR00322,TIGR00272	PF01866										UPA00559				
aly4966.15	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4966.16	14 kDa phosphohistidine phosphatase	GO:0008969,GO:0035774,GO:0007548,GO:2000249,GO:0070062,GO:0019855,GO:0006470,GO:0005829,GO:0051350,GO:0050860,GO:0004721,GO:0005575,GO:0003674,GO:2000147,GO:0035971,GO:2000984,GO:0044325	CG7933-PB						PF05005					SSF143724									
aly4966.17	Uncharacterized protein C19orf47 homolog		CG16812-PA										G3DSA:1.10.150.50	SSF47769									
aly4966.18	Unknown		n/a																				
aly4966.19	Unknown		n/a																				
aly4966.2	COP9 signalosome complex subunit 2	GO:0005737,GO:0000122,GO:0006909,GO:0005515,GO:0030182,GO:0051726,GO:0005634,GO:0003714,GO:0035257,GO:1903507,GO:0050821,GO:0045892,GO:0007165,GO:0004871,GO:0008231,GO:0007095,GO:0022008,GO:0042803,GO:0016922,GO:0008180	CG9556-PA				SM00753,SM00088		PF01399				G3DSA:1.10.10.10,G3DSA:1.25.40.10	SSF46785									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4966.20	Insulin-like growth factor-binding protein complex acid labile subunit	GO:0007155,GO:0042567,GO:0005654,GO:0070062	CG7896-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13306,PF13855,PF13855,PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058	81~101								
aly4966.21	Unknown		n/a																				
aly4966.22	Immunoglobulin-binding protein 1	GO:0005737,GO:2001234,GO:0060632,GO:0034047,GO:0031434,GO:0009966,GO:0005829,GO:0000122,GO:0042113,GO:0032873,GO:0035308,GO:0043154,GO:0051721,GO:0034612,GO:0045944,GO:0019904,GO:0008601,GO:0022008,GO:0005874,GO:0070555,GO:0035306	CG31852-PA						PF04177						162~182								
aly4966.3	Ribonucleoside-diphosphate reductase subunit M2	GO:0005971,GO:0005737,GO:0009186,GO:0006919,GO:0004748,GO:0006260,GO:0022008,GO:0046872,GO:0055114	CG8975-PA						PF00268			PS00368	G3DSA:1.10.620.20	SSF47240		00230+1.17.4.1,00480+1.17.4.1,00240+1.17.4.1	REACT_1698	PWY-7210,PWY-7198,PWY-7220,PWY-7184,PWY-7222,PWY-7226,PWY-7227,PWY-6545	UPA00326				
aly4966.4	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	GO:0006487,GO:0016021,GO:0008250,GO:0035010,GO:0016757,GO:0004579	CG6370-PA						PF05817,PF05817							00513+2.4.99.18,00510+2.4.99.18			UPA00378				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4966.5	ATP synthase subunit g, mitochondrial	GO:0000276,GO:0015992,GO:0005811,GO:0005753,GO:0015986,GO:0008553,GO:0015078	CG6105-PA			PIRSF017835			PF04718														
aly4966.6	28S ribosomal protein S29, mitochondrial	GO:0005654,GO:0008637,GO:0015935,GO:0005730,GO:0044822,GO:0006915,GO:0005739,GO:0032543,GO:0003735,GO:0005743,GO:0005761,GO:0005763,GO:0006412	CG3633-PA						PF10236		PR01716,PR01716,PR01716,PR01716,PR01716,PR01716,PR01716,PR01716		G3DSA:3.40.50.300,G3DSA:3.40.50.300										
aly4966.7	Unconventional prefoldin RPB5 interactor	GO:0006457,GO:0071383,GO:0010923,GO:0030425,GO:0005739,GO:0016272,GO:0005737,GO:0000122,GO:0009615,GO:0005634,GO:0051082,GO:2001243,GO:0019212,GO:0001106,GO:0001558,GO:0004864,GO:0071363,GO:0007283,GO:0005700,GO:0006357,GO:0005665,GO:0006351,GO:0003682	CG11416-PA						PF02996				G3DSA:1.10.287.370	SSF46579	92~119,261~288								
aly4966.8	Neuroblastoma-amplified sequence	GO:0005737,GO:0005794,GO:0006890,GO:0005783,GO:0200623,GO:0000149,GO:0016020,GO:0031965,GO:0005789,GO:0000956,GO:0070939,GO:0005515,GO:0015031,GO:0005730	n/a						PF15492,PF08314,PF08314				G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978									
aly4966.9	Neuroblastoma-amplified sequence	GO:0005737,GO:0005794,GO:0006890,GO:0005783,GO:0200623,GO:0000149,GO:0016020,GO:0031965,GO:0005789,GO:0000956,GO:0070939,GO:0015031,GO:0005730	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4975.1	Unknown	GO:0016324,GO:0007605,GO:0005886,GO:0007293,GO:0007297,GO:0035324	CG13636-PA																				
aly4975.2	Protein HGH1 homolog	GO:0005575,GO:0008150,GO:0003674	CG6073-PA						PF04064,PF04063				G3DSA:1.25.10.10	SSF48371									
aly4975.3	Gametocyte-specific factor 1	GO:0046872	CG34283-PA						PF05253,PF05253					SSF57667									
aly4975.4	Inactive peptidyl-prolyl cis-trans isomerase shutdown	GO:0005737,GO:0003755,GO:0006457,GO:0070725,GO:0051321,GO:0051879,GO:0016020,GO:0005528,GO:0031047,GO:0005515,GO:0043186,GO:0034587,GO:0048477,GO:0018208	CG4735-PA				SM00028,SM00028		PF07719,PF00254	PS50059,PS50293,PS50005			G3DSA:3.10.50.40,G3DSA:1.25.40.10	SSF54534,SSF48452									
aly4975.5	Multiple coagulation factor deficiency protein 2 homolog	GO:0005794,GO:0032504,GO:0005783,GO:0005793,GO:0005509,GO:0015031,GO:0016192,GO:0005615	CG17271-PA						PF13499			PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									
aly4975.6	Unknown	GO:0005509	n/a							PS50222		PS00018	G3DSA:1.10.238.10	SSF47473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4975.7	Cholesterol desaturase daf-36	GO:0005737,GO:0047598,GO:0008203,GO:0051537,GO:0016021,GO:0007552,GO:0046872,GO:0035264,GO:0045456,GO:0002168,GO:0055114,GO:0016491	CG40050-PA						PF00355	PS51296			G3DSA:2.102.10.10	SSF55961,SSF50022									
aly4975.8	Unknown		n/a																				
aly4975.9	Unknown		n/a																				
aly498.1	Solute carrier family 22 member 1	GO:0005333,GO:0005277,GO:0006855,GO:0015651,GO:0005329,GO:0010248,GO:0005215,GO:0016021,GO:0016020,GO:0051260,GO:0016323,GO:0048241,GO:0015101,GO:0044281,GO:0005887,GO:0015874,GO:0015872,GO:0015695,GO:0005886,GO:0008513,GO:0055085	CG7458-PA						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly498.2	Solute carrier family 22 member 21	GO:0015879,GO:0015226,GO:0016021,GO:1902603,GO:0005777,GO:0008513,GO:0031231,GO:0055085,GO:0005524	CG7442-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly498.3	Carbonyl reductase [NADPH] 3	GO:0005737,GO:0000253,GO:0005615,GO:0042376,GO:0005829,GO:0050890,GO:0005654,GO:0004090,GO:0008152,GO:0070402,GO:0016491	CG2064-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly498.4	(+)-neomenthol dehydrogenase	GO:0006952,GO:0047501,GO:0008152,GO:0016491	n/a						PF00106		PR00081,PR00081,PR0081		G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735									
aly498.5	Carbonyl reductase [NADPH] 3	GO:0005737,GO:0000253,GO:0005615,GO:0042376,GO:0005829,GO:0050890,GO:0005654,GO:0004090,GO:0008152,GO:0070402,GO:0016491	CG11200-PB						PF00106,PF00106		PR00080,PR00080,PR0080,PR00081,PR00081,PR00081,PR00081,PR0081		G3DSA:3.40.50.720	SSF51735									
aly498.6	Carbonyl reductase [NADPH] 3	GO:0005737,GO:0000253,GO:0005615,GO:0042376,GO:0005829,GO:0050890,GO:0005654,GO:0004090,GO:0008152,GO:0070402,GO:0016491	CG2064-PA						PF00106,PF00106		PR00080,PR00080,PR0080,PR00081,PR00081,PR00081,PR00081,PR0081		G3DSA:3.40.50.720	SSF51735									
aly498.7	Unknown		n/a																				
aly498.8	Lachesin	GO:0007424,GO:0016331,GO:0035151,GO:0043005,GO:0050767,GO:0009986,GO:0019991,GO:0035160,GO:0042803,GO:0005918,GO:0061343,GO:0005515,GO:0005886,GO:0016337,GO:0007156,GO:0043025,GO:0031225	CG14521-PA				SM00408,SM00408,SM00408,SM00406,SM00409,SM00409,SM00409		PF00047,PF07679,PF07679	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4988.1	Probable phosphoglucomutase-2	GO:0005975,GO:0005978,GO:0005829,GO:0000287,GO:0016052,GO:0004614,GO:0004615,GO:0016868,GO:0006006,GO:0019388	CG8073-PA						PF02878				G3DSA:3.40.120.10	SSF53738		00520+5.4.2.10		PWY-6749					
aly4988.2	Acylphosphatase-2	GO:0006796,GO:0003998,GO:0005739	CG14022-PA						PF00708	PS51160	PR00112,PR00112,PR00112		G3DSA:3.30.70.100	SSF54975		00620+3.6.1.7,00627+3.6.1.7							
aly4988.3	Unknown	GO:0070073,GO:0043195,GO:0042734,GO:0005886,GO:0007270,GO:0007274	CG14021-PB						PF15993														
aly4988.4	Unknown	GO:0070073,GO:0043195,GO:0042734,GO:0005886,GO:0007270,GO:0007274	CG14021-PB						PF15993														
aly4988.5	ATP-dependent DNA helicase pif1	GO:0000723,GO:0006310,GO:0006281,GO:0003677,GO:0003678,GO:0005524	CG3238-PA						PF05970				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540									
aly4988.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly4988.7	PCTP-like protein	GO:0031514,GO:0032782,GO:0016020,GO:0008289,GO:0035360,GO:0005902,GO:0046581,GO:0005829	n/a						PF01852	PS50848			G3DSA:3.30.530.20	SSF55961									
aly4988.8	Unknown	GO:0070073,GO:0043195,GO:0042734,GO:0005886,GO:0007270,GO:0007274	CG14021-PB						PF15993														
aly4988.9	Unknown	GO:0070073,GO:0043195,GO:0042734,GO:0005886,GO:0007270,GO:0007274	CG14021-PB						PF15993														
aly499.1	2-oxoglutarate dehydrogenase, mitochondrial	GO:0030976,GO:0009353,GO:0006096,GO:0006099,GO:0031966,GO:0005759,GO:0004591,GO:0006091,GO:0046872,GO:0005875,GO:0055114	CG11661-PA			PIRSF000157	SM00861	TIGR00239	PF16870,PF00676,PF16078,PF02779				G3DSA:3.40.50.970,G3DSA:3.40.50.970	SSF52518,SSF52518	541~561	00380+1.2.4.2,00020+1.2.4.2,00310+1.2.4.2		PWY-5084					
aly499.10	Translocation protein SEC63 homolog	GO:0008565,GO:0005785,GO:0006620,GO:0005047,GO:0016020,GO:0044822,GO:0006614,GO:0045169,GO:0006807,GO:0010259,GO:0001889,GO:0031204,GO:0072001,GO:0005789,GO:0016021	CG8583-PA				SM00611,SM00973,SM00271		PF00226,PF02889	PS50076	PR00625,PR00625		G3DSA:1.10.287.110,G3DSA:1.10.150.20,G3DSA:1.10.3380.10	SSF158702,SSF46565									
aly499.11	Iron-sulfur cluster assembly 1 homolog, mitochondrial	GO:0046872,GO:0051536,GO:0016226,GO:0005739,GO:0005198	CG8198-PB					TIGR00049	PF01521			PS01152	G3DSA:2.60.300.12	SSF89360									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.12	39S ribosomal protein L55, mitochondrial	GO:0005730,GO:0003700,GO:0005634,GO:0005739,GO:0007275,GO:0003735,GO:0005762,GO:0006412,GO:0003729	CG14283-PA						PF09776				G3DSA:3.30.780.10										
aly499.13	CTL-like protein 1	GO:0005575,GO:0003674,GO:0016021,GO:0008150	CG1311-PA						PF04515								REACT_20679,REACT_15518						
aly499.14	Ribosome biogenesis protein BRX1 homolog	GO:0042273,GO:0005730,GO:0019843,GO:0003674,GO:0003723,GO:0022008,GO:0000027	CG32253-PA				SM00879		PF04427	PS50833				SSF52954									
aly499.15	D-2-hydroxyglutarate dehydrogenase, mitochondrial	GO:0032025,GO:0044267,GO:0050660,GO:0008762,GO:0005739,GO:0003824,GO:0055114,GO:0010043,GO:0010042,GO:0051990	CG3835-PB						PF01565,PF02913	PS51387			G3DSA:3.30.43.10,G3DSA:3.30.465.10,G3DSA:1.10.45.10	SSF55103,SSF56176		00520+1.3.1.98,00550+1.3.1.98		PWY-6386,PWY-6387	UPA00219				
aly499.16	Polyadenylate-binding protein-interacting protein 1	GO:0031987,GO:0005737,GO:0000288,GO:0000289,GO:0042048,GO:0048854,GO:0005829,GO:0010467,GO:0001964,GO:0003723,GO:0048255,GO:0008494,GO:0002121,GO:0045727,GO:0006413,GO:0005488	CG8963-PA										G3DSA:1.25.40.180	SSF48371									
aly499.17	Cytochrome c-type heme lyase	GO:0009887,GO:0004408,GO:0018063,GO:0005739,GO:0005743,GO:0046872,GO:0055114	CG6022-PA						PF01265			PS00821,PS00822				00860+4.4.1.17							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.18	BRCA1-A complex subunit BRE	GO:0005737,GO:0031572,GO:0006302,GO:0005634,GO:0006915,GO:0070552,GO:0031593,GO:0070531,GO:0010212,GO:0045739,GO:0016568	n/a						PF06113														
aly499.19	Uncharacterized protein YJR142W	GO:0016787,GO:0004788,GO:0008152,GO:0044715	CG12567-PA						PF15916,PF00293	PS51462			G3DSA:3.90.79.10	SSF55811									
aly499.2	Calcium uptake protein 1 homolog, mitochondrial	GO:0005758,GO:0005509,GO:0051561,GO:0006816	CG4495-PB				SM00054,SM00054		PF13202,PF13833	PS50222,PS50222,PS50222		PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473,SSF47473									
aly499.20	Methionine aminopeptidase 2	GO:0005737,GO:0004177,GO:0070084,GO:0070006,GO:0006508,GO:0046872,GO:0008235	CG4008-PC	MF_03175				TIGR00501	PF00557		PR00599,PR00599,PR00599,PR00599	PS01202	G3DSA:3.90.230.10,G3DSA:3.90.230.10,G3DSA:1.10.10.10	SSF46785,SSF55920,SSF55920									
aly499.21	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.22	cAMP-specific 3',5'-cyclic phosphodiesterase, isoform I	GO:0048675,GO:0009187,GO:0006198,GO:0048149,GO:0007619,GO:0004114,GO:0007617,GO:0007614,GO:0007612,GO:0007613,GO:0007611,GO:0007165,GO:0046958,GO:0019933,GO:0001661,GO:0040040,GO:0008355,GO:0000003,GO:0004115,GO:0046872,GO:0048477,GO:0007623,GO:0008306,GO:0045475,GO:0007268,GO:0005622,GO:0046331,GO:0010738	CG32498-PB																				
aly499.23	cAMP-specific 3',5'-cyclic phosphodiesterase, isoforms N/G	GO:0048675,GO:0009187,GO:0006198,GO:0048149,GO:0007619,GO:0004114,GO:0007617,GO:0007614,GO:0007612,GO:0007613,GO:0007611,GO:0007165,GO:0046958,GO:0019933,GO:0001661,GO:0040040,GO:0008355,GO:0000003,GO:0004115,GO:0046872,GO:0048477,GO:0007623,GO:0008306,GO:0045475,GO:0007268,GO:0005622,GO:0046331,GO:0010738	CG32498-PB				SM00471		PF00233		PR00387,PR00387,PR00387,PR00387,PR00387	PS00126	G3DSA:1.10.1300.10	SSF109604									
aly499.24	Serine/threonine-protein kinase Nek8	GO:0005737,GO:0005856,GO:0006468,GO:0007017,GO:0004672,GO:0009887,GO:0097543,GO:0004674,GO:0048812,GO:0097546,GO:0004702,GO:0046872,GO:0035330,GO:0072372,GO:0005524	CG10951-PA			PIRSF000654	SM00220		PF00069	PS50011	PR00109,PR00109,PR00109	PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly499.25	U2 small nuclear ribonucleoprotein A'	GO:0030532,GO:0071011,GO:0071013,GO:0000398,GO:0007052,GO:0003723,GO:0005686,GO:0007067,GO:0006397,GO:0008380,GO:0005681,GO:0003729	CG1406-PA						PF14580				G3DSA:3.80.10.10	SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.26	NADH dehydrogenase [ubiqui] 1 beta subcomplex subunit 7	GO:0008137,GO:0005739,GO:0006120,GO:0005743,GO:0005747,GO:0005758,GO:0070469,GO:0003954	CG5548-PA						PF05676														
aly499.27	Helicase ARIP4	GO:0006281,GO:0003677,GO:0005634,GO:0005524,GO:0004386	CG4049-PA				SM00490,SM00487		PF00271,PF00176	PS51194,PS51192			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	667~687								
aly499.28	Unknown	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG32029-PA						PF00379	PS51155		PS00233											
aly499.29	Deoxyribose-phosphate aldolase	GO:0005737,GO:0004139,GO:0046386,GO:0005634,GO:0016052,GO:0003824,GO:0046121,GO:0009264,GO:0070062	CG8525-PA						PF01791				G3DSA:3.20.20.70	SSF51569									
aly499.3	PDZ and LIM domain protein 3	GO:0030239,GO:0007498,GO:0051371,GO:0008157,GO:0008270,GO:0005515,GO:0030018	CG6416-PE				SM00228,SM00735		PF15936,PF00595	PS50106			G3DSA:2.30.42.10	SSF50156									
aly499.30	2-succinylbenzoate--CoA ligase	GO:0008756,GO:0009234,GO:0016207,GO:0005524,GO:0008152	CG8834-PB						PF00501				G3DSA:3.40.50.980,G3DSA:2.30.38.10	SSF56801									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.31	Unknown	GO:0007157,GO:0005576,GO:0003674,GO:0005515,GO:0031225	CG14064-PA							PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726									
aly499.32	Unknown		n/a																				
aly499.33	Zinc finger matrin-type protein 2	GO:0005634,GO:0008270,GO:0003676,GO:0003677	CG11586-PA				SM00451		PF12171					SSF57667	19~39,117~167								
aly499.34	Unknown		n/a																				
aly499.35	Unknown		n/a										G3DSA:1.10.760.10	SSF46689	41~61								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.36	Rapamycin-insensitive companion of mTOR	GO:0051124,GO:0031932,GO:0033135,GO:0009790,GO:0018105,GO:0005488,GO:0043087,GO:0051896,GO:0030838,GO:0031532,GO:0051897,GO:2000114,GO:0050727,GO:0043022,GO:0010468,GO:0031929,GO:0019901,GO:0032956,GO:0006974,GO:0050731,GO:0001938,GO:0048813,GO:0032008,GO:0001932	CG8002-PA						PF14668,PF14664,PF14663,PF14666				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371	1389~1409								
aly499.37	Oocyte zinc finger protein XlCOF28 (Fragment)	GO:0005737,GO:0005819,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0005876,GO:0006351	CG8474-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57716									
aly499.38	Prothoracicotropic hormone	GO:0007218	n/a										G3DSA:2.10.90.10	SSF57501									
aly499.39	Zinc finger protein 714	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG3407-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF13912,PF13912,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57716,SSF57667									
aly499.4	E3 ubiquitin-protein ligase MARCH8	GO:0005764,GO:0005765,GO:0016874,GO:0016021,GO:0035220,GO:0002376,GO:0030659,GO:0022416,GO:0004842,GO:0008270,GO:0005768,GO:0031901	CG4080-PA				SM00744		PF12906	PS51292			G3DSA:3.30.40.10	SSF57850					UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.40	Unknown		n/a																				
aly499.41	Putative ATPase N2B	GO:0016887,GO:0005524	CG8520-PA						PF03969				G3DSA:3.40.50.300	SSF52540									
aly499.42	General transcription factor IIE subunit 1	GO:0043565,GO:0045111,GO:0006355,GO:0005634,GO:0005654,GO:0005673,GO:0045944,GO:0006367,GO:0046872	CG10415-PA				SM00531		PF11521,PF02002	PS51344			G3DSA:3.30.40.10	SSF57783	49~69								
aly499.43	Tyrosine-protein kinase transmembrane receptor Ror2	GO:0006468,GO:0042052,GO:0072499,GO:0016021,GO:0046716,GO:0004714,GO:0004713,GO:0018108,GO:0005886,GO:0007169,GO:0005524,GO:0007165	CG4007-PA				SM00130,SM00219		PF00051,PF07714,PF01392	PS50070,PS50011,PS50038	PR00109,PR00109,PR00109,PR00109,PR00109,PR00018,PR00018,PR00018,PR00018	PS00107,PS00021,PS00109	G3DSA:2.40.20.10,G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF57440,SSF56112									
aly499.44	Rab-like protein 3	GO:0006886,GO:0003924,GO:0005622,GO:0005575,GO:0032482,GO:0008150,GO:0008152,GO:0007264,GO:0005525	CG4789-PA				SM00175,SM00174,SM00173		PF00071	PS51419			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	106~126		REACT_11044						
aly499.45	Beta-1,3-glucan-binding protein	GO:0005975,GO:0008329,GO:0002758,GO:0045087,GO:0006955,GO:0030247,GO:0001530,GO:0050832,GO:0046658,GO:0050830,GO:0005576,GO:0005515,GO:0009253,GO:0050829,GO:0052736,GO:0004553,GO:0042834,GO:0001872	CG6895-PA						PF00722				G3DSA:2.60.120.200,G3DSA:2.60.120.200	SSF49899,SSF49899									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.46	Beta-1,3-glucan-binding protein	GO:0005975,GO:0008329,GO:0002758,GO:0045087,GO:0004553,GO:0030247,GO:0001530,GO:0050832,GO:0046658,GO:0050830,GO:0005576,GO:0001872,GO:0005515,GO:0009253,GO:0050829,GO:0052736,GO:0042834,GO:0006955	CG6895-PA						PF00722				G3DSA:2.60.120.200,G3DSA:2.60.120.200	SSF49899,SSF49899	375~375								
aly499.47	Uncharacterized protein C2orf47 homolog, mitochondrial	GO:0005739	CG3092-PA																				
aly499.48	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	GO:0042645,GO:0006909,GO:0006099,GO:0005739,GO:0009353,GO:0031625,GO:0048037,GO:0004147,GO:0046949,GO:0043754	CG5599-PA						PF00364,PF02817,PF00198	PS50968		PS00189	G3DSA:2.40.50.100,G3DSA:3.30.559.10,G3DSA:4.10.320.10	SSF47005,SSF51230,SSF52777									
aly499.49	Blood vessel epicardial substance	GO:0005923,GO:0089717,GO:0034446,GO:0071944,GO:0043087,GO:0031227,GO:0005737,GO:0003201,GO:0016021,GO:0016020,GO:0051260,GO:0005198,GO:0048471,GO:0001921,GO:0016328,GO:0008360,GO:0005886,GO:0090136,GO:0090132,GO:0016192,GO:0040017,GO:0044214,GO:0005623	CG32513-PA						PF04831				G3DSA:2.60.120.10	SSF51206									
aly499.5	Nucleolar and coiled-body phosphoprotein 1	GO:0005737,GO:0005730,GO:0044822,GO:0005654,GO:0006364,GO:0005524,GO:0015030,GO:0007067,GO:0007000,GO:0007049,GO:0005525	n/a						PF05022														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.50	Popeye domain-containing protein 3	GO:0016021,GO:0016020	CG32513-PA						PF04831														
aly499.51	Probable cation-transporting ATPase 13A3	GO:0042625,GO:0000166,GO:0006812,GO:0016021,GO:0016020,GO:0019829,GO:0016887,GO:0046872,GO:0005524	CG32000-PH					TIGR01657,TIGR01494,TIGR01494	PF00122,PF12409,PF12710,PF00690		PR00119,PR00119,PR00119,PR00119	PS00154	G3DSA:3.40.1110.10,G3DSA:3.40.1110.10,G3DSA:3.40.50.1000,G3DSA:3.40.50.1000,G3DSA:2.70.150.10	SSF81665,SSF81665,SSF81665,SSF56784,SSF56784,SSF56784,SSF81653,SSF81660,SSF81660									
aly499.52	Sodium channel protein Nach	GO:0005272,GO:0016021,GO:0016020,GO:0006814,GO:0035002,GO:0002121,GO:0008049,GO:0019236	CG8527-PC						PF00858		PR01078,PR01078,PR01078,PR01078		G3DSA:2.60.470.10,G3DSA:2.60.470.10,G3DSA:1.10.287.770										
aly499.53	Adenylate kinase 7	GO:0005737,GO:0007420,GO:0035082,GO:0005829,GO:0004127,GO:0002437,GO:0007283,GO:0004550,GO:0004017,GO:0006165,GO:0005634,GO:0003351,GO:0009142,GO:0005524	n/a						PF13207,PF05186				G3DSA:3.40.50.720,G3DSA:3.40.50.300	SSF51735,SSF52540	695~715,588~622								
aly499.54	Band 4.1-like protein 5	GO:0007492,GO:0048617,GO:0031032,GO:0008258,GO:0019898,GO:0070986,GO:0003383,GO:0007390,GO:0022408,GO:0051894,GO:0005737,GO:0032091,GO:0035088,GO:0005925,GO:0007509,GO:0010608,GO:0005634,GO:0009826,GO:0032525,GO:0010718,GO:0005856,GO:0070201,GO:0032092,GO:0048319,GO:0048339,GO:0016323,GO:0005915,GO:0001701,GO:0005886,GO:0046665,GO:0032587,GO:0005918,GO:0010634,GO:0001839,GO:0008092,GO:0007398,GO:0007391,GO:0001837,GO:0071560,GO:0042462,GO:0006931	CG9764-PA						PF08736,PF09380	PS50057			G3DSA:2.30.29.30	SSF50729									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.55	Eukaryotic translation initiation factor 3 subunit G	GO:0005852,GO:0051726,GO:0016282,GO:0006446,GO:0000166,GO:0001731,GO:0007052,GO:0008270,GO:0003676,GO:0033290,GO:0000022,GO:0003729,GO:0006413,GO:0007067,GO:0003743	CG8636-PA	MF_03006		PIRSF037949	SM00360		PF00076,PF12353	PS50102			G3DSA:3.30.70.330	SSF54928										
aly499.56	Unknown		CG13220-PA																				
aly499.57	Probable tRNA N6-adenosine threonylcarbamoyltransferase, mitochondrial	GO:0004222,GO:0070526,GO:0000408,GO:0005739,GO:0005575,GO:0003674,GO:0016747,GO:0008150,GO:0046872,GO:0002949	CG14231-PB	MF_01445				TIGR00329,TIGR03723	PF00814		PR00789,PR00789,PR00789,PR00789,PR00789,PR00789		G3DSA:3.30.420.40	SSF53067									
aly499.58	Cytochrome P450 302a1, mitochondrial	GO:0007494,GO:0020037,GO:0008258,GO:0016705,GO:0007391,GO:0031966,GO:0005743,GO:0005739,GO:0006697,GO:0008205,GO:0008362,GO:0042767,GO:0009055,GO:0005506,GO:0055114,GO:0007417	CG12028-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly499.59	Unknown	GO:0042302	CG1136-PA						PF00379	PS51155													
aly499.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.60	Protein lethal(3)malignant blood neoplasm 1	GO:0005737,GO:0042387,GO:0040003,GO:0005214,GO:0008010,GO:0035220,GO:0031012,GO:0022416,GO:0005886,GO:0048471,GO:0042302	CG12755-PB						PF00379,PF00379	PS51155,PS51155,PS51257		PS00233											
aly499.61	Endocuticle structural glycoprotein SgAbd-3	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG2555-PA						PF00379	PS51155		PS00233											
aly499.62	Flexible cuticle protein 12	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG6956-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly499.63	Endocuticle structural glycoprotein ABD-5	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34270-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly499.64	Endocuticle structural glycoprotein ABD-5	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG13224-PA						PF00379	PS51155													
aly499.65	Endocuticle structural glycoprotein SgAbd-5	GO:0040003,GO:0005214,GO:0008010,GO:0008012,GO:0031012,GO:0042302	CG10297-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.66	Endocuticle structural protein SgAbd-6	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG32405-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly499.67	Endocuticle structural glycoprotein SgAbd-2	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG30045-PB						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly499.68	Endocuticle structural glycoprotein SgAbd-2	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG30045-PB						PF00379	PS51155		PS00233											
aly499.69	Endocuticle structural glycoprotein SgAbd-2	GO:0040003,GO:0005214,GO:0008010,GO:0031012,GO:0022008,GO:0042302	CG8515-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly499.7	PDZ and LIM domain protein Zasp	GO:0001725,GO:0045177,GO:0015629,GO:0030239,GO:0051371,GO:0005915,GO:0045178,GO:0016323,GO:0003779,GO:0031252,GO:0008270,GO:0005515,GO:0001952,GO:0061061,GO:0005927,GO:0005925,GO:0030018	CG30084-PF				SM00132,SM00132		PF00412,PF00412	PS50023,PS50023		PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716,SSF57716	1566~1572,1511~1531								
aly499.70	Endocuticle structural glycoprotein SgAbd-2	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG8511-PA						PF00379	PS51155		PS00233											

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.71	Unknown		n/a																				
aly499.72	Endocuticle structural glycoprotein ABD-4	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG8505-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly499.73	Larval cuticle protein LCP-22	GO:0040003,GO:0005615,GO:0032504,GO:0005214,GO:0008010,GO:0031012,GO:0042302	CG18348-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly499.74	Larval cuticle protein LCP-30	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG30042-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly499.75	Unknown		n/a																				
aly499.76	Serpin-Z4	GO:0060570,GO:0005783,GO:0006952,GO:0005576,GO:0030162,GO:0045735,GO:0004867,GO:0010951,GO:0004869,GO:0010955,GO:0005615	CG9453-PB						PF00079				G3DSA:3.30.497.10,G3DSA:2.30.39.10	SSF56574										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.77	Unknown		n/a																				
aly499.78	Carbohydrate sulfotransferase 11	GO:0030206,GO:0030204,GO:0030203,GO:0048589,GO:0016232,GO:0008146,GO:0009791,GO:0044281,GO:0016051,GO:0016021,GO:0016020,GO:0036342,GO:0043066,GO:0002063,GO:0033037,GO:0042127,GO:0005794,GO:0048703,GO:0007585,GO:0047756,GO:0001537,GO:0030512,GO:0042733,GO:0050659,GO:0005975,GO:0000139	CG14024-PA						PF03567														
aly499.79	Unknown		n/a												356~376								
aly499.8	PDZ and LIM domain protein Zasp	GO:0001725,GO:0045177,GO:0015629,GO:0030239,GO:0051371,GO:0005915,GO:0045178,GO:0016323,GO:0003779,GO:0031252,GO:0008270,GO:0005515,GO:0001952,GO:0061061,GO:0005927,GO:0005925,GO:0030018	CG30084-PF				SM00132,SM00228,SM00735		PF00595,PF00412,PF15936	PS50023,PS50106			G3DSA:2.30.42.10,G3DSA:2.10.110.10	SSF50156,SSF57716,SSF57716										
aly499.80	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly499.81	Unknown		n/a																				
aly499.82	Unknown		n/a																				
aly499.9	Unknown	GO:0008565,GO:0031204,GO:0005047,GO:0005785,GO:0045169	CG8583-PA																				
aly49924.1	Unknown		n/a																				
aly49954.1	Formin-like protein CG32138	GO:0003779,GO:0005575,GO:0048812,GO:0017048,GO:0030036	CG32138-PA																				
aly49995.1	Formin-like protein CG32138	GO:0003779,GO:0005575,GO:0048812,GO:0017048,GO:0030036	CG32138-PA												9~53								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5.1	Unknown		n/a																				
aly5.10	26S protease regulatory subunit 7	GO:0005737,GO:0004175,GO:0005838,GO:0022624,GO:0043161,GO:0005634,GO:0009987,GO:0017111,GO:0006974,GO:0006511,GO:0030163,GO:0016887,GO:0000502,GO:0006508,GO:0005524,GO:0008540	CG1341-PA						PF00004			PS00674	G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540	415~442								
aly5.11	TBC1 domain family member 31	GO:0032313,GO:0005097	CG16896-PA				SM00320,SM00320,SM00320,SM00320		PF00566	PS50086,PS50294			G3DSA:2.130.10.10	SSF47923,SSF50978	664~687								
aly5.12	Protein phosphatase 1 regulatory subunit 7	GO:0008285,GO:0016336,GO:0016334,GO:0005634,GO:0000164,GO:0005515,GO:0007059,GO:0005694,GO:0008599,GO:0035307,GO:0070062	CG5851-PA				SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly5.13	Fumarylacetoacetase	GO:0006572,GO:0070062,GO:0006559,GO:0005829,GO:0006527,GO:0004334,GO:0003824,GO:0034641,GO:0044281,GO:0008152,GO:0046872,GO:0009072	CG14993-PA						PF01557,PF09298				G3DSA:2.30.30.230,G3DSA:3.90.850.10	SSF56529,SSF63433		00643+3.7.1.2,00350+3.7.1.2			UPA00139				
aly5.14	H/ACA ribonucleoprotein complex non-core subunit NAF1	GO:0005732,GO:0005634,GO:0042254,GO:0006364,GO:0022008,GO:0001522,GO:0003723	CG10341-PA						PF04410				G3DSA:2.40.10.230	SSF50447									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5.15	Protein bric-a-brac 2	GO:0007478,GO:0005515,GO:0007480,GO:0003700,GO:0007455,GO:0005634,GO:0008585,GO:0005701,GO:0006355,GO:0061040,GO:0006351,GO:0003676,GO:0003677,GO:0003680,GO:0005700	CG9102-PA				SM00384,SM00384,SM00384,SM00225,SM00355,SM00355		PF00651	PS50157,PS50097,PS50157	PR00930,PR00930,PR00929,PR00929,PR00929	PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.710.10	SSF54695,SSF57667	733~736,163~183,208~239								
aly5.16	Inositol-3-phosphate synthase	GO:0005737,GO:0004512,GO:0006021,GO:0008654	CG11143-PA			PIRSF015578			PF01658,PF07994				G3DSA:3.40.50.720,G3DSA:3.40.50.720,G3DSA:3.30.360.10	SSF55347,SSF51735,SSF51735		00562+5.5.1.4,00521+5.5.1.4		PWY-2301,PWY-6580,PWY-6372,PWY-4661,PWY-6664	UPA00823				
aly5.17	Atypical protein kinase C	GO:0016332,GO:0055059,GO:0045198,GO:0003382,GO:0016334,GO:0034332,GO:0045197,GO:0045196,GO:0017022,GO:0035003,GO:0007163,GO:0007043,GO:0008270,GO:0007294,GO:0030011,GO:0007309,GO:0035556,GO:0004697,GO:0007416,GO:0045176,GO:0045179,GO:0051491,GO:0090163,GO:0004674,GO:0060446,GO:0072659,GO:0046872,GO:0005524,GO:0006468,GO:0051601,GO:0016324,GO:0016327,GO:0007613,GO:0035011,GO:0045186,GO:0001738,GO:0005938,GO:0046667,GO:0045167,GO:0010592,GO:0000132,GO:0007423,GO:0007283,GO:0002052,GO:0007314,GO:0005515	CG42783-PJ				SM00109		PF00130	PS50081	PR00008,PR00008,PR00008,PR00008	PS00479	G3DSA:3.30.200.20,G3DSA:3.30.60.20	SSF57889										
aly5.18	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5.19	Unknown		n/a																				
aly5.2	Unknown		n/a											SSF53850									
aly5.20	Protein kinase C iota type	GO:0090004,GO:0006612,GO:0045197,GO:0061024,GO:0043524,GO:0046326,GO:0032869,GO:0035556,GO:0043220,GO:0004697,GO:0005923,GO:0005737,GO:0035089,GO:0045171,GO:0070062,GO:0005634,GO:0005543,GO:0004674,GO:0043066,GO:0004672,GO:0016477,GO:0005524,GO:0048194,GO:0042462,GO:0006468,GO:0015630,GO:0051092,GO:0016324,GO:0034351,GO:0031252,GO:2000353,GO:0010976,GO:0045216,GO:0005886,GO:0048011,GO:0060252,GO:0034329,GO:0043234,GO:0007015,GO:0046903,GO:0046872,GO:0007010,GO:0016192,GO:0005829,GO:0070830,GO:0000139,GO:0005515,GO:0005768,GO:0070555	n/a				SM00666		PF00564	PS51745			G3DSA:3.10.20.240	SSF54277										
aly5.21	F-actin-capping protein subunit beta	GO:0010591,GO:0007015,GO:0030832,GO:0071203,GO:0000902,GO:0046982,GO:0051016,GO:0030036,GO:0051490,GO:0003779,GO:0045887,GO:0007303,GO:0051015,GO:0035220,GO:0046329,GO:0007298,GO:0008290,GO:0005737,GO:0005884	CG17158-PB						PF01115		PR00192,PR00192,PR00192,PR00192,PR00192	PS00231		SSF90096	210~230								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5.22	Death domain-associated protein 6	GO:2001235,GO:0097190,GO:0006979,GO:0042981,GO:0016605,GO:0070603,GO:0030521,GO:0005634,GO:0003714,GO:0000281,GO:0000775,GO:0031396,GO:0042803,GO:0008134,GO:0000792,GO:0045892,GO:0045893,GO:1901216,GO:0008340,GO:0030295,GO:0006338,GO:0005829,GO:0005730,GO:0006351,GO:0005515,GO:0006334	CG9537-PA												209~229									
aly5.23	Eukaryotic translation initiation factor 5A	GO:0005737,GO:0006452,GO:0045901,GO:0032504,GO:0045905,GO:0006413,GO:0005829,GO:0035220,GO:0048102,GO:0045182,GO:0003746,GO:0043022,GO:0035071,GO:0008612,GO:0003743	CG3186-PA			PIRSF003025		TIGR00037	PF01287			PS00302	G3DSA:2.30.30.30,G3DSA:2.40.50.140	SSF50104,SSF50249										
aly5.24	Dorsal root ganglia homeobox protein	GO:0043565,GO:0007517,GO:0009593,GO:0016048,GO:0007399,GO:0003700,GO:0050954,GO:0005634,GO:0021516,GO:0021559,GO:0006355,GO:0048813,GO:0001764,GO:0006351,GO:0007409,GO:0003677,GO:0030182,GO:0007411	CG34340-PE				SM00389		PF03826,PF00046	PS50071,PS50803		PS00027	G3DSA:1.10.10.60	SSF46689										
aly5.25	Chromosome transmission fidelity protein 18 homolog	GO:0005737,GO:0008283,GO:0005634,GO:0016020,GO:0017111,GO:0005654,GO:0006260,GO:0007049,GO:0003677,GO:0005524	CG33122-PA				SM00382		PF00004				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	210~230									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5.3	Aquaporin-12	GO:0005737,GO:0005215,GO:0016021,GO:0005575,GO:0006833,GO:0005372	CG12251-PA			PIRSF017529							G3DSA:1.20.1080.10	SSF81338									
aly5.4	Aladin	GO:0016020,GO:0019221,GO:0034605,GO:0019083,GO:0007612,GO:0010827,GO:0003674,GO:0044281,GO:0051028,GO:0005737,GO:0044267,GO:0005813,GO:0005634,GO:0005635,GO:0015758,GO:0010467,GO:0019058,GO:0000278,GO:0043687,GO:0031965,GO:0006913,GO:0007077,GO:0016925,GO:0055085,GO:0005975,GO:0005643,GO:1900034,GO:0009566,GO:0046822,GO:0005515,GO:0008645,GO:0015031,GO:0005654,GO:0016032	CG16892-PB				SM00320,SM00320,SM00320,SM00320		PF00400	PS50294			G3DSA:2.130.10.10	SSF50978									
aly5.5	Unknown	GO:0031941,GO:0009913,GO:0051017,GO:0008407,GO:0003779,GO:0007605,GO:0048800,GO:0035017,GO:0035317	CG42864-PF												230~250								
aly5.6	Espin	GO:0005737,GO:0007626,GO:0031941,GO:0035017,GO:0032420,GO:0009913,GO:0032426,GO:0051494,GO:0051017,GO:0008407,GO:0051015,GO:0017124,GO:0003779,GO:0007605,GO:0048800,GO:0005903,GO:0051491,GO:0005515,GO:0035317,GO:0030046	CG42864-PF				SM00248,SM00248,SM00248,SM00248,SM00248		PF13637,PF12796	PS50297,PS50088,PS50088,PS50088,PS50088			G3DSA:1.25.40.20	SSF48403									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5.7	Protein MCM10 homolog	GO:0045931,GO:1901693,GO:0035214,GO:0051726,GO:0046872,GO:0005634,GO:0006270,GO:0016321,GO:0030261,GO:0042023,GO:0005656,GO:0006267,GO:0006260,GO:0031298,GO:0070868,GO:0003690,GO:0003682,GO:0003697,GO:0045678,GO:0003688	CG9241-PA						PF09329,PF09332														
aly5.8	GMP synthase [glutamine-hydrolyzing]	GO:0043234,GO:0005737,GO:0005829,GO:0003921,GO:0003922,GO:0006541,GO:0005700,GO:0006144,GO:2000152,GO:0016462,GO:0009113,GO:0055086,GO:0009168,GO:0007411,GO:0035800,GO:0006177,GO:0016578,GO:0005524,GO:0044281	CG9242-PB					TIGR00888	PF00117,PF02540,PF00958	PS51553,PS51273	PR00097,PR00097,PR00097,PR00096,PR00096,PR00096		G3DSA:3.40.50.880,G3DSA:3.30.300.10,G3DSA:3.30.300.10,G3DSA:3.40.50.620	SSF52317,SSF54810,SSF54810,SSF52402		00983+6.3.5.2,00230+6.3.5.2	REACT_1698	PWY-7221	UPA00189				
aly5.9	26S protease regulatory subunit 7	GO:0005737,GO:0004175,GO:0005838,GO:0022624,GO:0043161,GO:0005634,GO:0009987,GO:0000932,GO:0017111,GO:0006974,GO:0006511,GO:0030163,GO:0016887,GO:0000502,GO:0006508,GO:0005524,GO:0008540	CG1341-PA																				
aly50.1	TAR DNA-binding protein 43	GO:0006351,GO:0003729,GO:0008380,GO:0048812,GO:0008345,GO:0005634,GO:0000166,GO:0007528,GO:0006355,GO:0006397,GO:0045886,GO:0003723,GO:0003676,GO:0003677,GO:0048471,GO:0007628,GO:0007274,GO:0008344,GO:0007417	CG10327-PB				SM00360,SM00360		PF00076,PF14259	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly50.10	Ras-related protein Rab-10	GO:0055038,GO:0005794,GO:0055037,GO:0045200,GO:0005789,GO:0045202,GO:0007295,GO:0032869,GO:0032593,GO:0071786,GO:0071782,GO:0045175,GO:0072372,GO:0031982,GO:0045178,GO:0043001,GO:0030859,GO:0043025,GO:0005525,GO:0005737,GO:0061467,GO:0031254,GO:0003924,GO:0007264,GO:0032482,GO:0046331,GO:0007409,GO:0072659,GO:0006893,GO:0016192,GO:0030670,GO:0016197,GO:0005802,GO:0097051,GO:0019003,GO:0015031,GO:0005768	CG17060-PA				SM00174,SM00173,SM00176,SM00175,SM00177	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly50.11	Cohesin subunit SA-1	GO:0005721,GO:0016925,GO:0005829,GO:0007067,GO:0044267,GO:0043687,GO:0005634,GO:0001228,GO:0016322,GO:0000922,GO:0005654,GO:0000780,GO:0035327,GO:0007059,GO:0000785,GO:0000775,GO:0003682,GO:0005694,GO:0008278,GO:0051301,GO:0000278	CG3423-PA						PF08514	PS51425				SSF48371,SSF48371,SSF48371,SSF48371	309~348									
aly50.12	Unknown		n/a																				
aly50.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly50.14	BTB/POZ domain-containing protein 19	GO:0005515	CG7102-PA				SM00225,SM00584,SM00875		PF00651,PF07707,PF07534	PS50097			G3DSA:3.30.710.10	SSF54695									
aly50.15	Frizzled-2	GO:0048675,GO:0050808,GO:0035206,GO:0008587,GO:0008585,GO:0006928,GO:0030139,GO:0009790,GO:0007165,GO:0007166,GO:0008045,GO:0007411,GO:0005634,GO:0004930,GO:0007435,GO:0016021,GO:0016020,GO:0001944,GO:0008407,GO:0031290,GO:0007186,GO:0016201,GO:0060070,GO:0030165,GO:0005887,GO:0005886,GO:0042995,GO:0035567,GO:0016477,GO:0007420,GO:0006898,GO:0016055,GO:0042813,GO:0005770,GO:0004888,GO:0006357,GO:0017147,GO:0005769	CG9739-PF						PF01534	PS50261	PR00489,PR00489,PR00489,PR00489						REACT_14797						
aly50.16	Unknown	GO:0043565,GO:0031935,GO:0031519,GO:0009880,GO:0042048,GO:0006342,GO:0005634,GO:0007476,GO:0007315,GO:0008595,GO:0016458,GO:0031208,GO:0003677,GO:0042803	CG2368-PM						PF05225,PF05225	PS50960,PS50960,PS50960				SSF46689,SSF46689										
aly50.17	Longitudinals lacking protein, isoforms H/M/V	GO:0045476,GO:0019730,GO:0035167,GO:0045467,GO:0003676,GO:0007411,GO:0002121,GO:0031987,GO:0005634,GO:0044719,GO:0008406,GO:0005654,GO:0001964,GO:0046872,GO:0045893,GO:0007409,GO:0022008,GO:0007526,GO:0003700,GO:0048854,GO:0007464,GO:0016199,GO:0006355,GO:0048813,GO:0006357,GO:0006351,GO:0005515	CG12052-PI				SM00355,SM00355,SM00225		PF00651	PS50097,PS50157			G3DSA:3.30.710.10	SSF54695									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly50.18	Cytochrome c oxidase assembly protein COX11, mitochondrial	GO:0004129,GO:1902600,GO:0016021,GO:0007585,GO:0005739,GO:0008535,GO:0005743,GO:0033132,GO:0005507,GO:0009055	CG31648-PA	MF_00155					PF04442				G3DSA:2.60.370.10	SSF110111									
aly50.19	Tektin-3	GO:0080154,GO:0060271,GO:0036126,GO:0002080,GO:0000226,GO:0005874,GO:0030317,GO:0046692	CG17450-PB						PF03148		PR00511,PR00511,PR00511,PR00511				376~396,168~195,237~257,319~339								
aly50.2	Serine/threonine-protein kinase MAK	GO:0005737,GO:0006351,GO:0006468,GO:0072686,GO:0006355,GO:0005813,GO:0005634,GO:0030496,GO:0046777,GO:0005575,GO:0004674,GO:0001917,GO:0045494,GO:0004672,GO:0004693,GO:0001750,GO:0005524,GO:0003713	CG42366-PA				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									
aly50.20	Cytosolic Fe-S cluster assembly factor nubp1-A	GO:0046872,GO:0051539,GO:0051536,GO:0000166,GO:0016226,GO:0005829,GO:0005524	CG17904-PA	MF_03038					PF10609			PS01215	G3DSA:3.40.50.300	SSF52540									
aly50.21	FAD-linked sulfhydryl oxidase ALR	GO:0016971,GO:0005737,GO:0016972,GO:0051726,GO:0042246,GO:0005739,GO:0050660,GO:0005758,GO:0015035,GO:0055114	CG12534-PB						PF04777	PS51324			G3DSA:1.20.120.310	SSF69000				PWY-7533					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly50.22	Histone-lysine N-methyltransferase E(z)	GO:0042054,GO:0046974,GO:0046976,GO:0003677,GO:0051567,GO:0007411,GO:0007517,GO:0035186,GO:0006342,GO:0005634,GO:0016458,GO:0016571,GO:0006723,GO:0000790,GO:0045892,GO:0022008,GO:0035098,GO:0070734,GO:0003700,GO:0035097,GO:0048813,GO:0042810,GO:0006351,GO:0005515,GO:0003682	CG6502-PC				SM00317,SM00717		PF00856	PS51633,PS50280			G3DSA:2.170.270.10	SSF46689,SSF82199	182~220	00310+2.1.1.43							
aly50.23	Uncharacterized protein C19orf43	GO:0005751,GO:0004129,GO:0006123,GO:0008340	CG18809-PA																				
aly50.24	Cytochrome c oxidase subunit 6B1	GO:0004129,GO:1902600,GO:0044237,GO:0005751,GO:0005743,GO:0010467,GO:0021762,GO:0005739,GO:0006367,GO:0022904,GO:0005758,GO:0022008,GO:0044281	CG14235-PA			PIRSF000278			PF02297				G3DSA:1.10.10.140	SSF47694									
aly50.25	Unknown		n/a																				
aly50.26	Cytochrome c oxidase subunit 6b-3	GO:0005751,GO:0004129,GO:0022008,GO:0005739	CG14235-PA						PF02297				G3DSA:1.10.10.140	SSF47694	76~76								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly50.27	Oxysterol-binding protein-related protein 11	GO:0005794,GO:0006869,GO:0008289,GO:0010890,GO:0045444,GO:0031902	CG9205-PA				SM00233		PF00169	PS50003			G3DSA:2.30.29.30	SSF50729									
aly50.28	Aprataxin and PNK-like factor	GO:0006974,GO:0008408,GO:0051106,GO:0006302,GO:0045191,GO:0000012,GO:0035861,GO:0005829,GO:0005654,GO:0004520,GO:0000166,GO:0003906,GO:0090305,GO:0005515,GO:0046872,GO:0005634	n/a										G3DSA:2.60.200.20	SSF49879									
aly50.29	Translin-associated protein X	GO:0005737,GO:0043565,GO:0005794,GO:0005634,GO:0030154,GO:0004521,GO:0003697,GO:0090502,GO:0007283,GO:0044822,GO:0048471,GO:0046872,GO:0007275	CG5063-PB						PF01997				G3DSA:1.20.58.190,G3DSA:1.20.58.200	SSF74784	78~98,141~164								
aly50.3	Unknown		n/a						PF13873						168~188								
aly50.30	Actin-related protein 2/3 complex subunit 1A	GO:0005737,GO:0005200,GO:0007010,GO:0000902,GO:0030029,GO:0007413,GO:0030589,GO:0006886,GO:0051015,GO:0008407,GO:0051491,GO:0030037,GO:0003779,GO:0045747,GO:0022416,GO:0005885,GO:0034314,GO:0005515,GO:0030041,GO:0001745,GO:0007409	CG8978-PA			PIRSF038093	SM00320,SM00320,SM00320,SM00320,SM00320		PF00400	PS50294,PS50082			G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly50.31	Brefeldin A-inhibited guanine nucleotide-exchange protein 1	GO:0090303,GO:0005085,GO:0017022,GO:0005086,GO:0034237,GO:0031175,GO:0051897,GO:0005737,GO:0090284,GO:0006888,GO:0043547,GO:0030837,GO:2000114,GO:0010256,GO:0005654,GO:0032012,GO:0016363,GO:0005794,GO:0005730,GO:0007030,GO:0034260,GO:0048471,GO:0006891,GO:0016192,GO:0030532,GO:0005829,GO:0005802,GO:0000139,GO:0005515,GO:0015031	CG7578-PA				SM00222		PF12783,PF09324,PF01369,PF16213	PS50190			G3DSA:1.10.1000.11,G3DSA:1.10.220.20,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48425										
aly50.32	Mitotic checkpoint protein BUB3	GO:0051321,GO:0005634,GO:0005654,GO:0007052,GO:0051301,GO:0007094,GO:0007059,GO:0007067,GO:0000777,GO:0005875,GO:0000776,GO:0007093	CG7581-PB				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400	PS50082,PS50294,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10	SSF50978									
aly50.33	Protein embryonic gonad	GO:0043565,GO:0006351,GO:0030522,GO:0003700,GO:0005634,GO:0030154,GO:0003707,GO:0006355,GO:0008270,GO:0004879,GO:0007417	CG7383-PB				SM00399		PF00105	PS51030	PR00047,PR00047,PR00047,PR00047	PS00031	G3DSA:3.30.50.10,G3DSA:1.10.565.10	SSF57716			REACT_71						
aly50.34	Fatty acid synthase	GO:0006633,GO:0047451,GO:0004320,GO:0008144,GO:0008270,GO:0001649,GO:0005737,GO:0016020,GO:0070062,GO:0016295,GO:0005811,GO:0071353,GO:0005739,GO:0030879,GO:0005794,GO:0044822,GO:0004315,GO:0009058,GO:0042587,GO:0005886,GO:0055114,GO:0006084,GO:0044240,GO:0047117,GO:0004312,GO:0004313,GO:0016296,GO:0016297,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319	CG3523-PC										G3DSA:1.10.1470.20,G3DSA:3.40.50.1820	SSF53474		00061+1.1.1.100+2.3.1.85+4.2.1.59+2.3.1.39+2.3.1.41+3.1.2.14,00780+1.1.1.100+4.2.1.59+2.3.1.41		PWY-5965,PWY-6113,PWY-6519,PWY-7664,PWY-7388,PWY-5367,PWY-5366,PWY-6799,PWY-5971,PWY-6282,PWY-5147,PWY-5973,PWY-5989,PWY-5966,PWY G-321,PWY-5142,PWY-					
aly50.35	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly50.36	Longitudinals lacking protein, isoforms A/B/D/L	GO:0045476,GO:0019730,GO:0035167,GO:0045467,GO:0003676,GO:0003677,GO:0007411,GO:0002121,GO:0031987,GO:0005634,GO:0044719,GO:0008406,GO:0005654,GO:0001964,GO:0046872,GO:0045893,GO:0007409,GO:0022008,GO:0007526,GO:0003700,GO:0048854,GO:0007464,GO:0016199,GO:0006355,GO:0048813,GO:0006357,GO:0006351,GO:0005515	CG12052-PI				SM00355,SM00355			PS50157,PS50157				SSF57667									
aly50.37	Longitudinals lacking protein, isoform G	GO:0007409,GO:0019730,GO:0035167,GO:0045467,GO:0003677,GO:0007411,GO:0002121,GO:0031987,GO:0005634,GO:0044719,GO:0008406,GO:0005654,GO:0001964,GO:0046872,GO:0045893,GO:0045476,GO:0022008,GO:0007526,GO:0003700,GO:0048854,GO:0007464,GO:0016199,GO:0006355,GO:0048813,GO:0006351	CG44025-PB				SM00355,SM00355			PS50157			G3DSA:3.30.160.60	SSF57667									
aly50.38	Longitudinals lacking protein, isoforms A/B/D/L	GO:0007409,GO:0019730,GO:0035167,GO:0045467,GO:0003677,GO:0007411,GO:0002121,GO:0031987,GO:0005634,GO:0044719,GO:0008406,GO:0005654,GO:0001964,GO:0046872,GO:0045893,GO:0045476,GO:0022008,GO:0007526,GO:0003700,GO:0048854,GO:0007464,GO:0016199,GO:0006355,GO:0048813,GO:0006351	CG44025-PB				SM00355,SM00355		PF00096	PS50157			G3DSA:3.30.160.60	SSF57667									
aly50.4	Tryptophan--tRNA ligase, mitochondrial	GO:0005737,GO:0001570,GO:0006436,GO:0005739,GO:0000166,GO:0005759,GO:0004830,GO:0005524	CG7441-PA					TIGR00233	PF00579		PR01039,PR01039,PR01039,PR01039	PS00178	G3DSA:3.40.50.620,G3DSA:1.10.240.10	SSF52374		00970+6.1.1.2	REACT_71						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly50.5	Fatty acid synthase	GO:0047117,GO:0047451,GO:0006633,GO:0005811,GO:0016295,GO:0004320,GO:0016296,GO:0004312,GO:0004313,GO:0009058,GO:0004316,GO:0004317,GO:0004314,GO:0004315,GO:0004319,GO:0055114,GO:0008270	CG3523-PC				SM00822,SM00823,SM00827,SM00825,SM00829,SM00826		PF00550,PF08659,PF02801,PF00107,PF00698,PF00698,PF14765,PF16197,PF00975,PF00109	PS50075		PS00606	G3DSA:3.90.180.10,G3DSA:3.40.50.1820,G3DSA:3.40.366.10,G3DSA:3.40.50.720,G3DSA:3.40.47.10,G3DSA:3.40.50.720,G3DSA:1.10.1200.10,G3DSA:3.40.47.10	SSF53474,SSF50129,SSF51735,SSF51735,SSF52151,SSF47336,SSF53901,SSF53901										
aly50.6	Myosin-3	GO:0005737,GO:0045927,GO:0042623,GO:0042067,GO:0008586,GO:0035220,GO:0035218,GO:0003774,GO:0016459,GO:0009506,GO:0030048,GO:0005886,GO:0045572,GO:0001736,GO:0005524	CG42840-PE				SM00242		PF00063,PF00063	PS51456				SSF52540									
aly50.7	Unknown		n/a												19~39								
aly50.8	Proteasome subunit alpha type-6	GO:0005737,GO:0030016,GO:0004175,GO:0005839,GO:0005844,GO:0019773,GO:0005634,GO:0005654,GO:0000932,GO:0010499,GO:0004298,GO:0006974,GO:0030017,GO:0006511,GO:0051603,GO:0003723,GO:0043161,GO:0051092,GO:0016363,GO:0070062	CG30382-PA				SM00948		PF10584,PF00227	PS51475		PS00388	G3DSA:3.60.20.10	SSF56235			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045							
aly50.9	Unknown	GO:0016787,GO:0046872,GO:0003676	CG14120-PA										G3DSA:3.40.570.10	SSF54060									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5005.1	Inositol 1,4,5-trisphosphate receptor type 1	GO:0016319,GO:0030322,GO:0005635,GO:0005783,GO:0005262,GO:0005220,GO:0007591,GO:0050849,GO:0005789,GO:0009791,GO:0042594,GO:0005218,GO:0050909,GO:0005737,GO:0031094,GO:0001666,GO:0019855,GO:0005730,GO:0005637,GO:0016021,GO:0016020,GO:0000280,GO:0051209,GO:0032469,GO:0060259,GO:0042045,GO:0050882,GO:0006874,GO:0006816,GO:0007629,GO:0055089,GO:0014069,GO:0006979,GO:0005955,GO:0048016,GO:0043234,GO:0030536,GO:0070059,GO:0035091,GO:0070588,GO:0031088,GO:0016529	CG1063-PB																					
aly5007.1	Apyrase	GO:0016787,GO:0008253,GO:0017110,GO:0017111,GO:0016788,GO:0000166,GO:0009166,GO:0005576,GO:0046872,GO:0005524	CG1961-PA						PF02872		PR01607,PR01607,PR01607		G3DSA:3.60.21.10,G3DSA:3.90.780.10	SSF55816,SSF56300									
aly5007.2	Apyrase	GO:0016787,GO:0008253,GO:0017110,GO:0017111,GO:0016788,GO:0000166,GO:0009166,GO:0005576,GO:0046872,GO:0005524	CG1961-PA						PF00149,PF02872		PR01607,PR01607,PR01607,PR01607		G3DSA:3.90.780.10,G3DSA:3.60.21.10	SSF56300,SSF55816									
aly5007.3	Apyrase	GO:0016787,GO:0008253,GO:0017110,GO:0017111,GO:0016788,GO:0000166,GO:0009166,GO:0005576,GO:0046872,GO:0005524	CG42249-PC						PF00149,PF02872		PR01607,PR01607,PR01607,PR01607,PR01607,PR01607		G3DSA:3.90.780.10,G3DSA:3.60.21.10	SSF55816,SSF56300									
aly5007.4	TWiK family of potassium channels protein 18	GO:0040011,GO:0005267,GO:0006936,GO:0071805,GO:0006813,GO:0016021,GO:0016020,GO:0015271	CG42594-PB						PF07885,PF07885		PR01333,PR01333		G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324,SSF81324									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5007.5	Unknown	GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG33966-PA										G3DSA:3.40.525.10	SSF46938									
aly5013.1	Alpha-centractin	GO:0005737,GO:0019896,GO:0005200,GO:0007010,GO:0015629,GO:0043209,GO:0005813,GO:0070062,GO:0008089,GO:0003779,GO:0005884,GO:0005869,GO:0007067,GO:0005875,GO:0005524,GO:0008090	CG6174-PA						PF00022			PS00432	G3DSA:3.30.420.40	SSF53067									
aly502.1	CDC42 small effector protein homolog	GO:0005856,GO:0009966,GO:0035023,GO:0017048,GO:0005198,GO:0008360,GO:0005938,GO:0005886,GO:0007165	CG14672-PA						PF00786	PS50108			G3DSA:3.90.810.10										
aly502.2	Trithorax group protein osa	GO:0035060,GO:0007476,GO:0008587,GO:0008586,GO:0042058,GO:0003677,GO:0014017,GO:0005634,GO:0003713,GO:0005654,GO:0048190,GO:0007480,GO:0045893,GO:0007406,GO:0022008,GO:0006338,GO:0007379,GO:0016055,GO:0046530,GO:0006355,GO:0006357,GO:0006351	CG7467-PD						PF12031					SSF48371	1407~1427,820~840,947~974								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly502.3	Trithorax group protein osa	GO:0035060,GO:0007476,GO:0008587,GO:0008586,GO:0042058,GO:0003677,GO:0014017,GO:0005634,GO:0003713,GO:0005654,GO:0048190,GO:0007480,GO:0045893,GO:0007406,GO:0022008,GO:0006338,GO:0007379,GO:0016055,GO:0046530,GO:0006355,GO:0006357,GO:0006351	CG7467-PD				SM00501,SM01014		PF01388	PS51011			G3DSA:1.10.150.60	SSF46774									
aly502.4	Unknown	GO:0035060,GO:0048190,GO:0007480,GO:0007379,GO:0008587,GO:0005634,GO:0016055,GO:0003713,GO:0008586,GO:0042058,GO:0046530,GO:0006355,GO:0045893,GO:0003677,GO:0022008,GO:0007476	CG7467-PD								PR01217,PR01217,PR01217,PR01217,PR01217,PR01217												
aly502.5	Katanin p60 ATPase-containing subunit A-like 1	GO:0005737,GO:0030336,GO:0035220,GO:0007017,GO:0051013,GO:0005813,GO:0008017,GO:0000091,GO:0007019,GO:0017022,GO:0008568,GO:0070462,GO:0031252,GO:0000070,GO:0005938,GO:0005874,GO:0008352,GO:0031122,GO:0005694,GO:0005524,GO:0022416	CG10229-PB	MF_03023			SM00382		PF00004,PF09336			PS00674	G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540									
aly502.6	Trafficking protein particle complex subunit 10	GO:0006891,GO:0043204,GO:0032313,GO:1990071,GO:0030425,GO:0017112,GO:0043087,GO:0030008,GO:0034498,GO:0043547	CG6623-PA						PF12584				G3DSA:1.25.40.10,G3DSA:1.25.40.10										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly502.7	Mothers against decapentaplegic homolog 4	GO:0048589,GO:0030509,GO:0001076,GO:0001077,GO:0014033,GO:0032444,GO:0030511,GO:0031290,GO:0045705,GO:0060548,GO:0000790,GO:0030513,GO:0007179,GO:0044212,GO:0060395,GO:0030616,GO:0060391,GO:0005667,GO:0005829,GO:0003251,GO:0003677,GO:0072133,GO:0035556,GO:0010862,GO:0072134,GO:0005654,GO:0006367,GO:0000987,GO:0007183,GO:0001702,GO:0017015,GO:0035019,GO:0042733,GO:0048733,GO:0009953,GO:0009950,GO:0006355,GO:0006351,GO:0000978,GO:0007492,GO:0042078,GO:0030308,GO:0007498,GO:0046872,GO:0042177,GO:0060956,GO:0007411,GO:0001666,GO:0005737,GO:0043565,GO:0001701,GO:0000122,GO:0005634,GO:0030707,GO:0003190,GO:0003198,GO:0042802,GO:0042803,GO:0008285,GO:0007480,GO:0045892,GO:0045893,GO:0001658,GO:0030718,GO:0051797,GO:0051098,GO:0010718,GO:0045944,GO:0005515,GO:0003682,GO:0042118,GO:0032909,GO:0060021,GO:0045887,GO:0036302,GO:0003360,GO:0005813,GO:0008283,GO:0007476,GO:0010467,GO:0070412,GO:0070411,GO:0071559,GO:0048666,GO:0032525,GO:0048663,GO:0007507,GO:0048859,GO:0003279,GO:0003700,GO:0071141	CG1775-PA				SM00524,SM00523		PF03165,PF03166	PS51076,PS51075			G3DSA:2.60.200.10,G3DSA:3.90.520.10	SSF56366,SSF49879	33~60								
aly502.8	Unknown		CG44085-PO																				
aly502.9	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5021.1	SET and MYND domain-containing protein 4	GO:0005737,GO:0005634,GO:0010629,GO:0008168,GO:0046872,GO:0042826	CG1868-PB				SM00317		PF00856	PS50280			G3DSA:2.170.270.10,G3DSA:2.170.270.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF144232,SSF82199,SSF82199	607~627								
aly5021.10	ADP-ribosylation factor GTPase-activating protein 1	GO:0005795,GO:0044267,GO:0006890,GO:0030660,GO:0030968,GO:0032312,GO:0005829,GO:0097481,GO:0005096,GO:0048205,GO:0043547,GO:0036498,GO:0061024,GO:0008060,GO:0008270,GO:0015031,GO:0032012,GO:0046872,GO:0030100,GO:0005525	CG4237-PA				SM00105		PF01412	PS50115	PR00405,PR00405,PR00405			SSF57863									
aly5021.11	Tyrosine-protein phosphatase non-receptor type 61F	GO:0031647,GO:0006470,GO:0043407,GO:0035335,GO:0007411,GO:0032880,GO:0005737,GO:0005634,GO:0016020,GO:0071456,GO:0048471,GO:0048477,GO:0008285,GO:0046426,GO:0000278,GO:0046627,GO:0007176,GO:0012505,GO:0014067,GO:0007377,GO:0004725,GO:0050732,GO:0005740,GO:0005515,GO:0046580	CG9181-PA				SM00194,SM00404		PF00102	PS50055,PS50056	PR00700,PR00700,PR00700,PR00700,PR00700,PR00700,PR00700	PS00383	G3DSA:3.90.190.10	SSF52799									
aly5021.12	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5021.13	Protein tramtrack, beta isoform	GO:0035147,GO:0048750,GO:0045467,GO:0035001,GO:0031208,GO:0003677,GO:0043388,GO:0007298,GO:0001078,GO:0002121,GO:0031987,GO:0040003,GO:0000122,GO:0005634,GO:0001709,GO:0007476,GO:0030707,GO:0001964,GO:0060446,GO:0042682,GO:0016476,GO:0046872,GO:0000980,GO:0048666,GO:0035151,GO:0017053,GO:0042803,GO:0042675,GO:0008360,GO:0045892,GO:0048053,GO:0007426,GO:0007422,GO:0048854,GO:0005700,GO:0048813,GO:0045944,GO:0006351,GO:0000978,GO:0003682,GO:0046843	CG43365-PF				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695	204~224								
aly5021.14	Zinc-type alcohol dehydrogenase like protein C1773.06c	GO:0071361,GO:0005829,GO:0004022,GO:0006066,GO:0008270,GO:0006091,GO:0001666,GO:0055114,GO:0016491	CG1600-PC				SM00829		PF13602				G3DSA:3.90.180.10,G3DSA:3.40.50.720	SSF50129,SSF50129,SSF51735									
aly5021.15	Plexin domain containing protein 2	GO:0070062,GO:0016021,GO:0016020,GO:0007275,GO:0004872	CG2221-PA						PF01437				G3DSA:3.30.1680.10										
aly5021.16	Glucose transporter type 1	GO:0005355,GO:0022891,GO:0016021,GO:0055085,GO:0008643	CG43946-PP					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171,PR00171,PR00171	PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473	391~411,101~155		REACT_15518						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5021.17	Biogenesis of lysosome-related organelles complex 1 subunit 2	GO:0008150,GO:0031083,GO:0005515,GO:0042803	CG14145-PA						PF10046						76~96								
aly5021.18	Tubulin alpha-1 chain	GO:0045298,GO:0051258,GO:0005200,GO:0019730,GO:0005813,GO:0005634,GO:0009987,GO:0003924,GO:0005737,GO:0007052,GO:0005819,GO:0000235,GO:0007094,GO:0006184,GO:0048471,GO:0005874,GO:0005525	CG1913-PA				SM00865,SM00864		PF03953,PF00091		PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161	PS00227	G3DSA:3.30.1330.20,G3DSA:3.40.50.1440,G3DSA:1.10.287.600	SSF52490,SSF55307	418~438								
aly5021.19	Unknown		n/a																				
aly5021.2	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1	GO:0005737,GO:0016020,GO:0030246,GO:0005576,GO:0005509,GO:0007155,GO:0003682	CG9095-PB				SM00034,SM00032,SM00032,SM00032,SM00607		PF00059,PF00084,PF00084,PF00084,PF00084	PS50923,PS50041,PS50923,PS50923,PS50923		PS00615	G3DSA:3.10.100.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.60.120.260,G3DSA:2.10.70.10	SSF57535,SSF57535,SSF57535,SSF49785,SSF57535,SSF56436									
aly5021.20	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5021.21	Unknown		n/a																				
aly5021.22	Unknown	GO:0003677	n/a						PF05225	PS50960													
aly5021.3	Protein-methionine sulfoxide oxidase Mical	GO:0007015,GO:0055114,GO:0043195,GO:0060386,GO:0007526,GO:0005829,GO:0016709,GO:0019417,GO:0016322,GO:0003779,GO:0048813,GO:0045214,GO:0008270,GO:0005886,GO:0007411,GO:0030042,GO:0030047,GO:0070995,GO:0071949,GO:0043914	CG33208-PL				SM00132		PF00890,PF00412	PS50023	PR00420,PR00420		G3DSA:2.10.110.10,G3DSA:3.50.50.60	SSF51905,SSF51905	2078~2098,1064~1084,2332~2333								
aly5021.4	Solute carrier family 35 member C2	GO:0005794,GO:0015297,GO:0036066,GO:0005793,GO:0005801,GO:0016021,GO:0033116,GO:0015786,GO:0000138,GO:0045747,GO:0010629,GO:0098656	CG14971-PA						PF03151														
aly5021.5	Protein KBP homolog	GO:0005856,GO:0006839,GO:0019894,GO:0007399,GO:0005739	CG14043-PA						PF12309						20~40								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5021.6	Muscle M-line assembly protein unc-89	GO:0031430,GO:0005089,GO:0006468,GO:0004687,GO:0043547,GO:0004683,GO:0032041,GO:0031672,GO:0031034,GO:0017048,GO:0004674,GO:0005200,GO:0004672,GO:0019902,GO:0005875,GO:0005524	CG44162-PU				SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00406,SM00406,SM00406,SM00460		PF00041,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679	PS50835,PS50835,PS50835,PS50835,PS50853,PS50835,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726	3663~3693,2663~2711,1924~1995,1856~1876,2200~2384,2023~2048,1397~1417,3051~3645,2813~2865,2872~3009,2059~2148,666~686,1879~1906,1269~1289,3016~3049,2152~2197,755~782,2762~2809,1041~1061,2535~2646,2388~2426							
aly5021.7	Muscle M-line assembly protein unc-89	GO:0031430,GO:0005089,GO:0006468,GO:0004687,GO:0043547,GO:0004683,GO:0032041,GO:0031672,GO:0031034,GO:0017048,GO:0004674,GO:0005200,GO:0005515,GO:0004672,GO:0019902,GO:0005875,GO:0005524	CG44162-PU				SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409,SM00409		PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679	PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726	1453~1473,1402~1429,639~659							
aly5021.8	Mitogen-activated protein kinase kinase kinase 12	GO:0048674,GO:0006468,GO:0018105,GO:2000331,GO:0005829,GO:0007254,GO:0007030,GO:0030424,GO:0018107,GO:0004674,GO:0007283,GO:0046777,GO:0005886,GO:0004672,GO:0004709,GO:0016572,GO:0005524,GO:0042803	CG8789-PA				SM00220		PF07714	PS50011	PR00109,PR00109,PR00109,PR00109,PR00109,PR00109	PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112	364~384								
aly5021.9	Peroxisomal membrane protein PEX16	GO:0007031,GO:0016021,GO:0005777,GO:0042760,GO:0007283,GO:0005778,GO:0048137	CG3947-PA						PF08610														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5024.1	Unknown		n/a																				
aly5024.2	Unknown		n/a																				
aly5024.3	Protein fem-1 homolog CG6966	GO:0005575,GO:0016567,GO:0004842,GO:0051438	CG11896-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF13637,PF12796	PS50088,PS50088,PS50297,PS50088			G3DSA:1.25.40.20	SSF48403									
aly5024.4	Protein fem-1 homolog A	GO:0005737,GO:0050728,GO:0005575,GO:0016567,GO:0051438,GO:0004842	CG11896-PA										G3DSA:1.25.40.20										
aly5024.5	Protein Skeletor, isoforms B/C	GO:0060439,GO:0007067,GO:0005874,GO:0051225,GO:0051301,GO:0007362,GO:0005819,GO:0051321,GO:0004500,GO:0005634,GO:0006031,GO:0006035,GO:0035151,GO:0035152,GO:0007424,GO:0035158,GO:0006584,GO:0008362,GO:0055114,GO:0001838,GO:0006997,GO:0005730,GO:0005700,GO:0005737,GO:0008293	CG6217-PA				SM00686,SM00686,SM00664		PF10517,PF10517,PF03351	PS51549,PS50836,PS51549													
aly5024.6	Protein Skeletor, isoforms B/C	GO:0005737,GO:0006997,GO:0005819,GO:0051321,GO:0004500,GO:0005874,GO:0005634,GO:0005730,GO:0006584,GO:0005700,GO:0005198,GO:0055114,GO:0005652,GO:0007067,GO:0016363,GO:0005694,GO:0051225,GO:0051301	CG43161-PE				SM00686,SM00686		PF10517,PF10517	PS51549,PS51549													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5024.7	Unknown		n/a												14~37								
aly5027.1	Protein msta, isoform A	GO:0008168,GO:0010629,GO:0042826	CG18136-PA						PF01753,PF00856	PS50865,PS50280		PS01360	G3DSA:2.170.270.10,G3DSA:2.170.270.10	SSF82199,SSF82199,SSF144232									
aly5027.2	Neuropeptide Y receptor	GO:0004930,GO:0016021,GO:0005886,GO:0007218,GO:0004983,GO:0001653,GO:0007165,GO:0007166,GO:0008188,GO:0007186	CG30340-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly5029.1	Phosphatidylserine decarboxylase proenzyme	GO:0006646,GO:0004609,GO:0005739,GO:0008654	CG5991-PA					TIGR00163	PF02666							00564+4.1.1.65		PWY-5669	UPA00558				
aly5029.2	Zinc finger protein 836	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG6654-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028		SSF57667,SSF57667,SSF57667	58~78								
aly5029.3	Cytoplasmic FMR1-interacting protein	GO:0005737,GO:0045177,GO:0006909,GO:0000902,GO:0030031,GO:0050807,GO:0030866,GO:0017048,GO:0008360,GO:0045202,GO:0007411,GO:0001745,GO:0022416,GO:0031209	CG4931-PA			PIRSF008153			PF05994,PF07159		PR01698,PR01698,PR01698,PR01698,PR01698				351~371,173~193								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly50373.1	Unknown		n/a																				
aly5041.1	IQ and AAA domain-containing protein 1	GO:0005524,GO:0005515	CG16789-PA						PF00004	PS50096			G3DSA:3.40.50.300	SSF52540	348~368,419~439								
aly5044.1	Unknown		n/a																				
aly5044.2	Unknown		n/a												639~659								
aly50525.1	Endoribonuclease Dcr-1	GO:0033227,GO:0042078,GO:0030422,GO:0007279,GO:0070883,GO:0031054,GO:0007294,GO:0005737,GO:0007367,GO:0004525,GO:0005634,GO:0030727,GO:0035087,GO:0006309,GO:0016246,GO:0046872,GO:0005524,GO:0004386,GO:0090502,GO:0090501,GO:0042594,GO:0035195,GO:0035196,GO:0004530,GO:0003727,GO:0048813,GO:0003725,GO:0003723,GO:0005515,GO:0016443,GO:0016442,GO:0006396,GO:0045448	CG4792-PA						PF00636	PS50142			G3DSA:1.10.1520.10,G3DSA:1.10.1520.10,G3DSA:3.30.160.20	SSF69065,SSF69065,SSF54768,SSF54768										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly506.1	Unknown		n/a																				
aly506.10	Unknown		CG4281-PA																				
aly506.11	Unknown	GO:0071630,GO:0005634,GO:0031965,GO:0031144	CG5199-PA						PF08559														
aly506.12	Unknown		n/a																				
aly506.13	Xanthine dehydrogenase	GO:0008762,GO:0004855,GO:0004854,GO:0005875,GO:0006650,GO:0050660,GO:0043546,GO:0006206,GO:0005777,GO:0006525,GO:0006568,GO:0005506,GO:0048072,GO:0045471,GO:0016903,GO:0009115,GO:0008340,GO:0055114,GO:0009055,GO:0016614,GO:0005829,GO:0051537,GO:0006144	CG18522-PA				SM01092,SM01008		PF03450,PF01315,PF01799,PF00111,PF02738			PS00197	G3DSA:3.30.390.50,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.10.20.30,G3DSA:3.90.1170.50,G3DSA:1.10.150.120,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10	SSF55447,SSF47741,SSF54292,SSF56003,SSF54665,SSF56176									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly506.14	Uncharacterized protein CG43867	GO:0005575,GO:0005856,GO:0003674,GO:0008150	CG43867-PK				SM00139,SM00233,SM00233,SM00295		PF00784,PF00784,PF00373,PF00169,PF00169	PS50003,PS50057,PS50003,PS51016			G3DSA:1.20.80.10,G3DSA:2.30.29.30,G3DSA:2.30.29.30	SSF50729,SSF50729,SSF54236,SSF47031	17~58,102~136								
aly506.15	Unknown		n/a																				
aly506.16	Unknown		n/a																				
aly506.17	Unknown		n/a																				
aly506.2	Unknown		n/a										G3DSA:1.10.287.70	SSF53850									
aly506.3	Pancreatic lipase-related protein 3	GO:0005575,GO:0004806,GO:0005576,GO:0016298,GO:0016042	CG6472-PB						PF00151		PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly506.4	Unknown		n/a																				
aly506.5	Xanthine dehydrogenase	GO:0008762,GO:0004855,GO:0004854,GO:0005875,GO:0006650,GO:0050660,GO:0043546,GO:0006206,GO:0005777,GO:0006525,GO:0006568,GO:0005506,GO:0048072,GO:0045471,GO:0016903,GO:0009115,GO:0008340,GO:0055114,GO:0009055,GO:0016614,GO:0005829,GO:0051537,GO:0006144	CG6045-PA				SM01092,SM01092,SM01008,SM01008		PF03450,PF03450,PF00111,PF02738,PF02738,PF00941,PF00941,PF01799,PF01799,PF01315,PF01315	PS51387,PS51387,PS51085		PS00197,PS00197	G3DSA:3.30.390.50,G3DSA:3.30.390.50,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:1.10.150.120,G3DSA:1.10.150.120,G3DSA:3.90.1170.50,G3DSA:3.90.1170.50,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.365.10,G3DSA:3.30.465.10,G3DSA:3.30.465.10,G3DSA:3.10.20.30,G3DSA:3.10.20.30	SSF56003,SSF56176,SSF56003,SSF54292,SSF54292,SSF47741,SSF47741,SSF54665,SSF55447,SSF55447,SSF56176,SSF546665	477~497								
aly506.6	Sensory neuron membrane protein 1	GO:0006952,GO:0050896,GO:0035073,GO:0005887,GO:0005044,GO:0016021,GO:0016020,GO:0030425,GO:0055088,GO:0007166,GO:0005886,GO:0007155,GO:0043025,GO:0019236,GO:0007608	CG7000-PA						PF01130		PR01609,PR01609,PR01609,PR01609,PR01609,PR01609,PR01609												
aly506.7	2-hydroxyacylsphingosine 1-beta-galactosyltransferase	GO:0043231,GO:0052696,GO:0007422,GO:0016021,GO:0009813,GO:0006682,GO:0032870,GO:0008152,GO:0016758,GO:0015020,GO:0008489,GO:0003851,GO:0007417	CG30438-PB						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									
aly506.8	Zinc finger protein 2	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG6654-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF13912,PF13912,PF13912,PF13912,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57716,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly506.9	Pyruvate carboxylase, mitochondrial	GO:0009374,GO:0010629,GO:0005739,GO:0019074,GO:0003677,GO:0006090,GO:0005875,GO:0006094,GO:0005737,GO:0005811,GO:0004736,GO:0005759,GO:0046872,GO:0044794,GO:0006767,GO:0006766,GO:0006629,GO:0006768,GO:0004075,GO:0044791,GO:0005975,GO:0005829,GO:0005524,GO:0006006,GO:0044281	CG1516-PI				SM00878	TIGR01235	PF02786,PF00682,PF02785,PF02436,PF00289,PF00364	PS50968,PS50975,PS50979,PS50991		PS00867,PS00188	G3DSA:3.10.600.10,G3DSA:3.30.470.20,G3DSA:3.20.20.70,G3DSA:1.10.10.60,G3DSA:2.40.50.100,G3DSA:3.30.1490.20,G3DSA:3.40.50.20	SSF51569,SSF89000,SSF51230,SSF56059,SSF52440,SSF51246		00620+6.4.1.1,00720+6.4.1.1,00020+6.4.1.1		PWY-6142,PWY-6146,PWY-5750	UPA00138				
aly50623.1	Unknown	GO:0006909	CG16791-PA																				
aly50660.1	Unknown		n/a																				
aly5076.1	Unknown		n/a						PF08574														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5076.2	Zinc finger protein ush	GO:0009996,GO:0008258,GO:0035167,GO:0030154,GO:0003677,GO:0001078,GO:0004879,GO:0007362,GO:0042440,GO:0000122,GO:0005634,GO:0046872,GO:0048749,GO:0002805,GO:0008134,GO:0022416,GO:0001102,GO:0030097,GO:0046665,GO:0043433,GO:0007507,GO:0007398,GO:0003700,GO:0007393,GO:0007391,GO:0007390,GO:0006355,GO:0006351,GO:0005515,GO:0042690,GO:0008293,GO:0048542	CG2762-PC				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157			G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly5076.3	Unknown		n/a																				
aly5076.4	Unknown		n/a																				
aly5076.5	Krueppel-like factor 11	GO:0000083,GO:0048102,GO:0043565,GO:0007254,GO:0000122,GO:0007472,GO:0005634,GO:0043065,GO:0006366,GO:0046872,GO:0000981,GO:0008285,GO:0048190,GO:0035071,GO:0090098,GO:0048592,GO:0006915,GO:0045893,GO:0001736,GO:0044212,GO:0007423,GO:0003700,GO:0007391,GO:0007390	CG4427-PA				SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5076.6	Coiled-coil and C2 domain-containing protein 1-like	GO:0008586,GO:0045035,GO:0005737,GO:0007219,GO:0000122,GO:0007472,GO:0006886,GO:0005543,GO:0000281,GO:0045746,GO:0000981,GO:0048749,GO:0016324,GO:0036257,GO:0008593,GO:0048132,GO:0030100,GO:0016197,GO:0007423,GO:0045732,GO:0005515,GO:0005634	CG4713-PB				SM00685,SM00685		PF00168				G3DSA:2.60.40.150	SSF49562	27~47								
aly50908.1	Unknown		n/a												50~88,110~165								
aly5092.1	Unknown		n/a																				
aly5098.1	Unknown		n/a																				
aly5098.2	Lipase 1	GO:0004806,GO:0006629,GO:0007586,GO:0016788,GO:0016042,GO:0048812,GO:0005576	CG31871-PA			PIRSF000862			PF00561				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5098.3	Gastric triacylglycerol lipase	GO:0005576,GO:0004806,GO:0006629,GO:0016788,GO:0016042	CG18301-PA			PIRSF000862			PF00561				G3DSA:3.40.50.1820	SSF53474									
aly51064.1	Unknown	GO:0048802,GO:0045214,GO:0048734,GO:0035220,GO:0007527	CG13366-PB												31~100								
aly51077.1	Long-chain fatty acid transport protein 4	GO:0006631,GO:0005783,GO:0005324,GO:0031957,GO:0005789,GO:0005902,GO:0044539,GO:0042760,GO:0016021,GO:0016020,GO:0000166,GO:0004467,GO:0005886,GO:0043588,GO:0015909,GO:0007584,GO:0003824,GO:0008152,GO:0000038,GO:0001676,GO:0001579,GO:0031526	CG3394-PA						PF00501				G3DSA:3.40.50.980	SSF56801									
aly5112.1	Unknown		n/a																				
aly5112.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5112.3	Unknown		n/a												64~84								
aly51219.1	Unknown		n/a												39~59								
aly5125.1	Apyrase	GO:0008253,GO:0017110,GO:0017111,GO:0016788,GO:0000166,GO:0009166,GO:0005576,GO:0046872,GO:0005524	CG1961-PA						PF00149		PR01607,PR01607,PR01607	PS00786	G3DSA:3.60.21.10,G3DSA:3.90.780.10	SSF56300,SSF55816									
aly5125.2	Apyrase	GO:0016787,GO:0008253,GO:0017110,GO:0017111,GO:0016788,GO:0000166,GO:0009166,GO:0005576,GO:0046872,GO:0005524	CG1961-PA						PF02872,PF00149		PR01607,PR01607,PR01607,PR01607,PR01607	PS00786	G3DSA:3.90.780.10,G3DSA:3.60.21.10	SSF56300,SSF55816									
aly5125.3	Unknown		n/a																				
aly5126.1	Apyrase	GO:0008253,GO:0017110,GO:0017111,GO:0016788,GO:0000166,GO:0009166,GO:0005576,GO:0046872,GO:0005524	CG42249-PC										G3DSA:3.60.21.10	SSF56300									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly51364.1	Protein C21orf2	GO:0005737,GO:0007010,GO:0035071,GO:0060271,GO:0007224,GO:0048102,GO:0008360,GO:0005515,GO:0005886	CG14995-PA							PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									
aly51367.1	Dedicator of cytokinesis protein 4	GO:0005089,GO:0005737,GO:0016020,GO:0043547,GO:0032420,GO:0005085,GO:0005829,GO:0060326,GO:0005096,GO:0048365,GO:0045466,GO:0032863,GO:0030165,GO:0012505,GO:0005886,GO:0032421,GO:0007264,GO:0030971,GO:0007417	CG31048-PE																				
aly5145.1	Unknown		n/a																				
aly515.1	Major heat shock 70 kDa protein Bc	GO:0006986,GO:0035080,GO:0031427,GO:0009408,GO:0001666,GO:0005875,GO:0005524	CG31449-PA						PF00012		PR00301,PR00301,PR00301,PR00301,PR00301,PR00301,PR00301	PS00329,PS00297,PS01036	G3DSA:2.60.34.10,G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.90.640.10,G3DSA:3.30.30.30,G3DSA:1.20.1270.10	SSF53067,SSF100920,SSF100934,SSF53067										
aly515.10	60S ribosomal protein L4-B	GO:0003735,GO:0022625,GO:0005840,GO:0051298,GO:0006412	CG5502-PA						PF00573				G3DSA:3.40.1370.10	SSF52166									
aly515.11	60S ribosomal protein L4	GO:0003735,GO:0022625,GO:0005840,GO:0051298,GO:0006412	CG5502-PA						PF00573,PF14374				G3DSA:3.40.1370.10	SSF52166									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly515.12	Unknown	GO:0003676	n/a				SM00980		PF05485	PS50950				SSF57716									
aly515.13	Unknown		n/a						PF14214						1214~1239								
aly515.2	Unknown		n/a																				
aly515.3	Putative aminopeptidase W07G4.4	GO:0005737,GO:0004177,GO:0008240,GO:0030145,GO:0005622,GO:0008239,GO:0006508,GO:0008235	CG9285-PA						PF00883		PR00481,PR00481,PR00481		G3DSA:3.40.630.10,G3DSA:3.40.630.10	SSF53187		00480+3.4.11.1		PWY-5988,PWY-6018					
aly515.4	Meprin A subunit beta	GO:0004222,GO:0016021,GO:0016020,GO:0008270,GO:0006954,GO:0005886,GO:0006508,GO:1901998	CG11865-PA						PF01400				G3DSA:3.40.390.10	SSF55486									
aly515.5	28S ribosomal protein S35, mitochondrial	GO:0044822,GO:0006412,GO:0003735,GO:0005743,GO:0005763,GO:0032543	CG2101-PA						PF10213														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly515.6	Unknown		n/a																				
aly515.7	La-related protein 1	GO:0005737,GO:0051299,GO:0035186,GO:0035071,GO:0000001,GO:0005829,GO:0005739,GO:0048102,GO:0007053,GO:0003674,GO:0003723,GO:0007076,GO:0051225,GO:0007140	CG14066-PB				SM00715,SM00684,SM00684		PF05383	PS50961			G3DSA:1.10.10.10	SSF46785	321~341								
aly515.8	Unknown		n/a																				
aly515.9	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5150.1	Cytoskeleton-associated protein 5	GO:0035371,GO:0007411,GO:0007067,GO:0000922,GO:0005875,GO:0051301,GO:0007344,GO:0000022,GO:0007029,GO:0005813,GO:0090063,GO:0016020,GO:0007143,GO:0043021,GO:0048477,GO:0008017,GO:0005737,GO:0015631,GO:0016325,GO:0051297,GO:0031122,GO:0007051,GO:0045450,GO:0043234,GO:0050658,GO:0007017,GO:0030951,GO:0005515	CG5000-PD																				
aly5150.2	Zinc finger CCCH domain containing protein 11A	GO:0046872	n/a				SM00356,SM00356,SM00356		PF15663	PS50103,PS50103,PS50103													
aly5150.3	Unknown		n/a																				
aly5150.4	Paired box protein Pax-6	GO:0016319,GO:0008284,GO:0030307,GO:0001745,GO:0043565,GO:0043567,GO:0006355,GO:0007455,GO:0005634,GO:0006351,GO:0048749,GO:0005667,GO:0030182,GO:0007628,GO:0048036,GO:0008347,GO:0007420,GO:0043704,GO:0040018,GO:0003705,GO:0003700,GO:0006357,GO:0045944,GO:0000977,GO:0005515,GO:0048854,GO:0045893	CG1464-PD				SM00389		PF00046	PS50071	PR00031,PR00031	PS00027	G3DSA:1.10.10.60	SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5150.5	Paired box protein Pax-6	GO:0016319,GO:0071380,GO:0021510,GO:0070094,GO:0042660,GO:0035690,GO:0001764,GO:0003700,GO:0032869,GO:0001745,GO:0007417,GO:0043565,GO:0043567,GO:0060041,GO:0003309,GO:0021593,GO:0016567,GO:0003322,GO:0007455,GO:0005634,GO:0044344,GO:0050768,GO:0045664,GO:0006357,GO:0061351,GO:0071333,GO:1901142,GO:0003690,GO:0002064,GO:2001224,GO:0048749,GO:0005667,GO:0030182,GO:0050767,GO:0030902,GO:0006366,GO:0048708,GO:0007628,GO:0045471,GO:0000790,GO:0022027,GO:0048036,GO:0010975,GO:0021772,GO:0001755,GO:0021549,GO:0004842,GO:0008347,GO:0003310,GO:0007420,GO:0043704,GO:0040018,GO:0003705,GO:0006355,GO:0010628,GO:0045944,GO:0000981,GO:0005515,GO:0048854,GO:0003680,GO:0000979,GO:0045893	CG1464-PD				SM00351		PF00292	PS51057	PR00027,PR00027,PR00027,PR00027	PS00034	G3DSA:1.10.10.10,G3DSA:1.10.10.10	SSF46689									
aly5156.1	Unknown		n/a																				
aly5167.1	Beclin-1-like protein	GO:0006897,GO:0035071,GO:0009306,GO:0006914,GO:0005623,GO:0035096,GO:0048102,GO:0045824,GO:0016322,GO:0050829,GO:0030097,GO:1902350,GO:0034271,GO:0006979	CG5429-PA						PF04111						126~202,222~242								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5167.2	Homeobox protein SIX4	GO:0034504,GO:0007498,GO:0008582,GO:0061551,GO:0008584,GO:0001077,GO:0043524,GO:0098528,GO:0003677,GO:0051451,GO:0072075,GO:0032880,GO:0005737,GO:0043565,GO:0009653,GO:0005634,GO:0030910,GO:0008406,GO:0043586,GO:0043066,GO:0048538,GO:0072095,GO:0061197,GO:0048701,GO:0030238,GO:0060037,GO:0090190,GO:0045892,GO:0045893,GO:0007520,GO:0061055,GO:0046661,GO:0072107,GO:0048699,GO:0042472,GO:0050678,GO:0007503,GO:0003700,GO:0006355,GO:0048812,GO:0007519,GO:0045214,GO:0000978,GO:1902725	CG3871-PA				SM00389		PF16878,PF00046	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689									
aly517.1	Unknown		n/a																				
aly517.10	Tubulin beta chain	GO:0045298,GO:0051258,GO:0007017,GO:0003924,GO:0005737,GO:0007435,GO:0005200,GO:0006184,GO:0005874,GO:0005525	CG9359-PA				SM00864,SM00865		PF00091,PF03953		PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163	PS00227,PS00228	G3DSA:1.10.287.600,G3DSA:3.30.1330.20,G3DSA:3.40.50.1440	SSF55307,SSF52490			REACT_152						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly517.11	Tubulin beta-4 chain	GO:0045298,GO:0051258,GO:0007017,GO:0003924,GO:0005737,GO:0005200,GO:0007435,GO:0006184,GO:0005874,GO:0005525	CG9359-PA				SM00865,SM00864		PF00091,PF03953		PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161	PS00227,PS00228	G3DSA:3.40.50.1440,G3DSA:1.10.287.600,G3DSA:3.30.1330.20	SSF55307,SSF52490	408~428		REACT_152						
aly517.12	Unknown		n/a																				
aly517.13	Tubulin beta-4 chain	GO:0045298,GO:0051258,GO:0007017,GO:0003924,GO:0005879,GO:0005200,GO:0007435,GO:0006184,GO:0005874,GO:0005525	CG9359-PA				SM00864,SM00865		PF00091,PF03953		PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161	PS00227,PS00228	G3DSA:1.10.287.600,G3DSA:3.30.1330.20,G3DSA:3.40.50.1440	SSF52490,SSF55307	408~428		REACT_152						
aly517.14	Diacylglycerol kinase eta	GO:0005737,GO:0051259,GO:0019992,GO:0016310,GO:0007205,GO:0008152,GO:0003951,GO:0035556,GO:0046872,GO:0004143,GO:0005768,GO:0005524	CG34384-PE				SM00109,SM00109,SM00046		PF00130,PF00130,PF00781	PS50081,PS50146,PS50081,PS50003		PS00479,PS00479	G3DSA:3.30.60.20,G3DSA:3.30.60.20,G3DSA:2.30.29.30	SSF111331,SSF50729,SSF57889,SSF57889	317~337								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly517.15	Diacylglycerol kinase eta	GO:0005737,GO:0051259,GO:0019992,GO:0016310,GO:0007205,GO:0008152,GO:0003951,GO:0035556,GO:0046872,GO:0004143,GO:0005768,GO:0005524	CG34384-PE				SM00454,SM00045		PF00536,PF00609	PS50105			G3DSA:1.10.150.50	SSF111331,SSF47769		00561+2.7.1.107,00564+2.7.1.107	REACT_14797,REACT_604	PWY-7039					
aly517.16	Probable glutamate--tRNA ligase, mitochondrial	GO:0005737,GO:0006424,GO:0000049,GO:0004818,GO:0043039,GO:0016876,GO:0005759,GO:0005524	CG4573-PA	MF_00022_B				TIGR00464	PF00749		PR00987,PR00987,PR00987,PR00987,PR00987	PS00178	G3DSA:1.10.10.350,G3DSA:3.40.50.620,G3DSA:3.40.50.620,G3DSA:3.90.800.10,G3DSA:1.10.1160.10	SSF52374,SSF48163		00970+6.1.1.17,00860+6.1.1.17	REACT_71	PWY-5188					
aly517.17	DCN1-like protein 1	GO:0005634,GO:0000151	CG7427-PC						PF03556,PF14555	PS51229			G3DSA:1.10.8.10	SSF46934									
aly517.18	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 2	GO:0005747,GO:0031966,GO:0003954,GO:0055114,GO:0006120	CG15434-PA			PIRSF005822	SM00916		PF05047				G3DSA:3.40.30.10	SSF52833									
aly517.19	Probable pseudouridine-5'-phosphatase	GO:0016787,GO:1990738,GO:0042060,GO:0009117,GO:0008152,GO:0046872	CG15441-PA					TIGR01509	PF13419				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF56784									
aly517.2	Cytochrome P450 6B5 (Fragment)	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0042742,GO:0005506,GO:0055114,GO:0009055	CG2397-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00464,PR00464,PR00464	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly517.20	Glypican-6	GO:0008589,GO:0008101,GO:0008587,GO:0031594,GO:0030177,GO:0045880,GO:0007411,GO:0050908,GO:0030178,GO:0031225,GO:0007367,GO:0005634,GO:0016020,GO:0016477,GO:0048749,GO:0005796,GO:0048190,GO:0007528,GO:0043395,GO:0005887,GO:0005615,GO:0007224,GO:0016055,GO:0005576,GO:0017147,GO:0045570,GO:0005578,GO:0045202	CG32146-PA						PF01153														
aly517.21	Kelch domain-containing protein 4		CG4069-PA						PF01344,PF13418,PF13418				G3DSA:2.120.10.80,G3DSA:2.120.10.80	SSF117281,SSF117281	40~60,18~38								
aly517.22	General transcription factor IIF subunit 1	GO:0001096,GO:0060261,GO:0005674,GO:0005634,GO:0006366,GO:0003824,GO:0016740,GO:0045944,GO:0006367,GO:0003677,GO:0022008,GO:0032968	CG10281-PA						PF05793,PF05793				G3DSA:1.10.10.10	SSF50916,SSF46785			REACT_6185,REACT_769,REACT_1788,REACT_1892,REACT_1675,REACT_71						
aly517.23	Solute carrier family 22 member 1	GO:0015075,GO:0016021,GO:0016323,GO:0055085,GO:0008513	CG6231-PC																				
aly517.24	Organic cation transporter 1	GO:0016021,GO:0015695,GO:0008513,GO:0022857,GO:0015101,GO:0008340,GO:0055085	CG42269-PE						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473	67~87,95~129								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly517.25	Organic cation transporter protein	GO:0006811,GO:0006915,GO:0055085,GO:0022857,GO:0008513,GO:0016021	CG42269-PE						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly517.26	Solute carrier family 22 member 3	GO:0015651,GO:0019534,GO:0006855,GO:0051615,GO:0005329,GO:0015697,GO:0032098,GO:0016021,GO:0016020,GO:0015872,GO:0098779,GO:0015101,GO:0044281,GO:0005887,GO:0005886,GO:0015695,GO:0008513,GO:0055085	CG42269-PE						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	12~32								
aly517.27	Solute carrier family 22 member 3	GO:0015651,GO:0019534,GO:0006855,GO:0051615,GO:0005329,GO:0015697,GO:0032098,GO:0016021,GO:0016020,GO:0015872,GO:0098779,GO:0015101,GO:0044281,GO:0005887,GO:0005886,GO:0015695,GO:0008513,GO:0055085	CG42269-PE						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly517.28	Solute carrier family 22 member 3	GO:0015651,GO:0019534,GO:0006855,GO:0051615,GO:0005329,GO:0015697,GO:0032098,GO:0016021,GO:0016020,GO:0015872,GO:0098779,GO:0015101,GO:0044281,GO:0005887,GO:0005886,GO:0015695,GO:0008513,GO:0055085	CG42269-PE						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly517.29	Transposon Tf2-6 polyprotein	GO:0006310,GO:0004519,GO:0003887,GO:0015074,GO:0004190,GO:0003723,GO:0003677,GO:0003964,GO:0046872	n/a						PF00665	PS50994			G3DSA:3.30.420.10	SSF53098									
aly517.3	Cytochrome P450 6k1	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0042742,GO:0005506,GO:0055114,GO:0009055	CG2397-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly517.30	Unknown		n/a										G3DSA:3.30.420.10	SSF56672,SSF53098									
aly517.4	Cytochrome P450 6B4	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0035220,GO:0005789,GO:0070330,GO:0022416,GO:0005506,GO:0055114,GO:0009055	CG12800-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly517.5	Cytochrome P450 6k1	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG8345-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly517.6	Unknown		n/a										G3DSA:3.40.630.30	SSF55729									
aly517.7	DNA topoisomerase 2-binding protein 1-A	GO:0071165,GO:0033138,GO:0071163,GO:0071168,GO:0030174,GO:0000785,GO:0003677,GO:0007067,GO:0000922,GO:0005737,GO:0005634,GO:0005815,GO:0048477,GO:0033314,GO:0006281,GO:0006974,GO:0019900,GO:0035563,GO:0003682,GO:0000076,GO:0006270,GO:0007095,GO:0045860	CG11156-PA				SM00292,SM00292,SM00292,SM00292,SM00292		PF12738,PF12738,PF00533	PS50172,PS50172,PS50172,PS50172			G3DSA:3.40.50.10190,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190	SSF52113,SSF52113,SSF52113,SSF52113,SSF52113										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly517.8	Pre-rRNA-processing protein TSR2 homolog	GO:0022008,GO:0006364	CG14543-PA						PF10273														
aly517.9	Alpha-1,2-mannosyltransferase ALG9	GO:0052926,GO:0006486,GO:0016021,GO:0016020,GO:0097502,GO:0005789,GO:0016757,GO:0052918,GO:0000030	CG11851-PA						PF03901,PF03901														
aly5174.1	Sodium-coupled monocarboxylate transporter 2	GO:0006810,GO:0008507,GO:0070062,GO:0015129,GO:0016324,GO:0016021,GO:0016020,GO:0006814,GO:0015293,GO:0055085	CG7720-PB					TIGR00813	PF00474	PS50283													
aly518.1	Unknown		n/a																				
aly518.2	Probable RNA directed DNA polymerase from transposon X-element	GO:0003964,GO:0006278,GO:0006313	n/a						PF00078	PS50878,PS50879			G3DSA:3.60.10.10,G3DSA:3.30.420.10	SSF56672,SSF53098,SSF56219									
aly5180.1	Homeobox protein invected	GO:0048100,GO:0043565,GO:0003700,GO:0005634,GO:0007476,GO:0007386,GO:0050832,GO:0006355,GO:0006357,GO:0000976,GO:0007474,GO:0007275,GO:0007400	CG17835-PD																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5180.2	Aldo-keto reductase AKR2E4	GO:0004032,GO:0008202,GO:0006081,GO:0055114,GO:0016491	CG10638-PA			PIRSF000097			PF00248		PR00069,PR00069,PR00069,PR00069,PR00069	PS00798,PS00062	G3DSA:3.20.20.100	SSF51430									
aly5180.3	Aldo-keto reductase AKR2E4	GO:0004032,GO:0008202,GO:0055114,GO:0016491	CG9436-PA			PIRSF000097			PF00248		PR00069,PR00069,PR00069,PR00069,PR00069	PS00798,PS00062	G3DSA:3.20.20.100	SSF51430									
aly5181.1	Unknown	GO:0006470,GO:0004725	CG7180-PA																				
aly5181.2	Unknown	GO:0005575,GO:0008150,GO:0003674,GO:0008080	CG34010-PA						PF08445				G3DSA:3.40.630.30	SSF55729									
aly5181.3	Unknown	GO:0016747,GO:0008080	CG17681-PA						PF08445	PS51186			G3DSA:3.40.630.30	SSF55729									
aly5181.4	Unknown	GO:0008080	CG12560-PB						PF06021,PF08445	PS51186			G3DSA:3.40.630.30	SSF55729									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5181.5	Unknown	GO:0006030,GO:0005576,GO:0008061	CG5756-PC				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly5181.6	Dynein heavy chain 10, axonemal	GO:0005737,GO:0042623,GO:0007018,GO:0005858,GO:0000166,GO:0005875,GO:0003777,GO:0016887,GO:0005929,GO:0030286,GO:0005874,GO:0003774,GO:0005524	CG1842-PB				SM00382,SM00382,SM00382,SM00382		PF07728,PF12774,PF08393,PF03028,PF08385,PF12780,PF12777,PF12775,PF12781				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540	1362~1382,3229~3277,3020~3064,3578~3605,1854~1874									
aly5181.7	Ufm1-specific protease 1	GO:0005575,GO:0008150,GO:0016790,GO:0071567,GO:0070062	CG16979-PA						PF07910														
aly5181.8	Ufm1-specific protease 2	GO:0005737,GO:0016790,GO:0005634,GO:0005575,GO:0008150,GO:0071567,GO:0006508,GO:0005783	CG16979-PA						PF07910														
aly5181.9	Dynein heavy chain 10, axonemal	GO:0005737,GO:0042623,GO:0007018,GO:0005858,GO:0000166,GO:0003774,GO:0005524,GO:0016887,GO:0005929,GO:0030286,GO:0005874,GO:0005875,GO:0003777	CG1842-PB												4~24								
aly51842.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5196.1	GATA-binding factor C	GO:0043565,GO:0009887,GO:0003700,GO:0005634,GO:0009888,GO:0006355,GO:0006357,GO:0008270,GO:0008045,GO:0000981,GO:0006351	CG9656-PC				SM00401,SM00401		PF00320,PF00320	PS50114,PS50114	PR00619,PR00619	PS00344,PS00344	G3DSA:3.30.50.10,G3DSA:3.30.50.10	SSF57716,SSF57716									
aly5196.10	Forkhead box protein N4	GO:0048749,GO:0008105,GO:0035881,GO:0060579,GO:0001158,GO:0009790,GO:0000785,GO:0007391,GO:0036302,GO:0007000,GO:0051302,GO:0043565,GO:0007517,GO:0005730,GO:0006325,GO:0005634,GO:0007476,GO:0001947,GO:0003690,GO:0000981,GO:0048666,GO:0030154,GO:0007389,GO:0008134,GO:0008016,GO:0035050,GO:0009888,GO:0050832,GO:0000791,GO:0008301,GO:0045893,GO:0007400,GO:0051090,GO:0010842,GO:0003700,GO:0000122,GO:0003705,GO:0005700,GO:0005701,GO:0006355,GO:0048813,GO:0006357,GO:0000976,GO:0006351,GO:0005667,GO:0003682	CG4029-PA				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00658	G3DSA:1.10.10.10	SSF46785									
aly5196.11	Unknown	GO:0005819,GO:0007420,GO:0005730,GO:0005634,GO:0003674,GO:0007000,GO:0005875	CG12819-PB												1170~1190								
aly5196.12	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5196.13	Unknown		n/a																				
aly5196.2	Unknown		n/a																				
aly5196.3	Unknown	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG6955-PA						PF00379	PS51155													
aly5196.4	Protein FAM32A-like	GO:0005634,GO:0006915,GO:0007049	CG15432-PA												56~76,25~50								
aly5196.5	Unknown	GO:0005575,GO:0003674,GO:0042060	CG10217-PA																				
aly5196.6	Transcription elongation factor 1 homolog	GO:0005634,GO:0005575,GO:0006355,GO:0008150,GO:0006351,GO:0003674,GO:0046872	CG40228-PC						PF05129					SSF57783									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5196.7	Vesicle-fusing ATPase 1	GO:0008021,GO:0006909,GO:0008152,GO:0034214,GO:0016887,GO:0007274,GO:0005737,GO:0006888,GO:0051260,GO:0043001,GO:0032403,GO:0046872,GO:0005524,GO:0005795,GO:0016082,GO:0006891,GO:0048211,GO:0035540,GO:0048172,GO:0007269,GO:0007030,GO:0043195,GO:0031629,GO:0035494	CG1618-PB				SM01073,SM00382,SM00382		PF00004,PF00004,PF02359,PF02933			PS00674	G3DSA:3.10.330.10,G3DSA:2.40.40.20,G3DSA:1.10.8.60,G3DSA:1.10.8.60,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF54585,SSF52540,SSF52540,SSF50692	295~315									
aly5196.8	Calcium homeostasis endoplasmic reticulum protein	GO:0005737,GO:0008285,GO:0005783,GO:0006874,GO:0044822,GO:0016020,GO:0000398,GO:0051533,GO:0005681,GO:0003676,GO:0044325,GO:0051209,GO:0048471,GO:0006396,GO:0003729	CG33522-PA				SM00443,SM00648,SM00582		PF01585,PF01805,PF04818	PS50174,PS50128,PS51391			G3DSA:1.25.40.90	SSF48464,SSF109905	803~807,134~154,163~183,365~392								
aly5196.9	Protein misato	GO:0005856,GO:0005737,GO:0000070,GO:0003924,GO:0005739,GO:0090307,GO:0003674	CG1424-PA						PF10644,PF14881				G3DSA:3.40.50.1440,G3DSA:3.40.50.1440	SSF52490,SSF52490									
aly522.1	Dihydroxyacetone phosphate acyltransferase	GO:0006654,GO:0005782,GO:0016287,GO:0061024,GO:0044281,GO:0042594,GO:0007416,GO:0004366,GO:0005778,GO:0030913,GO:0016020,GO:0005777,GO:0005739,GO:0016746,GO:0006644,GO:0007584,GO:0008152,GO:0044255,GO:0008611,GO:0021587,GO:0070542,GO:0042493,GO:0016290,GO:0046474,GO:0005102	CG4625-PC				SM00563		PF01553					SSF69593									
aly522.10	WD repeat-containing protein 92	GO:0006915,GO:0005515	CG14353-PA				SM00320,SM00320,SM00320,SM00320		PF00400	PS50294,PS50082			G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly522.11	Serine protease easter	GO:0004252,GO:0009950,GO:0045087,GO:0008063,GO:0031638,GO:0006952,GO:0050830,GO:0005576,GO:0007311,GO:0045752,GO:0006508,GO:0008233,GO:0008236	CG5896-PB				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly522.12	CXXC-type zinc finger protein 1	GO:0051568,GO:0006355,GO:0048188,GO:0008270,GO:0003677,GO:0006351	CG17446-PA				SM00249		PF12269,PF02008,PF00628	PS50016,PS51058		PS01359	G3DSA:3.30.40.10	SSF57903									
aly522.13	Unknown		n/a																				
aly522.14	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0035006,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG1102-PC				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly522.15	Unknown		n/a																				
aly522.16	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0035006,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG1102-PC				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly522.17	Serine protease easter	GO:0004252,GO:0009950,GO:0050832,GO:0045087,GO:0045752,GO:0031638,GO:0006964,GO:0006952,GO:0050830,GO:0005576,GO:0007311,GO:0008063,GO:0050829,GO:0006508,GO:0008233,GO:0006959,GO:0008236	CG16705-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly522.18	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG3505-PA						PF00089				G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly522.19	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0035006,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG1102-PC				SM00020		PF00089	PS50240	PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly522.2	Alpha-mannosidase 2	GO:0005795,GO:0004572,GO:0015923,GO:0005783,GO:0006486,GO:0006487,GO:0016021,GO:0030246,GO:0000139,GO:0006013,GO:0035010,GO:0008270,GO:0016063,GO:0006491,GO:0006517	CG18802-PB				SM00872		PF07748,PF01074,PF09261				G3DSA:3.20.110.10,G3DSA:2.60.40.1180,G3DSA:2.70.98.30,G3DSA:1.20.1270.50	SSF88688,SSF88713,SSF74650									
aly522.20	BTB/POZ domain-containing protein 6	GO:0005575,GO:0000932,GO:0022008,GO:0003674,GO:0005515	CG43226-PD				SM00225,SM00875		PF00651,PF08005,PF07707	PS50097			G3DSA:3.30.710.10	SSF54695									
aly522.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly522.4	Sodium/potassium-transporting ATPase subunit alpha	GO:0007630,GO:0051124,GO:0060439,GO:0007268,GO:0005890,GO:0050905,GO:0005737,GO:0001700,GO:0005634,GO:0019991,GO:0009612,GO:0000166,GO:0005391,GO:0035158,GO:0035725,GO:0005886,GO:0006812,GO:0046872,GO:0015672,GO:0005524,GO:0007626,GO:0035152,GO:0007605,GO:0035159,GO:0008324,GO:0016323,GO:0008360,GO:0009266,GO:0008340,GO:0001894,GO:0008344,GO:0005918,GO:0098655,GO:0006754	CG5670-PA				SM00831	TIGR01106,TIGR01494,TIGR01494	PF00122,PF13246,PF00689,PF006690		PR00119,PR00119,PR00119,PR00119,PR00119,PR00119,PR00121,PR00121,PR00121,PR00121,PR00121,PR00121	PS00154	G3DSA:2.70.150.10,G3DSA:2.70.150.10,G3DSA:1.20.1110.10,G3DSA:4.10.6.10,G3DSA:3.40.50.1000,G3DSA:3.40.1110.10	SSF81653,SSF81665,SSF81665,SSF81665,SSF81665,SSF56784,SSF56784,SSF81660										
aly522.5	Synaptotagmin 16	GO:0016192,GO:0016079,GO:0016021,GO:0005543,GO:0005544,GO:0048812,GO:0030276,GO:0005515,GO:0007269,GO:0005886,GO:0019905,GO:0005509	CG9778-PD				SM00239,SM00239		PF00168,PF00168	PS50004,PS50004			G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562									
aly522.6	Unknown	GO:0016020,GO:0005272,GO:0006814	n/a						PF00858														
aly522.7	Proto-oncogene c-Fos	GO:0048674,GO:0016330,GO:0019730,GO:0035220,GO:0001077,GO:0007297,GO:0003677,GO:0007298,GO:0070491,GO:0005737,GO:0043565,GO:0007254,GO:0005634,GO:0009611,GO:0046529,GO:0048749,GO:0005515,GO:0008134,GO:0042060,GO:0007281,GO:0045475,GO:0001736,GO:0003700,GO:0031660,GO:0007464,GO:0007391,GO:0051124,GO:0048813,GO:0006357,GO:0045944,GO:0000981,GO:0005667,GO:0046982	CG15509-PA				SM00338		PF00170	PS50217	PR00042,PR00042,PR00042,PR00042	PS00036	G3DSA:1.20.5.170	SSF57959	155~175,182~219								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly522.8	Transcription factor IIIB 90 kDa subunit	GO:0000126,GO:0005667,GO:0043488,GO:0017025,GO:0005634,GO:0008134,GO:0006355,GO:0048812,GO:0008270,GO:0006352,GO:0001046,GO:0006384,GO:0006383,GO:0006359,GO:0045893	CG31256-PA				SM00385,SM00385		PF07741,PF08271,PF00382,PF00382	PS51134	PR00685,PR00685,PR00685,PR00685,PR00685		G3DSA:1.10.472.10,G3DSA:1.10.472.10,G3DSA:1.20.5.650,G3DSA:2.20.25.10	SSF47954,SSF57783,SSF47954	311~331		REACT_1788							
aly522.9	Protein pellino	GO:0042325,GO:0006952,GO:0019207,GO:0006955,GO:0005737,GO:0005575,GO:0008348,GO:0045751,GO:0007165,GO:0005886,GO:0008063,GO:1902524	CG5212-PA			PIRSF038886			PF04710								REACT_6900		UPA00143				
aly52248.1	Glutathione S-transferase 2	GO:0005737,GO:0004364,GO:0006979,GO:0004602,GO:0006749	CG8938-PD							PS50405			G3DSA:1.20.1050.10	SSF47616									
aly52266.1	Unknown		n/a																				
aly523.1	Unknown		n/a																				
aly5235.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5235.2	Low-density lipoprotein receptor-related protein 6	GO:0019534,GO:0034392,GO:0090118,GO:0005783,GO:0007616,GO:0007268,GO:0060021,GO:0035261,GO:0090245,GO:0090244,GO:0090009,GO:0071901,GO:0001745,GO:0003344,GO:0021987,GO:0014033,GO:2000055,GO:0045787,GO:0090263,GO:0044340,GO:0016021,GO:0005770,GO:0030917,GO:0034185,GO:0060026,GO:1901998,GO:0001843,GO:0043025,GO:0031901,GO:0030901,GO:0090090,GO:0019210,GO:0060059,GO:0006469,GO:0009880,GO:0043235,GO:0048076,GO:0009986,GO:0071397,GO:0006622,GO:0060070,GO:0045893,GO:0005886,GO:0042475,GO:0044332,GO:0021794,GO:0044335,GO:0021587,GO:0051091,GO:0071936,GO:0007399,GO:0014029,GO:0016055,GO:0005041,GO:0005102,GO:0042813,GO:0005109,GO:0005576,GO:0045944,GO:0042802,GO:0060535,GO:0031410,GO:0017147,GO:0060325,GO:0001933,GO:0042803,GO:0005769,GO:0045202	CG5912-PA				SM00135,SM00181,SM00181		PF00058,PF00058,PF00058,PF00058,PF00058,PF00058,PF00058,PF14670,PF14670	PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120		G3DSA:2.120.10.30,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.10.30	SSF63825,SSF57196,SSF63825,SSF63825,SSF63825,SSF57196								
aly5235.3	Unknown		n/a																				
aly52379.1	Unknown		n/a												61~76								
aly5241.1	D-xylulose reductase A	GO:0019569,GO:0003939,GO:0019697,GO:0042843,GO:0046526,GO:0008270,GO:0055114,GO:0016491	CG1982-PA						PF08240			PS00059	G3DSA:3.90.180.10	SSF51735,SSF50129									
aly5241.2	Lachesin	GO:0007424,GO:0016331,GO:0004714,GO:0035151,GO:0019991,GO:0035160,GO:0019898,GO:0031225,GO:0005918,GO:0061343,GO:0007409,GO:0005886,GO:0007155,GO:0007169,GO:0007156,GO:0042803	CG12369-PA				SM00408,SM00408,SM00408,SM00409,SM00409,SM00409		PF07679,PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.1	Unknown		CG12075-PA				SM00462						G3DSA:2.30.29.30	SSF50729									
aly525.10	Vacuolar protein sorting associated protein 37C	GO:0016197,GO:0070062,GO:0048306,GO:0019082,GO:0032509,GO:0000813,GO:0075733,GO:0061024,GO:0019058,GO:0003674,GO:0016032,GO:0015031,GO:0019068,GO:0031902,GO:0010008	CG1115-PA						PF07200	PS51314				SSF140111									
aly525.100	Alpha/beta hydrolase domain-containing protein 11	GO:0005575,GO:0016787,GO:0008150,GO:0052689	CG2059-PA						PF00561		PR00111,PR00111,PR00111,PR00111		G3DSA:3.40.50.1820	SSF53474									
aly525.101	Phenoloxidase subunit 2	GO:0006952,GO:0036264,GO:0036263,GO:0005615,GO:0006583,GO:0042417,GO:0005576,GO:0008152,GO:0004503,GO:0046872	CG8193-PA						PF03722,PF00372,PF03723		PR00187,PR00187,PR00187,PR00187	PS00210,PS00498,PS00209	G3DSA:1.20.1370.10,G3DSA:1.10.1280.10,G3DSA:2.60.40.1520	SSF81296,SSF48050,SSF48056									
aly525.102	Alpha/beta hydrolase domain-containing protein 11	GO:0005575,GO:0003824,GO:0008150,GO:0052689,GO:0016787	CG2059-PA						PF00561		PR00412,PR00412		G3DSA:3.40.50.1820	SSF53474									
aly525.103	Phenoloxidase subunit 2	GO:0006952,GO:0036264,GO:0036263,GO:0005615,GO:0006583,GO:0042417,GO:0005576,GO:0008152,GO:0004503,GO:0046872	CG8193-PA						PF03722,PF03723,PF00372		PR00187,PR00187,PR00187,PR00187	PS00210,PS00498	G3DSA:1.20.1370.10,G3DSA:2.60.40.1520,G3DSA:1.10.1280.10	SSF81296,SSF48056,SSF48050									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.104	MOG interacting and ectopic P-granules protein 1	GO:0007506,GO:0048599,GO:0003682,GO:0070615,GO:0000122,GO:0040025,GO:0008134,GO:0005634,GO:0002119,GO:0008406,GO:0005700,GO:0048813,GO:0042802,GO:0003723,GO:0005515,GO:0017151,GO:0046872,GO:0042826,GO:0010468,GO:0040035,GO:0016581	CG1244-PC				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13909,PF13909			PS00028,PS00028,PS00028,PS00028			264~305,316~344								
aly525.105	Protein unc-45 homolog B	GO:0005737,GO:0031034,GO:0030239,GO:0034605,GO:0031672,GO:0007519,GO:0048747,GO:0061077,GO:0048738,GO:0002088,GO:0045824,GO:0060538,GO:0050829,GO:0048471,GO:0007525,GO:0030018	CG2708-PA				SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00028,SM00028,SM00028		PF11701,PF13414	PS50293,PS50005,PS50005,PS50005			G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.40.10	SSF48371,SSF48371,SSF48452,SSF48371,SSF48371									
aly525.106	T-complex protein 1 subunit zeta	GO:0006457,GO:0070062,GO:0042623,GO:0044822,GO:0005811,GO:0044297,GO:0005832,GO:0031122,GO:1901998,GO:0007052,GO:0002199,GO:0001669,GO:0051082,GO:0007339,GO:0007067,GO:0005874,GO:0005875,GO:0005524,GO:0007099	CG8231-PA					TIGR02347	PF00118		PR00304,PR00304,PR00304,PR00304,PR00304	PS00995,PS00751,PS00750	G3DSA:3.30.260.10,G3DSA:3.30.260.10,G3DSA:3.50.7.10,G3DSA:1.10.560.10,G3DSA:1.10.560.10	SSF52029,SSF54849,SSF54849,SSF48592,SSF48592			REACT_17015					
aly525.107	CDP-diacylglycerol-inositol 3-phosphatidyltransferase	GO:0005794,GO:0030145,GO:0016780,GO:0046341,GO:0008654,GO:0019992,GO:0016021,GO:0016020,GO:0006644,GO:0030246,GO:0007602,GO:0043178,GO:0005789,GO:0044281,GO:0003881,GO:0006661,GO:0046474,GO:0005886,GO:0000139	CG9245-PA			PIRSF000848			PF01066			PS00379				00564+2.7.8.11,00562+2.7.8.11		PWY-6352,PWY-6351,PWY-7625					
aly525.108	Unknown		n/a												240~260								
aly525.109	Oxysterol-binding protein 1	GO:0005737,GO:0005794,GO:0007030,GO:0005783,GO:0006869,GO:0008142,GO:0006886,GO:0016020,GO:0008289,GO:0000139,GO:0005654,GO:0007291,GO:0044128,GO:0005634,GO:0005730,GO:0030054,GO:0019904	CG6708-PA				SM00233		PF01237,PF00169	PS50003			G3DSA:2.30.29.30	SSF50729,SSF144000	222~249								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.11	DnaJ homolog subfamily C member 30	GO:0009408,GO:0051087,GO:0005739	CG11035-PA				SM00271		PF00226	PS50076	PR00625,PR00625,PR00625	PS00636	G3DSA:1.10.287.110	SSF46565									
aly525.110	Apoptosis-inducing factor 3	GO:0050660,GO:0005783,GO:0097194,GO:0051537,GO:0005739,GO:0005743,GO:0045454,GO:0046872,GO:0055114,GO:0016491	CG4199-PC						PF00355,PF07992	PS51296	PR00411,PR00411,PR00411,PR00411,PR00368,PR00368,PR00368,PR00368,PR00368		G3DSA:3.50.50.60,G3DSA:2.102.10.10,G3DSA:3.30.390.30,G3DSA:3.50.50.60	SSF50022,SSF51905,SSF55424									
aly525.111	Unknown	GO:0005761	CG14817-PA						PF14978														
aly525.112	Signal peptide peptidase-like 3	GO:0005794,GO:0050852,GO:0005791,GO:0005783,GO:0032092,GO:0042500,GO:0016021,GO:0016020,GO:0033116,GO:0007204,GO:0006465,GO:0042803,GO:0071556,GO:0004190,GO:0033619,GO:0070886,GO:0071458,GO:0051533,GO:0005829,GO:0035307,GO:0030660	CG17370-PD				SM00730		PF04258														
aly525.113	Coiled-coil domain-containing protein 86	GO:0022008,GO:0005634	CG14210-PA						PF03879						81~130								
aly525.114	Actin-related protein 2/3 complex subunit 3	GO:0005856,GO:0005737,GO:0030833,GO:0070062,GO:0030027,GO:0016020,GO:0003779,GO:0005200,GO:0005885,GO:0034314,GO:0005925	CG4560-PC			PIRSF016315			PF04062				G3DSA:1.10.1760.10	SSF69060									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.115	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	GO:0033539,GO:0050660,GO:0042594,GO:0006635,GO:0051289,GO:0046359,GO:0000062,GO:0031966,GO:0001104,GO:0005759,GO:0048813,GO:0051384,GO:0005739,GO:0006367,GO:0004085,GO:0003995,GO:0016592,GO:0055114	CG4703-PA						PF02770,PF00441,PF02771			PS00073,PS00072	G3DSA:1.20.140.10,G3DSA:2.40.110.10,G3DSA:1.10.540.10	SSF47203,SSF56645	301~321								
aly525.116	Polymerase delta-interacting protein 2	GO:0070584,GO:0030674,GO:0005634,GO:0005739,GO:0003677,GO:0042645	CG12162-PB				SM00992		PF04379,PF08755	PS51087			G3DSA:2.60.40.1470	SSF110069,SSF141255									
aly525.117	5'-AMP-activated protein kinase catalytic subunit alpha-2	GO:0047322,GO:0006633,GO:0006909,GO:0006950,GO:0071380,GO:0045197,GO:0008286,GO:0042593,GO:0035690,GO:0007165,GO:0042595,GO:0042752,GO:0007411,GO:0035556,GO:0048511,GO:0007005,GO:0006629,GO:0005737,GO:0014850,GO:0042331,GO:0044058,GO:0005634,GO:0010508,GO:0005654,GO:0004674,GO:0010467,GO:0043066,GO:0006112,GO:0006367,GO:0004672,GO:0004712,GO:0046872,GO:0004679,GO:0035174,GO:0005524,GO:0006468,GO:0031588,GO:0006853,GO:0000278,GO:2000505,GO:0006914,GO:0007050,GO:0055089,GO:0050405,GO:0001558,GO:0009267,GO:0042149,GO:0044255,GO:0042304,GO:0045821,GO:0008610,GO:0006996,GO:0030730,GO:0061024,GO:0005829,GO:0016055,GO:0035404,GO:0006355,GO:0048813,GO:0031669,GO:0006695,GO:0016241,GO:0004703,GO:0032007,GO:0003682,GO:0044281	CG3051-PA				SM00220		PF16579,PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF103243									
aly525.118	Zinc finger protein 568	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG32772-PC				SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF00096,PF12171	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.119	Farnesol dehydrogenase	GO:0047886,GO:0006718,GO:0016614,GO:0008152	CG9150-PB						PF00106		PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly525.12	Myosin regulatory light chain sqh	GO:0007349,GO:0035277,GO:0032956,GO:0030707,GO:0007300,GO:0007298,GO:0035317,GO:0005737,GO:0060288,GO:0000281,GO:0045177,GO:0005509,GO:0048471,GO:0032036,GO:0035183,GO:0031941,GO:0016324,GO:0035159,GO:0019749,GO:0032154,GO:0042060,GO:0030048,GO:0005938,GO:0090254,GO:0005886,GO:0022008,GO:0035148,GO:0051233,GO:0001736,GO:0000910,GO:0003384,GO:0005911,GO:0030496,GO:0035191,GO:0016461,GO:0016460,GO:0005912	CG3595-PA				SM00054,SM00054		PF13405	PS50222,PS50222		PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly525.120	Unknown		n/a																				
aly525.121	Unknown		CG15252-PC																				
aly525.122	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.123	Unknown		n/a										G3DSA:1.25.10.10										
aly525.124	Armadillo repeat-containing protein 2	GO:0005575,GO:0008150,GO:0003674	CG32668-PA										G3DSA:1.25.10.10	SSF48371									
aly525.125	Zinc finger protein 410	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG7372-PA				SM00355,SM00355,SM00355,SM00868		PF07776	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57716									
aly525.126	Golgi SNAP receptor complex member 1	GO:0006891,GO:0006888,GO:0016192,GO:0048193,GO:0005801,GO:0016021,GO:0006906,GO:0000138,GO:0000139,GO:0015031,GO:0005484,GO:0031201	CG7700-PA			PIRSF027109			PF12352														
aly525.127	Cell cycle checkpoint protein RAD1	GO:0030896,GO:0008408,GO:0000077,GO:0043231,GO:0006281,GO:0008853,GO:0005634,GO:0004527,GO:0071479,GO:0005654,GO:0090305,GO:0021762,GO:0051598,GO:0005694,GO:0003684	CG3240-PA						PF02144	PS50966	PR01246,PR01246,PR01246,PR01246,PR01245,PR01245,PR01245,PR01245,PR01245		G3DSA:3.70.10.10	SSF55979									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.128	SH2B adapter protein 2	GO:0019221,GO:0019222,GO:0050851,GO:0046578,GO:0030036,GO:0007165,GO:0004871,GO:0035556,GO:0038202,GO:0005737,GO:0001725,GO:0001726,GO:0040008,GO:0016020,GO:0043568,GO:0001922,GO:0042802,GO:0046628,GO:0060180,GO:0008286,GO:0050873,GO:0005884,GO:0005886,GO:0007399,GO:0035591	CG17367-PD				SM00252,SM00233		PF00017,PF08916,PF00169	PS50001,PS50003	PR00401,PR00401,PR00401,PR00401		G3DSA:3.30.505.10,G3DSA:2.30.29.30	SSF55550,SSF50729,SSF109805									
aly525.129	T-box transcription factor TBX1	GO:0008284,GO:0007368,GO:0050679,GO:0007498,GO:2001054,GO:0060023,GO:0001945,GO:0060325,GO:0042693,GO:0003677,GO:0005634,GO:2001037,GO:0003151,GO:0007389,GO:0007517,GO:0001525,GO:0021644,GO:0090103,GO:0001974,GO:0006351,GO:0046983,GO:0001708,GO:0043410,GO:0044344,GO:0048844,GO:0048752,GO:0030878,GO:0048514,GO:0048538,GO:0030855,GO:0048644,GO:0042803,GO:0060017,GO:0043587,GO:0048701,GO:0048384,GO:0048703,GO:0008283,GO:0007605,GO:0060037,GO:0070166,GO:0042473,GO:0003007,GO:0045596,GO:0045893,GO:0001755,GO:0007525,GO:0042474,GO:0042471,GO:0007507,GO:0097152,GO:0042472,GO:0042475,GO:0009952,GO:0072513,GO:0003700,GO:0071600,GO:0003148,GO:0006355,GO:0043565,GO:0001934,GO:0002053,GO:0071300,GO:0006357,GO:0045944,GO:2000027,GO:0035176,GO:0035909,GO:0060982,GO:0001568,GO:0060415	CG11202-PA				SM00425		PF00907	PS50252	PR00937,PR00937,PR00937,PR00937,PR00937,PR00937	PS01264,PS01283	G3DSA:2.60.40.820	SSF49417									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.13	Glucose dehydrogenase [FAD, qui]	GO:0042335,GO:0016614,GO:0008812,GO:0004344,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0050660,GO:0055114	CG1152-PA						PF05199				G3DSA:3.50.50.60	SSF54373,SSF51905									
aly525.130	Unknown		n/a																				
aly525.131	Unknown	GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0008066,GO:0050907,GO:0004970	CG31718-PC										G3DSA:1.10.287.70	SSF53850,SSF53850									
aly525.132	Unknown		n/a																				
aly525.133	Fatty acid synthase	GO:0006633,GO:0047451,GO:0004320,GO:0008144,GO:0008270,GO:0001649,GO:0016491,GO:0005737,GO:0070062,GO:0016295,GO:0005835,GO:0016020,GO:0071353,GO:0005739,GO:0030879,GO:0005794,GO:0044822,GO:0004315,GO:0016788,GO:0047117,GO:0042587,GO:0005886,GO:0055114,GO:0006084,GO:0042470,GO:0004312,GO:0004313,GO:0016296,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319	CG17374-PC				SM00827,SM00829,SM00825		PF02801,PF00107,PF16197,PF00698,PF00109			PS00606	G3DSA:3.40.47.10,G3DSA:3.40.366.10,G3DSA:3.40.366.10,G3DSA:3.40.50.720,G3DSA:3.40.47.10,G3DSA:3.90.180.10	SSF55048,SSF52151,SSF52151,SSF50129,SSF53901,SSF51735,SSF53901									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.134	Unknown	GO:0006633,GO:0005835,GO:0016788,GO:0004312,GO:0009058,GO:0008270,GO:0055114,GO:0016491	CG17374-PC						PF00975				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474									
aly525.135	Fatty acid synthase	GO:0006633,GO:0047451,GO:0042470,GO:0005835,GO:0004320,GO:0016295,GO:0016296,GO:0016788,GO:0004317,GO:0004312,GO:0004313,GO:0047117,GO:0004316,GO:0008270,GO:0004314,GO:0004315,GO:0004319,GO:0055114,GO:0016491	CG17374-PC						PF00975				G3DSA:3.40.50.1820,G3DSA:1.10.1200.10	SSF53474									
aly525.136	Fatty acid synthase	GO:0006633,GO:0047451,GO:0006631,GO:0004320,GO:0042587,GO:0015939,GO:0031325,GO:0008144,GO:0035338,GO:0008270,GO:0001649,GO:0016491,GO:0005737,GO:0070062,GO:0016295,GO:0005835,GO:0016020,GO:0071353,GO:0005739,GO:0006112,GO:0030879,GO:0005794,GO:0006767,GO:0006766,GO:0044822,GO:0004315,GO:0016788,GO:0003824,GO:0047117,GO:0008152,GO:0005886,GO:0044255,GO:0055114,GO:0006084,GO:0042470,GO:0005829,GO:0004312,GO:0004313,GO:0016296,GO:0019432,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319,GO:0044281	CG17374-PC				SM00825,SM00827		PF02801,PF16197,PF00109,PF00698				G3DSA:3.40.47.10,G3DSA:3.40.366.10,G3DSA:3.40.366.10,G3DSA:3.40.47.10	SSF55048,SSF53901,SSF52151,SSF52151									
aly525.137	Asparagine--tRNA ligase, cytoplasmic	GO:0005737,GO:0006421,GO:0003676,GO:0005524,GO:0004816	CG10687-PA					TIGR00457	PF01336,PF00152	PS50862	PR01042,PR01042,PR01042,PR01042		G3DSA:3.30.930.10,G3DSA:2.40.50.140	SSF55681,SSF50249	84~106	00970+6.1.1.22	REACT_71						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.138	Aldo-keto reductase AKR2E4	GO:0004032,GO:0008202,GO:0055114,GO:0016491	CG10863-PA			PIRSF000097			PF00248		PR00069,PR00069,PR00069,PR00069,PR00069	PS00062,PS00798,PS00063	G3DSA:3.20.20.100	SSF51430									
aly525.139	Putative tricarboxylate transport protein, mitochondrial	GO:0006843,GO:0016021,GO:0005811,GO:0005740,GO:0005739,GO:0005743,GO:0022857,GO:0006810,GO:0016006,GO:0015746,GO:0005371	CG6782-PE						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly525.14	Glucose dehydrogenase [FAD, qui]	GO:0042335,GO:0016614,GO:0008812,GO:0004344,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0050660,GO:0055114	CG1152-PA						PF00732			PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905									
aly525.140	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1-A	GO:0035060,GO:0030154,GO:0008587,GO:0008586,GO:0002165,GO:0000228,GO:0008544,GO:0001700,GO:0005634,GO:0043044,GO:0003713,GO:0007474,GO:0008285,GO:0006281,GO:0007517,GO:0045893,GO:0090544,GO:0006338,GO:0006337,GO:0070983,GO:0070984,GO:0044772,GO:0006355,GO:0048813,GO:0006357,GO:0006351,GO:0005515	CG1064-PA			PIRSF038126			PF04855,PF04855														
aly525.141	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.142	Glucose dehydrogenase [FAD, qui]	GO:0042335,GO:0016614,GO:0008812,GO:0004344,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0050660,GO:0055114	CG1152-PA						PF05199				G3DSA:3.50.50.60	SSF51905									
aly525.143	Nardilysin	GO:0004222,GO:0052548,GO:0005739,GO:0006508,GO:0008233,GO:0046872,GO:0051044	CG10588-PA						PF16187				G3DSA:3.30.830.10,G3DSA:3.30.830.10,G3DSA:3.30.830.10,G3DSA:3.30.830.10	SSF63411									
aly525.144	Nardilysin	GO:0004222,GO:0052548,GO:0005739,GO:0006508,GO:0008233,GO:0046872,GO:0051044	CG10588-PA										G3DSA:3.30.830.10	SSF63411									
aly525.145	Unknown		CG8501-PA																				
aly525.146	Unknown		n/a																				
aly525.147	Tetratricopeptide repeat protein 28	GO:0005737,GO:0007346,GO:0005813,GO:0030496,GO:0000922,GO:0005575,GO:0003674,GO:0008150,GO:0007067,GO:0051301	CG43163-PD						PF12770														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.148	Diphthamide biosynthesis protein 1	GO:0017183,GO:0005737,GO:0005634,GO:0006909,GO:0008283	CG11652-PA			PIRSF004967		TIGR00322	PF01866										UPA00559				
aly525.149	Unknown		n/a																				
aly525.15	Glucose dehydrogenase [FAD, qui]	GO:0042335,GO:0016614,GO:0008812,GO:0004344,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0050660,GO:0055114	CG1152-PA			PIRSF000137			PF05199,PF00732			PS00624,PS00623	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly525.16	Unknown		n/a						PF15074														
aly525.17	39S ribosomal protein L44, mitochondrial	GO:0070126,GO:0006996,GO:0070124,GO:0070125,GO:0005840,GO:0004525,GO:0044822,GO:0003735,GO:0005743,GO:0003723,GO:0005762,GO:0022008,GO:0032543,GO:0006396	CG2109-PA				SM00535			PS50142			G3DSA:1.10.1520.10	SSF69065	611~631								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.18	Centromere protein J	GO:0000242,GO:0000086,GO:0008275,GO:0005874,GO:0051301,GO:0000278,GO:0007020,GO:0035186,GO:0005813,GO:0005814,GO:0046785,GO:0007140,GO:0046599,GO:0045298,GO:0015631,GO:0042384,GO:0051298,GO:0051297,GO:0019901,GO:0007052,GO:0019904,GO:0008356,GO:0040011,GO:0006996,GO:0005829,GO:0007099	CG10061-PA						PF07202						1203~1207,634~654,692~726,567~608,660~687									
aly525.19	Nardilysin	GO:0003824,GO:0008233,GO:0046872,GO:0004222,GO:0006508	CG2025-PA						PF05193,PF00675			PS00143	G3DSA:3.30.830.10,G3DSA:3.30.830.10,G3DSA:3.30.830.10,G3DSA:3.30.830.10,G3DSA:3.30.830.10	SSF63411,SSF63411,SSF63411,SSF63411,SSF63411										
aly525.2	Unknown		CG14395-PB												940~941								
aly525.20	Apyrase	GO:0016787,GO:0008253,GO:0017110,GO:0017111,GO:0016788,GO:0000166,GO:0009166,GO:0005576,GO:0046872,GO:0005524	CG1961-PA						PF02872		PR01607,PR01607,PR01607,PR01607,PR01607		G3DSA:3.60.21.10,G3DSA:3.90.780.10	SSF55816,SSF56300									
aly525.21	Cell cycle control protein 50A	GO:0005794,GO:0016324,GO:0016021,GO:0016020,GO:0030658,GO:0015914	CG9947-PA			PIRSF015840			PF03381														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.22	Cell cycle control protein 50A	GO:0005794,GO:0006855,GO:0005783,GO:0016324,GO:0016021,GO:0016020,GO:0036010,GO:0030658,GO:0045332,GO:0070863,GO:0010976	CG9947-PA			PIRSF015840			PF03381														
aly525.23	Septin-1	GO:0000910,GO:0031105,GO:0031625,GO:0005940,GO:0008152,GO:0045172,GO:0003924,GO:0007349,GO:0000281,GO:0043065,GO:0005515,GO:0006184,GO:0042803,GO:0005875,GO:0007049,GO:0005525	CG1403-PA			PIRSF006698			PF00735	PS51719	PR01740,PR01740,PR01740		G3DSA:3.40.50.300	SSF52540									
aly525.24	Squamous cell carcinoma antigen recognized by T-cells 3	GO:0042393,GO:0000244,GO:0003676,GO:0007417,GO:0005737,GO:0000387,GO:0000902,GO:0030621,GO:0005634,GO:1990381,GO:0030624,GO:0000166,GO:0005654,GO:1903586,GO:0010468,GO:0017070,GO:0016607,GO:0044822,GO:0048872,GO:0071425,GO:0006334,GO:0000398,GO:0005622,GO:0015030,GO:0006396,GO:0003729	CG3312-PB				SM00360,SM00360		PF00076	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF48452,SSF54928	379~406								
aly525.25	Uncharacterized protein C4orf29 homolog	GO:0005576	CG32112-PB						PF09752				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474	351~371								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.26	Neurogenic locus notch homolog protein 1	GO:0055016,GO:0021531,GO:0021514,GO:0031017,GO:0031016,GO:0021523,GO:0042663,GO:0004872,GO:0005634,GO:0021986,GO:0007219,GO:0016021,GO:0050768,GO:0002244,GO:0005509,GO:0035907,GO:0061314,GO:0048337,GO:0060271,GO:0001525,GO:0005886,GO:0048259,GO:0001756,GO:0048699,GO:0009952,GO:0001840,GO:0006355,GO:0048936,GO:0006351,GO:0007368	CG9572-PA				SM00181,SM00181,SM00181,SM00181,SM00181,SM00181		PF12661	PS50026,PS50026,PS50026,PS50026		PS01186,PS01186,PS01186,PS01186,PS01186	G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.10.25.10										
aly525.27	Exocyst complex component 8	GO:0000910,GO:0007110,GO:0045199,GO:0016192,GO:0046907,GO:0048812,GO:0016081,GO:0016080,GO:0006887,GO:0000916,GO:0005737,GO:0043147,GO:0007163,GO:0003674,GO:0015031,GO:0032456,GO:0007286,GO:0007269,GO:0072659,GO:0007111,GO:0000145	CG6095-PB				SM00233		PF08700,PF16528	PS50003			G3DSA:2.30.29.30	SSF50729,SSF74788	110~130								
aly525.28	Vacuolar protein sorting associated protein 33A	GO:0006904,GO:0008333,GO:0007040,GO:0031410,GO:0000149,GO:0016020,GO:0000046,GO:0031396,GO:0031902,GO:0030897,GO:0048072,GO:0006622,GO:0035542,GO:0019905,GO:0006727,GO:0008057,GO:0008593,GO:0008340,GO:0007032,GO:0007220,GO:0006897,GO:0016192,GO:0046907,GO:0016197,GO:0005829,GO:0032403,GO:0005764,GO:0005765,GO:0033263,GO:0005515,GO:0015031	CG12230-PC						PF00995				G3DSA:3.90.830.10,G3DSA:1.10.274.20,G3DSA:3.40.50.1910,G3DSA:3.40.50.1910	SSF56815		00360+4.3.1.24,00940+4.3.1.24		PWY-5883,PWY-6444,PWY-1121,PWY-6457	UPA00713				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.29	Small G protein signaling modulator 1	GO:0032313,GO:0005794,GO:0005097	CG1695-PC				SM00164,SM00593		PF02759,PF00566	PS50826,PS50086			G3DSA:1.10.8.270,G3DSA:1.10.8.270	SSF47923,SSF47923,SSF140741,SSF140741,SSF47923	23~43								
aly525.3	Unknown	GO:0005515	CG12581-PB				SM00462							SSF50729									
aly525.30	Peptidoglycan-recognition protein LB	GO:0004040,GO:0008745,GO:0045087,GO:0009253,GO:0000270,GO:0042834,GO:0006952,GO:0050830,GO:0005576,GO:0008270,GO:0005887,GO:0006955,GO:0061060,GO:0005875	CG9681-PA										G3DSA:3.40.80.10	SSF55846									
aly525.31	Peptidoglycan-recognition protein LB	GO:0005887,GO:0004040,GO:0008745,GO:0045087,GO:0006955,GO:0000270,GO:0006952,GO:0016045,GO:0050830,GO:0005576,GO:0008270,GO:0005515,GO:0009253,GO:0061060,GO:0042834	CG14704-PD				SM00644,SM00701		PF01510				G3DSA:3.40.80.10	SSF55846									
aly525.32	Peptidoglycan-recognition protein LB	GO:0005887,GO:0004040,GO:0008745,GO:0045087,GO:0006955,GO:0000270,GO:0006952,GO:0016045,GO:0050830,GO:0005576,GO:0008270,GO:0005515,GO:0009253,GO:0061060,GO:0042834	CG14704-PD				SM00644,SM00701		PF01510				G3DSA:3.40.80.10	SSF55846									
aly525.33	Peptidoglycan-recognition protein LB	GO:0005887,GO:0004040,GO:0008745,GO:0045087,GO:0006955,GO:0000270,GO:0006952,GO:0016045,GO:0050830,GO:0005576,GO:0008270,GO:0005515,GO:0009253,GO:0061060,GO:0042834	CG14704-PD			PIRSF037945	SM00701,SM00644		PF01510				G3DSA:3.40.80.10	SSF55846									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.34	Peptidoglycan-recognition protein LB	GO:0005887,GO:0004040,GO:0016045,GO:0045087,GO:0006955,GO:0000270,GO:0006952,GO:0008745,GO:0050830,GO:0005576,GO:0008270,GO:0005515,GO:0009253,GO:0061060,GO:0042834	CG14704-PD			PIRSF037945	SM00701,SM00644		PF01510				G3DSA:3.40.80.10	SSF55846										
aly525.35	Unknown	GO:0003779,GO:0030838,GO:0060297,GO:0051015	CG31374-PC				SM00246,SM00246		PF02205	PS51082,PS51082				SSF57997	511~562,719~765,669~689,576~636,798~853								
aly525.36	Condensin complex subunit 3	GO:0005720,GO:0000070,GO:0000819,GO:0005829,GO:0005634,GO:0000281,GO:0007052,GO:0070194,GO:0000796,GO:0007076,GO:0000785,GO:0022008,GO:0000775,GO:0051301	CG34438-PF						PF12719				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371	502~522,995~1022								
aly525.37	Glucose dehydrogenase [FAD, qui]	GO:0042335,GO:0016614,GO:0008812,GO:0004344,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0050660,GO:0055114	CG1152-PA			PIRSF000137			PF05199,PF00732			PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly525.38	Pupal cuticle protein	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG5494-PA																				
aly525.39	Chromobox protein homolog 3	GO:0005720,GO:0005654,GO:0005635,GO:0005719,GO:0048511,GO:0031452,GO:0005634,GO:0000122,GO:0010369,GO:0000792,GO:0000779,GO:0005819,GO:0045944,GO:0019904,GO:0031618,GO:0045892,GO:0000785,GO:0003682,GO:0016568,GO:0006351	CG7041-PA				SM00300		PF01393	PS50013			G3DSA:2.40.50.40,G3DSA:2.40.50.40	SSF54160									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.4	Protein Red	GO:0071011,GO:0071013,GO:0000398,GO:0007528,GO:0003674,GO:0005634,GO:0007274,GO:0072553	CG18005-PA						PF07808,PF07807						59~94								
aly525.40	Serine/threonine-protein kinase TAO1	GO:0016319,GO:0000186,GO:0097194,GO:0051493,GO:0030707,GO:0042981,GO:0033332,GO:0005737,GO:0007346,GO:0031572,GO:0005634,GO:0000165,GO:0045178,GO:0004674,GO:0023014,GO:0004672,GO:0005524,GO:0006468,GO:0006281,GO:0046621,GO:0006915,GO:0006974,GO:0045471,GO:0046330,GO:0048036,GO:0032874,GO:0005886,GO:0042220,GO:0035329,GO:0030295,GO:0019901,GO:0031098,GO:0035094,GO:0004702,GO:0045807,GO:0004709	CG14217-PE				SM00220		PF00069	PS50011		PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112	529~549,691~720,558~596,654~674,926~946								
aly525.41	Protein NipSnap	GO:0005575,GO:0008150,GO:0003674	CG9212-PB						PF07978,PF07978				G3DSA:3.30.70.900,G3DSA:3.30.70.900	SSF54909,SSF54909									
aly525.42	Rabankyrin-5	GO:0048598,GO:0030904,GO:0016020,GO:0006897,GO:0070062,GO:0005765,GO:0005773,GO:0032439,GO:0090160,GO:0017137,GO:0044354,GO:0042147,GO:0016023,GO:0048549,GO:0003382,GO:1901981,GO:0046872,GO:0005769,GO:0034058,GO:0010008	CG41099-PC				SM00064,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF13857,PF13637,PF13637,PF12796,PF12796,PF01363	PS50297,PS50097,PS50297,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50178,PS50088	PR01415,PR01415		G3DSA:3.30.40.10,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:3.30.710.10	SSF48403,SSF54695,SSF57903,SSF48403,SSF48403,SSF48403	19~39								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.43	Cytochrome b-c1 complex subunit 6, mitochondrial	GO:0032403,GO:0005750,GO:0008121,GO:0006122,GO:0051291	CG30354-PA			PIRSF000019			PF02320				G3DSA:1.10.287.20	SSF81531									
aly525.44	Histone-lysine N-methyltransferase SETD1	GO:0018024,GO:0046427,GO:0006338,GO:0005634,GO:0005700,GO:0000166,GO:0006355,GO:0000791,GO:0035327,GO:0003723,GO:0003676,GO:0051568,GO:0044648,GO:0048188,GO:0042800,GO:0080182,GO:0006351	CG40351-PA				SM00508,SM00360,SM00317		PF00076,PF11764,PF00856	PS50102,PS50280,PS50868			G3DSA:3.30.70.330,G3DSA:2.170.270.10	SSF54928,SSF82199	1072~1092	00310+2.1.1.43							
aly525.45	Rho-associated protein kinase 2	GO:0005083,GO:0005886,GO:0030036,GO:0010825,GO:0036464,GO:0031616,GO:0035556,GO:0008625,GO:0048511,GO:0019992,GO:0005813,GO:0005634,GO:0007109,GO:0000281,GO:0004674,GO:0004672,GO:0001843,GO:0046872,GO:0005524,GO:0006468,GO:0051298,GO:0006939,GO:0044822,GO:0042752,GO:0032956,GO:0007266,GO:0005826,GO:0000910,GO:0000915,GO:0006325,GO:0048813,GO:0045616,GO:2000431,GO:0016525	CG10522-PB				SM00220		PF00069,PF00780	PS50011		PS00108	G3DSA:1.10.510.10	SSF56112	613~654,495~515,992~1012,711~766,676~703,548~568,262~303,932~966,425~487,229~249,305~360,862~924									
aly525.46	Transmembrane emp24 domain-containing protein 2 (Fragment)	GO:0005783,GO:0090263,GO:0072661,GO:0033116,GO:0035220,GO:0005789,GO:0048042,GO:0070863,GO:0030137,GO:0006888,GO:0000003,GO:0030663,GO:0016021,GO:0061357,GO:0005794,GO:0005793,GO:0048193,GO:0005215,GO:0034260,GO:0032580,GO:0030126,GO:0007030,GO:0016192	CG3564-PB						PF01105,PF00650	PS50191,PS50866	PR00180,PR00180,PR00180		G3DSA:3.40.525.10	SSF46938,SSF52087,SSF101576	261~281,421~441								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.47	DNA replication ATP-dependent helicase/nuclease DNA2	GO:0017108,GO:0006260,GO:0003677,GO:0003678,GO:0043504,GO:0042645,GO:0000729,GO:0033567,GO:0006264,GO:0043142,GO:0045740,GO:0043137,GO:0046872,GO:0005524,GO:0006284,GO:0004003,GO:0016890,GO:0000076,GO:0000014,GO:0051539,GO:0004518,GO:0000737,GO:0005760,GO:0043139,GO:0005634	CG2990-PB				SM00852,SM00852	TIGR00177	PF13086,PF08696,PF03453,PF00994,PF00994,PF13245,PF13087			PS01079,PS01078	G3DSA:2.170.190.11,G3DSA:3.40.50.300,G3DSA:2.40.340.10,G3DSA:2.40.340.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.90.105.10,G3DSA:3.40.980.10,G3DSA:3.40.980.10	SSF52540,SSF52540,SSF63882,SSF53218,SSF53218				PWY-6823	UPA00344				
aly525.48	Probable 18S rRNA (guanine-N(7))-methyltransferase	GO:0005737,GO:0008757,GO:0005634,GO:0006355,GO:0006364,GO:0008152,GO:0008168,GO:0022008,GO:0044822,GO:0016568,GO:0006351	CG10903-PB						PF08241,PF12589				G3DSA:3.40.50.150	SSF53335									
aly525.49	Protein FAM173B	GO:0016021	CG3337-PA										G3DSA:3.40.50.150	SSF53335									
aly525.5	Macrophage migration inhibitory factor	GO:2000343,GO:0042056,GO:0090344,GO:1902166,GO:0048146,GO:0043406,GO:0010629,GO:0007166,GO:0033138,GO:0002906,GO:0005737,GO:0042289,GO:0005615,GO:0050178,GO:0043209,GO:0008283,GO:0005654,GO:0045087,GO:0033033,GO:0071157,GO:0004167,GO:0070207,GO:0030890,GO:0030330,GO:0090238,GO:0009986,GO:0001516,GO:0061078,GO:0043518,GO:0006954,GO:0070062,GO:0032269,GO:0007569,GO:0050715,GO:0050731,GO:0031666,GO:0061081,GO:0070374,GO:0010739	n/a						PF01187			PS01158	G3DSA:3.30.429.10	SSF55331									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.50	ATP-dependent RNA helicase Ddx1	GO:0033677,GO:0000245,GO:0008026,GO:0008143,GO:0042254,GO:0090305,GO:0003676,GO:0001700,GO:0006302,GO:0005634,GO:0003712,GO:0010501,GO:0032508,GO:0005524,GO:0006446,GO:0004004,GO:0004386,GO:1903506,GO:0004518,GO:0005575,GO:0003682,GO:0004527	CG9054-PA				SM00490,SM00449,SM00487		PF00271,PF00270,PF00622	PS51192,PS51194,PS51195,PS50188			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF49899										
aly525.51	Histone-lysine N-methyltransferase pr-set7	GO:0000077,GO:0035067,GO:0005634,GO:0005700,GO:0030261,GO:0006355,GO:0034771,GO:0034770,GO:0016571,GO:0042799,GO:0005515,GO:0007067,GO:0051301,GO:0006351	CG3307-PA				SM00317		PF00856	PS50280			G3DSA:2.170.270.10	SSF82199										
aly525.52	Histone deacetylase 8	GO:0032041,GO:0005705,GO:0006099,GO:0000785,GO:0007062,GO:0005737,GO:0070822,GO:0007517,GO:0071922,GO:0000122,GO:0004407,GO:0005634,GO:0003714,GO:0016458,GO:0016575,GO:2001229,GO:0022904,GO:0046872,GO:0048477,GO:0017053,GO:0045892,GO:0005886,GO:0008340,GO:0022008,GO:0007350,GO:0035098,GO:0016580,GO:0016581,GO:0050771,GO:0031523,GO:0070983,GO:0005700,GO:0006355,GO:0048813,GO:0006351,GO:0005515,GO:0006342	CG7471-PA			PIRSF037913			PF00850		PR01270,PR01270,PR01270,PR01271,PR01271,PR01271,PR01271,PR01271,PR01271		G3DSA:3.40.800.20	SSF52768										
aly525.53	Ubiquitin-conjugating enzyme E2 L3	GO:0005737,GO:0008283,GO:0070979,GO:0016874,GO:0071383,GO:0006355,GO:0071385,GO:0000209,GO:0044770,GO:0016567,GO:0006351,GO:0005515,GO:0022008,GO:0004842,GO:0005634,GO:0005524,GO:0003713	CG5788-PA				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.54	Eukaryotic translation initiation factor 3 subunit C	GO:0006446,GO:0005852,GO:0016282,GO:0005829,GO:0033290,GO:0031369,GO:0006413,GO:0001731,GO:0003743	CG4954-PA	MF_03002			SM00088		PF01399,PF05470				G3DSA:1.10.10.10	SSF46785	237~257								
aly525.55	Zinc finger protein 26	GO:0005737,GO:0005819,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0005876	CG8474-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF00096,PF13912,PF13912,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57716,SSF57667									
aly525.56	Soluble NSF attachment protein 29	GO:0055037,GO:0043005,GO:0030728,GO:0016192,GO:0016324,GO:0000149,GO:0000046,GO:0046903,GO:0065002,GO:0097352,GO:0045202,GO:0007269,GO:0005484,GO:0031201,GO:0030054	CG11173-PA				SM00397,SM00397		PF12352	PS50192			G3DSA:1.20.5.110,G3DSA:1.20.5.110	SSF58038,SSF58038	91~114,48~68								
aly525.57	Pickpocket protein 28	GO:0005272,GO:0071462,GO:0015280,GO:0016021,GO:0009415,GO:0006814,GO:0035002,GO:0035725,GO:0042756,GO:0005886	CG8546-PC						PF00858				G3DSA:1.10.287.770										
aly525.58	Pickpocket protein 28	GO:0005272,GO:0071462,GO:0016021,GO:0016020,GO:0006814,GO:0035002,GO:0035725,GO:0042756,GO:0009415,GO:0005886	CG4805-PA						PF00858		PR01078,PR01078,PR01078,PR01078,PR01078		G3DSA:2.60.470.10,G3DSA:2.60.470.10,G3DSA:2.60.470.10										
aly525.59	Pupal cuticle protein	GO:0042302	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.6	E3 ubiquitin-protein ligase SIAH1	GO:0008022,GO:0010498,GO:0030154,GO:0008270,GO:0007283,GO:0061630,GO:0007275,GO:0007049,GO:0005737,GO:0004842,GO:0005634,GO:0030877,GO:0042787,GO:0006508,GO:2001244,GO:0051402,GO:0005886,GO:0016874,GO:0043621,GO:0031648,GO:0007423,GO:0005829,GO:0007465,GO:0000151,GO:0045676,GO:0016567,GO:0006511,GO:0005515,GO:0043161,GO:0005769	CG9949-PA						PF03145	PS51081			G3DSA:3.90.890.10	SSF49599					UPA00143				
aly525.60	Tetratricopeptide repeat protein 28	GO:0005737,GO:0007346,GO:0005813,GO:0030496,GO:0000922,GO:0005575,GO:0003674,GO:0005515,GO:0008150,GO:0007067,GO:0051301	CG43163-PD				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF13414,PF12770,PF13424,PF13424,PF13424,PF13424,PF00515,PF13176,PF07719,PF07719	PS50005,PS50005,PS50005,PS50005,PS50293,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452,SSF48452,SSF48452,SSF48452	851~881,1014~1034								
aly525.61	Trichoplein keratin filament-binding protein	GO:0005737,GO:0005856	CG17230-PA												382~402,58~95,325~345,166~239,432~479								
aly525.62	Zinc finger protein 593 homolog	GO:0022008,GO:0046872,GO:0008270,GO:0003676	CG3224-PA				SM00451		PF12171			PS00028		SSF57667									
aly525.63	Serine--tRNA ligase, chloroplastic/mitochondrial	GO:0070584,GO:0006434,GO:0000049,GO:0004828,GO:0005737,GO:0005739,GO:0000166,GO:0009658,GO:0045333,GO:0007005,GO:0048481,GO:0005524,GO:0009507	CG31133-PA			PIRSF001529			PF00587	PS50862			G3DSA:1.10.287.40,G3DSA:3.30.930.10	SSF46589,SSF55681	49~69	00970+6.1.1.11	REACT_71	PWY-6281	UPA00906				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.64	LIM/homeobox protein Lhx1	GO:0042074,GO:0008270,GO:0009798,GO:0043565,GO:0007517,GO:0007479,GO:0005634,GO:0043009,GO:0010468,GO:0048749,GO:0007480,GO:0045892,GO:0045893,GO:0039020,GO:0022008,GO:0035565,GO:0039003,GO:0009952,GO:0003700,GO:0048793,GO:0006355,GO:0072080,GO:0045944,GO:0006351,GO:0005667,GO:0030903,GO:0003002	CG11354-PA				SM00132,SM00132,SM00389		PF00046,PF00412,PF00412	PS50071,PS50023,PS50023		PS00478,PS00478,PS00027	G3DSA:2.10.110.10,G3DSA:1.10.10.60,G3DSA:2.10.110.10	SSF57716,SSF57716,SSF46689										
aly525.65	Unknown		n/a																				
aly525.66	Unknown		n/a																				
aly525.67	JmjC domain-containing histone demethylation protein 1	GO:0006351,GO:0033522,GO:0007379,GO:0034721,GO:0005634,GO:0070544,GO:0031146,GO:0006355,GO:0051864,GO:0019005,GO:0034647,GO:0008270,GO:0005515,GO:0003677,GO:0007526,GO:0031519	CG11033-PB				SM00256,SM00558		PF13621,PF02008,PF12937,PF16866	PS51058,PS51184			G3DSA:2.60.120.650,G3DSA:3.80.10.10	SSF81383,SSF52047,SSF51197										
aly525.68	Methyl-CpG-binding domain protein 4	GO:0005737,GO:0006306,GO:0006284,GO:0008630,GO:0006281,GO:0009314,GO:0005634,GO:0005654,GO:0006974,GO:0003824,GO:0000785,GO:0008263,GO:0003677,GO:0007095	n/a										G3DSA:1.10.340.30	SSF48150			REACT_216						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.69	Calcium release-activated calcium channel protein 1	GO:0004252,GO:0015279,GO:0016020,GO:0007399,GO:0002115,GO:0016021,GO:0051928,GO:0051533,GO:0005887,GO:0005886	CG11430-PE						PF07856														
aly525.7	Protein unc-119 homolog	GO:0005575,GO:0015031,GO:0003674,GO:0008289,GO:0007399	CG1659-PA						PF05351				G3DSA:2.70.50.40	SSF81296									
aly525.70	Unknown		n/a						PF15810														
aly525.71	Peregrin	GO:0005737,GO:0006351,GO:0043966,GO:0033563,GO:0005634,GO:0070776,GO:0005654,GO:0006325,GO:0008270,GO:0003677,GO:0045893	CG1845-PA				SM00297,SM00293,SM00249,SM00249		PF00439,PF13832,PF00855,PF10513,PF13831	PS50157,PS50016,PS50014,PS50812	PR00503,PR00503,PR00503,PR00503	PS01359,PS00028	G3DSA:2.30.30.160,G3DSA:1.20.920.10,G3DSA:3.30.40.10	SSF63748,SSF47370,SSF57903									
aly525.72	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 7	GO:0032543,GO:0008137,GO:0042773,GO:0005739,GO:0006120,GO:0003735,GO:0005743,GO:0005747,GO:0003954,GO:0005761	CG3621-PA						PF07347														
aly525.73	Cytosolic 10-formyltetrahydrofolate dehydrogenase	GO:0005737,GO:0016155,GO:0006730,GO:0016620,GO:0016742,GO:0009058,GO:0008168,GO:0009258,GO:0055114	CG8665-PA			PIRSF036489			PF00550,PF00171,PF00551,PF02911	PS50075		PS00070,PS00687	G3DSA:3.40.50.170,G3DSA:1.10.1200.10,G3DSA:3.40.605.10,G3DSA:3.10.25.10,G3DSA:3.40.309.10	SSF50486,SSF47336,SSF53720,SSF53328		00670+1.5.1.6,00670+2.1.2.9,00970+2.1.2.9								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.74	L-asparaginase	GO:0004622,GO:0006520,GO:0006528,GO:0004067	CG6428-PA			PIRSF001220,PIRSF500176	SM00870		PF00710,PF00795	PS51732,PS50263	PR00139,PR00139,PR00139	PS00917	G3DSA:3.40.50.1170,G3DSA:3.40.50.40,G3DSA:3.40.50.40,G3DSA:3.60.110.10	SSF53774,SSF53774,SSF56317									
aly525.75	Flotillin-2	GO:0005737,GO:0016600,GO:0005829,GO:0005198,GO:0035011,GO:0005886,GO:0007155	CG32593-PJ				SM00244		PF01145					SSF117892	235~262								
aly525.76	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9503-PA			PIRSF000137			PF00732,PF05199			PS00623	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905,SSF54373		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly525.77	Glucose dehydrogenase [FAD, qui]	GO:0042600,GO:0050660,GO:0016614,GO:0008812,GO:0004344,GO:0006066,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG12398-PA						PF05199,PF05199,PF05199,PF00732,PF00732,PF00732			PS00624,PS00624,PS00623,PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905,SSF51905,SSF51905,SSF54373,SSF54373,SSF51905,SSF51905,SSF54373									
aly525.78	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0045455,GO:0055114,GO:0016491	CG9512-PA						PF00732				G3DSA:3.50.50.60	SSF51905									
aly525.79	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9512-PA						PF00732,PF05199			PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905,SSF54373									

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.8	Phosphatidylinositol transfer protein beta isoform	GO:0033206,GO:0005548,GO:0001700,GO:0001701,GO:0070062,GO:0043147,GO:0016006,GO:0005794,GO:0006810,GO:0031965,GO:0032154,GO:0008289,GO:0007112,GO:0005886,GO:0048137,GO:0070732,GO:0007111,GO:0007110,GO:0031566,GO:0000915,GO:0000916,GO:0035091	CG5269-PB						PF02121		PR00391,PR00391,PR00391,PR00391		G3DSA:3.30.530.20	SSF55961	272~292								
aly525.80	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0045455,GO:0055114,GO:0016491	CG9514-PA						PF05199,PF00732,PF00732			PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905									
aly525.81	Glucose dehydrogenase [FAD, qui]	GO:0005575,GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0045455,GO:0055114,GO:0016491	CG45065-PA			PIRSF000137			PF00732,PF05199			PS00623,PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905,SSF54373		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly525.82	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0046331,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9518-PA						PF00732,PF00732,PF05199,PF05199			PS00624,PS00624,PS00623	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905,SSF51905,SSF51905,SSF54373,SSF54373	1227~1227								
aly525.83	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0045455,GO:0055114,GO:0016491	CG9521-PA			PIRSF000137			PF00732,PF05199			PS00623,PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905,SSF54373		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.84	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0045455,GO:0055114,GO:0016491	CG9503-PA			PIRSF000137			PF00732,PF05199			PS00623,PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly525.85	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0055114	CG6142-PA			PIRSF000137			PF00732,PF05199			PS00623,PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905,SSF54373		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly525.86	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0055114	CG6142-PA			PIRSF000137			PF05199,PF00732			PS00623,PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly525.87	Serine/threonine-protein phosphatase 4 catalytic subunit	GO:0005737,GO:0016787,GO:0007346,GO:0007017,GO:0000278,GO:0006470,GO:0005634,GO:0004722,GO:0004721,GO:0005815,GO:0005813,GO:0022008,GO:0046872	CG32505-PG				SM00156		PF00149		PR00114,PR00114,PR00114,PR00114,PR00114,PR00114,PR00114	PS00125	G3DSA:3.60.21.10	SSF56300									
aly525.88	NAD-dependent protein deacylase Sirt4	GO:0034979,GO:0005759,GO:0006471,GO:0008270,GO:0070403	CG3187-PC	MF_01967					PF02146	PS50305			G3DSA:3.40.50.1220,G3DSA:3.40.50.1220,G3DSA:3.40.50.1220,G3DSA:3.30.1600.10,G3DSA:3.30.1600.10	SSF52467										
aly525.89	Elongator complex protein 5	GO:0005737,GO:0030335,GO:0005634,GO:0033588,GO:0006355,GO:0006351	n/a						PF10483														

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.9	N-acetylglucosaminyl-phosphatidylinositol de-N-acetylase	GO:0016021,GO:0000225,GO:0042406,GO:0006506	CG4433-PB						PF02585				G3DSA:3.40.50.10320	SSF102588									
aly525.90	Eukaryotic translation initiation factor 4H	GO:0048589,GO:0005829,GO:0016020,GO:0044822,GO:0019953,GO:0000166,GO:0003676,GO:0048471,GO:0003743,GO:0006413,GO:0005875,GO:0003729	CG4429-PD				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly525.91	Myb-binding protein 1A-like protein	GO:0048511,GO:0005730,GO:0003887,GO:0006355,GO:0006351,GO:0003677	CG6189-PA						PF04931						1085~1105								
aly525.92	Ubiquitin-conjugating enzyme E2 G1	GO:0005737,GO:0031625,GO:0070062,GO:0061630,GO:0000209,GO:0016881,GO:0016567,GO:0006511,GO:0004842,GO:0061631,GO:0070936,GO:0016874,GO:0070534,GO:0005524	CG40045-PA				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				
aly525.93	Cell cycle checkpoint control protein RAD9A	GO:0030896,GO:0005737,GO:0008408,GO:0000077,GO:0000076,GO:0006281,GO:1902231,GO:0005634,GO:0005654,GO:0031965,GO:0017124,GO:0019899,GO:0006974,GO:0090305,GO:0006260,GO:0071479,GO:0042826,GO:0008853,GO:0019901,GO:0031573	CG3945-PA						PF04139				G3DSA:3.70.10.10	SSF55979			REACT_1538						
aly525.94	Unknown		n/a												6~26								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly525.95	Unknown	GO:0022008	CG31344-PA						PF09995														
aly525.96	Unknown	GO:0022008	CG31344-PA						PF09995														
aly525.97	Protein DGCR14 homolog	GO:0007399,GO:0005634,GO:0071013,GO:0000398,GO:0004757	CG1474-PA						PF09751														
aly525.98	Elongation of very long chain fatty acids protein 7	GO:0009922,GO:0005783,GO:0016021,GO:0030497,GO:0005789,GO:0005575,GO:0016740,GO:0034626,GO:0019367,GO:0042761	CG5278-PA						PF01151			PS01188				00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					
aly525.99	Alpha/beta hydrolase domain-containing protein 11	GO:0005575,GO:0016787,GO:0008150,GO:0005739,GO:0052689	CG2059-PA						PF00561		PR00111,PR00111,PR00111,PR00111		G3DSA:3.40.50.1820	SSF53474									
aly526.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly526.10	Poly(A) RNA polymerase gld-2 homolog A	GO:0005737,GO:0007616,GO:0004652,GO:0005654,GO:0003723,GO:0043005,GO:0043631,GO:0046872,GO:0005524,GO:0006397	CG5732-PC										G3DSA:3.30.460.10	SSF81301,SSF81631									
aly526.11	Unknown		CG10435-PA							PS50030,PS51497					77~100								
aly526.12	Chondroitin sulfate synthase 1	GO:0030206,GO:0051216,GO:0002063,GO:0016021,GO:0016020,GO:0051923,GO:0031667,GO:0060349,GO:0050510,GO:0009954,GO:0005576,GO:0045880,GO:0030279,GO:0016758,GO:0047238,GO:0008375,GO:0015020,GO:0046872,GO:0032580,GO:0016757	CG9220-PC						PF05679					SSF53448									
aly526.13	Chondroitin sulfate synthase 1	GO:0030206,GO:0051216,GO:0002063,GO:0016021,GO:0016020,GO:0051923,GO:0031667,GO:0060349,GO:0050510,GO:0009954,GO:0005576,GO:0045880,GO:0030279,GO:0016758,GO:0047238,GO:0008375,GO:0015020,GO:0046872,GO:0032580,GO:0016757	CG9220-PC						PF05679				G3DSA:3.90.550.10,G3DSA:3.90.550.10,G3DSA:3.90.550.10	SSF53448,SSF53448,SSF53448,SSF53448									
aly526.14	Unknown		CG2150-PA																				
aly526.15	Retinol dehydrogenase 13	GO:0042462,GO:0016614,GO:0010842,GO:0005743,GO:0008152,GO:0009644,GO:0016491	CG7675-PB						PF00106		PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly526.16	Retinol dehydrogenase 13	GO:0042462,GO:0016614,GO:0005739,GO:0010842,GO:0008152,GO:0009644,GO:0016491	CG7675-PB						PF00106		PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly526.2	Immunoglobulin superfamily DCC subclass member 4	GO:0005575,GO:0007606,GO:0003674,GO:0005887,GO:0005515	CG33481-PF				SM00409,SM00409,SM00408,SM00408		PF00047,PF07686	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly526.3	Phosphate carrier protein, mitochondrial	GO:0070062,GO:0015293,GO:0043209,GO:0016021,GO:0016020,GO:0006817,GO:0005740,GO:0005739,GO:0005743,GO:0022857,GO:0032403,GO:0015114	CG9090-PC						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920,PS51257			G3DSA:1.50.40.10	SSF103506									
aly526.4	Fibrillin-1	GO:0005201,GO:0031012,GO:0001501,GO:0001527,GO:0009653,GO:0048048,GO:0090287,GO:0070062,GO:0005576,GO:0035583,GO:0005509,GO:0032403,GO:0022617,GO:0035582,GO:0005178,GO:0030023,GO:0048050,GO:0001656,GO:0005615,GO:0007507,GO:0005604,GO:0071560,GO:0030198,GO:0043010,GO:0005578,GO:1990314	n/a										G3DSA:2.10.25.10										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly526.5	Fibrillin-2	GO:0007424,GO:0005201,GO:0035108,GO:0051539,GO:0030326,GO:0040005,GO:0007475,GO:0060346,GO:0008362,GO:0046331,GO:0035583,GO:0005509,GO:0030501,GO:0001527,GO:0031012,GO:0045669,GO:0005578,GO:0005576	CG33196-PQ				SM00181,SM00179,SM00179		PF12662,PF12662,PF12662,PF07645,PF00683,PF00683,PF00683,PF00683,PF00683,PF00683,PF12947	PS50026,PS50026,PS51364,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS51364,PS50026,PS51364,PS51364,PS50026,PS50026,PS51364,PS51364,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS51364,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS51364,PS50026,PS50026		PS01186,PS01186,PS01186,PS01186,PS00010,PS01186,PS00010,PS01187,PS01187,PS01187,PS01187,PS00010,PS00010,PS01187,PS01186,PS01186,PS01186,PS01186,PS00010,PS00010,PS01187,PS01186,PS01186,PS00022,PS00010,PS01187,PS01187,PS00010,PS01186,PS01186,PS00010,PS01187,PS01187,PS00010,PS01187,PS00010,PS00010,PS01187,PS01187,PS01187,PS01187,PS01187,PS01186,PS00010,PS00010,PS01186,PS01186,PS00010,PS01186,PS01187,PS00010,PS00010,PS01187,PS00010,PS00010,PS00010,PS00010,PS01187,PS01187,PS00010,PS00010,PS01187,PS00010,PS00010,PS01187,PS01187,PS01186,PS00010,PS00010,PS01187,PS01187,PS01186,PS01186,PS01187,PS00010,PS00010,PS01187,PS01186,PS01186,PS01186,PS01186,PS00010,PS01187,PS01187,PS01186,PS01186,PS01187,PS01187,PS00010,PS01186,PS01187,PS01187,PS00010,PS01186,PS01187,PS00010,PS00010,PS01186,PS00010,PS01186,PS00010,PS01187,PS00022,PS00010,PS00010,PS00010,PS01187,PS01186,PS01186,PS01187,PS00010	G3DSA:2.170.300.10,G3DSA:3.90.290.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:3.90.290.10,G3DSA:3.90.290.10,G3DSA:3.90.290.10,G3DSA:3.90.290.10,G3DSA:3.90.290.10,G3DSA:3.90.290.10,G3DSA:3.90.290.10,G3DSA:3.90.290.10,G3DSA:2.10.25.10	SSF57196,SSF57581,SSF57184,SSF57196,SSF57196,SSF57184,SSF57196,SSF57581,SSF57581,SSF57196,SSF57196,SSF57581,SSF57581,SSF57184,SSF57581,SSF57581,SSF57196,SSF57581,SSF57184,SSF57196,SSF57196,SSF57184,SSF57196,SSF57196,SSF57184,SSF57184,SSF57184,SSF57184,SSF57184									
aly526.6	Zinc finger RNA-binding protein	GO:0005737,GO:0006909,GO:0071011,GO:0071013,GO:0000398,GO:0008270,GO:0003677,GO:0003723,GO:0005634,GO:0007275,GO:0003729	CG5215-PB				SM00572		PF07528	PS51703													
aly526.7	Zinc finger RNA-binding protein 2	GO:0006909,GO:0071011,GO:0071013,GO:0000398,GO:0008270,GO:0003676,GO:0003729	CG5215-PB				SM00355,SM00355,SM00451,SM00451		PF12874,PF12874	PS51703		PS00028,PS00028		SSF57667,SSF57667	355~375								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly526.8	snRNA-activating protein complex subunit 3	GO:0043565,GO:0005730,GO:0003677,GO:0006355,GO:0019185,GO:0006351,GO:0005515,GO:0065004,GO:0003681,GO:0042795,GO:0042796	CG11508-PA						PF12251														
aly526.9	Immediate early response 3-interacting protein 1	GO:0022008,GO:0016021,GO:0005789	CG32069-PA						PF08571														
aly52603.1	Unknown		n/a																				
aly5264.1	Breast cancer type 2 susceptibility protein homolog	GO:0006310,GO:0005737,GO:0032355,GO:0051298,GO:0000724,GO:0042127,GO:0005813,GO:0035264,GO:0007584,GO:0003697,GO:0006355,GO:0007283,GO:0031619,GO:0043015,GO:0005634,GO:0030879,GO:0051276	n/a						PF09169,PF00634,PF00634,PF00634,PF00634, PF00634,PF00634,PF00634,PF00634,PF00634, PF00634,PF09103	PS50138,PS50138,PS50138,PS50138,PS50138,PS50138,PS50138,PS50138,PS50138,PS50138,PS50222,PS50138			G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:2.40.50.140	SSF50249,SSF50249,SSF50249,SSF81872	1980~1981									
aly5264.10	Wee1-like protein kinase	GO:0006468,GO:0051299,GO:0000278,GO:0045448,GO:0005634,GO:0000287,GO:0000280,GO:0001700,GO:0018108,GO:0051225,GO:0004715,GO:0045736,GO:0051301,GO:0004672,GO:0007093,GO:0007067,GO:0007088,GO:0051642,GO:0005875,GO:0005524,GO:0004713	CG4488-PA			PIRSF037281	SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112	482~502								
aly5264.11	SID1 transmembrane family member 1	GO:0051033,GO:0033227,GO:0016021	n/a										G3DSA:3.90.25.10										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5264.12	Unknown		n/a																				
aly5264.2	Zinc finger protein 358	GO:0019827,GO:0035075,GO:0046872,GO:0021915,GO:0035115,GO:0003700,GO:0005634,GO:0007552,GO:0006355,GO:0010977,GO:0006351,GO:0003676,GO:0003677,GO:0045316	CG45074-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667	428~455								
aly5264.3	Enhancer of rudimentary homolog	GO:0006221,GO:0005634,GO:0006357,GO:0007049,GO:0045747	CG1871-PA			PIRSF016393			PF01133			PS01290		SSF143875									
aly5264.4	Uncharacterized protein C1orf198 homolog	GO:0005737	n/a						PF15797														
aly5264.5	Protein deglycase DJ-1	GO:0050821,GO:0051583,GO:0043523,GO:0008233,GO:0005737,GO:0005634,GO:0005739,GO:0006979,GO:0001963,GO:0042803,GO:2000277,GO:0060548,GO:0006914,GO:0070301,GO:0007338,GO:0006954,GO:0005886,GO:0034599,GO:0008344,GO:0042542,GO:0045121,GO:0006517,GO:0003729	CG1349-PA						PF01965				G3DSA:3.40.50.880,G3DSA:3.40.50.880	SSF52317,SSF52317									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5264.6	Myeloid zinc finger 1	GO:0044212,GO:0009649,GO:0042051,GO:0000122,GO:0003700,GO:0005634,GO:0006636,GO:0042803,GO:0003705,GO:0035271,GO:0006355,GO:0001077,GO:0045944,GO:0043153,GO:0003677,GO:0007605,GO:0010114,GO:0000978,GO:0046872,GO:0001078,GO:0001752	CG7672-PC				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13909,PF13909,PF13909,PF13909,PF13909	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly5264.7	Homeobox protein DBX1A	GO:0043565,GO:0048663,GO:0007399,GO:0003700,GO:0005634,GO:0006355,GO:0000976,GO:0021515,GO:0007411	CG42234-PC																				
aly5264.8	Homeobox protein DBX1	GO:0043565,GO:0048663,GO:0007399,GO:0021521,GO:0003700,GO:0005634,GO:0006355,GO:0006357,GO:0000976,GO:0003677,GO:0007411	CG42234-PC						PF00046	PS50071			G3DSA:1.10.10.60	SSF46689									
aly5264.9	Unknown		n/a																				
aly527.1	WD repeat-containing protein wdr-5.3	GO:0005515	n/a				SM00320,SM00320,SM00320,SM00320,SM00320			PS50294,PS50082			G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly527.10	pre-rRNA processing protein FTSJ3	GO:0030688,GO:0008649,GO:0005730,GO:0044822,GO:0006364,GO:0031167,GO:0000453	CG8939-PA	MF_01547,MF_03163					PF07780,PF01728,PF11861				G3DSA:3.40.50.150	SSF53335	356~384,724~761								
aly527.11	Probable Bax inhibitor 1	GO:0043234,GO:0006986,GO:0035071,GO:0060548,GO:0016021,GO:0006915,GO:0060702,GO:0005789,GO:0043066,GO:0003674,GO:0009267,GO:1900102,GO:0010507	CG7188-PA						PF01027														
aly527.12	tRNA-dihydrouridine (16/17) synthase [NAD(P)(+)]-like	GO:0017150,GO:0050660,GO:0008033,GO:0055114	CG3645-PA						PF01207			PS01136	G3DSA:3.20.20.70	SSF51395									
aly527.13	Sphingomyelin phosphodiesterase 4	GO:0016021,GO:0005789,GO:0004767,GO:0050290,GO:0046872,GO:0000139	CG6962-PA						PF14724,PF14724						511~531	00600+3.1.4.12		PWY-7277					
aly527.14	DNA-directed RNA polymerase III subunit RPC2	GO:0005666,GO:0005634,GO:0032549,GO:0003677,GO:0003899,GO:0046872,GO:0006383	CG8344-PA						PF04563,PF04565,PF04561,PF04566,PF04567,PF00562,PF04560			PS01166	G3DSA:3.90.1100.10,G3DSA:3.90.1100.10,G3DSA:3.90.1100.10,G3DSA:2.40.270.10,G3DSA:2.40.270.10,G3DSA:3.90.1110.10,G3DSA:2.40.50.150	SSF64484		00240+2.7.7.6,00230+2.7.7.6	REACT_1788						
aly527.15	Mitochondrial Rho GTPase	GO:0019725,GO:0097345,GO:0006915,GO:0047497,GO:0003924,GO:0005525,GO:0031122,GO:0034643,GO:0031307,GO:0000226,GO:0005509,GO:0008152,GO:0007268,GO:0051646,GO:0000287,GO:0007264,GO:0048489	CG5410-PE			PIRSF037488	SM00173,SM00174,SM00175,SM00054,SM00054		PF08355,PF08356,PF00071	PS50222,PS51423,PS51423,PS50222	PR00449,PR00449,PR00449	PS00018,PS00018	G3DSA:3.40.50.300,G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:3.40.50.300	SSF47473,SSF47473,SSF52540,SSF52540			REACT_11044						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly527.16	RNA-binding protein cabeza	GO:0048749,GO:0051124,GO:0006367,GO:0005634,GO:0000398,GO:0000166,GO:0005654,GO:0045887,GO:0035327,GO:0008270,GO:0003676,GO:0071013,GO:0005669,GO:0008345,GO:0008344,GO:0003729	CG3606-PB				SM00360		PF00076,PF00641	PS50199,PS50102		PS01358	G3DSA:4.10.1060.10,G3DSA:3.30.70.330	SSF54928,SSF90209									
aly527.17	Polymerase delta-interacting protein 3	GO:0005737,GO:0016607,GO:0016973,GO:0043231,GO:0044822,GO:0000166,GO:0005654,GO:0003676,GO:2001020,GO:0045727,GO:0003729	CG6961-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928	41~61								
aly527.18	Uncharacterized protein C17orf85 homolog	GO:0000166	n/a						PF10309				G3DSA:3.30.70.330										
aly527.19	MICAL-like protein 2	GO:0001725,GO:0055037,GO:0043005,GO:0032456,GO:0034446,GO:0031532,GO:0005829,GO:0031005,GO:0070830,GO:0051015,GO:0003779,GO:0034333,GO:1903955,GO:0008270,GO:0005911,GO:0031175,GO:0030041,GO:0005886,GO:0005923	CG11259-PA				SM00033,SM00132		PF00412,PF12130,PF00307	PS50021,PS50023		PS00478	G3DSA:2.10.110.10,G3DSA:1.10.418.10	SSF57716,SSF47576	698~718								
aly527.2	Protein phosphatase Slingshot	GO:0016319,GO:0008330,GO:0006470,GO:0030036,GO:0008064,GO:0003677,GO:0005856,GO:0045177,GO:0030833,GO:0000902,GO:0040023,GO:0003779,GO:0048749,GO:0005737,GO:0000278,GO:0008138,GO:0017017,GO:0007409,GO:0010591,GO:0050770,GO:0004725,GO:0030837,GO:0004721	CG6238-PB				SM00195		PF00782,PF08766	PS50054,PS50056		PS00383	G3DSA:1.10.10.60,G3DSA:3.90.190.10	SSF52799,SSF109715									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly527.20	Unknown		n/a											SSF57184,SSF57184,SSF57184									
aly527.3	LYR motif-containing protein 9		n/a						PF05347														
aly527.4	Serine/threonine-protein kinase PLK4	GO:0006468,GO:0007099,GO:0051298,GO:0004674,GO:0051297,GO:0031647,GO:0035186,GO:0005814,GO:0045732,GO:0007052,GO:0004713,GO:0007140,GO:0004672,GO:0007288,GO:0046777,GO:0005524,GO:0046599	CG7186-PA						PF00069	PS50011		PS00107,PS00109	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112	596~616								
aly527.5	60S ribosomal protein L23a	GO:0051298,GO:0022625,GO:0005634,GO:0000166,GO:0003735,GO:0019843,GO:0006412,GO:0005840	CG7977-PA	MF_01369_A				TIGR03636	PF03939,PF00276			PS00050	G3DSA:3.30.70.330	SSF54189									
aly527.6	NADPH--cytochrome P450 reductase	GO:0005783,GO:0016709,GO:0005829,GO:0005811,GO:0005789,GO:0003958,GO:0008150,GO:0010181,GO:0005506,GO:0055114,GO:0016491	CG11567-PD			PIRSF000208			PF00175,PF00667,PF00258	PS51384,PS50902	PR00371,PR00371,PR00371,PR00371,PR00371,PR00371,PR00371,PR00371,PR00369,PR00369,PR00369,PR00369		G3DSA:3.40.50.80,G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:3.40.50.360,G3DSA:1.20.990.10	SSF52218,SSF63380,SSF52343									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly527.7	A-kinase anchor protein 1, mitochondrial	GO:0008104,GO:0005783,GO:0007616,GO:0060269,GO:0031594,GO:0006099,GO:0007298,GO:0008069,GO:0040040,GO:0016020,GO:0071375,GO:0030837,GO:0016021,GO:0005811,GO:0005739,GO:0005741,GO:0005759,GO:0006403,GO:0005794,GO:0051018,GO:0044822,GO:0008070,GO:0035308,GO:0030061,GO:0051276,GO:0010614,GO:0045211,GO:0051534,GO:0071320,GO:0008298,GO:0003723,GO:0046843	CG3249-PC				SM00333,SM00322		PF00013,PF00567	PS50304,PS50084			G3DSA:3.30.1370.10,G3DSA:2.30.30.140	SSF63748,SSF54791,SSF50199	41~61								
aly527.8	Eukaryotic translation initiation factor 1A, X-chromosomal	GO:0006909,GO:0007224,GO:0016282,GO:0005829,GO:0044822,GO:0007052,GO:0000022,GO:0006413,GO:0006412,GO:0003743	CG8053-PA	MF_00216			SM00652	TIGR00523	PF01176	PS50832		PS01262	G3DSA:2.40.50.140	SSF50249									
aly527.9	Ecdysone-inducible protein E75	GO:0043565,GO:0035075,GO:0006351,GO:0018990,GO:0019730,GO:0003700,GO:0005634,GO:0007591,GO:0003707,GO:0020037,GO:0006355,GO:0008270,GO:0043401,GO:0003677,GO:0004887,GO:0048477,GO:0010468,GO:0004879,GO:0007553	CG8127-PB				SM00430,SM00399		PF00105,PF00104	PS51030	PR00398,PR00398,PR00398,PR00398,PR00047,PR00047,PR00047,PR00047,PR00546,PR00546	PS00031	G3DSA:1.10.565.10,G3DSA:1.10.565.10,G3DSA:3.30.50.10	SSF48508,SSF57716	727~729		REACT_71							
aly52716.1	Unknown	GO:0005096,GO:0007165	n/a										G3DSA:1.25.40.200	SSF69099									
aly52775.1	Ankyrin repeat domain-containing protein 50	GO:1990126,GO:0005575,GO:0008150,GO:0015031,GO:0003674,GO:0005768	CG10011-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly528.1	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly528.10	Transcriptional regulator ATRX homolog	GO:0005722,GO:0051276,GO:0007399,GO:0006281,GO:0006336,GO:0005524,GO:0005634,GO:0003677,GO:0007411,GO:0005700,GO:0004386,GO:0042585,GO:0006351,GO:0016887,GO:0070868,GO:0003678,GO:0046328,GO:0097193,GO:0000775,GO:0008347	CG4548-PA				SM00487,SM00384,SM00384		PF00176	PS51192			G3DSA:3.40.50.300	SSF52540	1953~1982								
aly528.11	Guanine nucleotide exchange factor subunit Rich	GO:0043234,GO:0005794,GO:0050808,GO:0016021,GO:0043547,GO:0042147,GO:1903363,GO:0016023,GO:0034066,GO:0005829,GO:0016020,GO:0017137,GO:0017112,GO:0045467,GO:0032483,GO:0032851,GO:0005515,GO:0007411,GO:0060078,GO:0000139,GO:0035418	CG9063-PA						PF07064				G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978									
aly528.12	Protein bicaudal D	GO:0008103,GO:0030154,GO:0007293,GO:0007294,GO:0007309,GO:0051028,GO:0048488,GO:0005737,GO:0070727,GO:0045502,GO:0030727,GO:0030669,GO:0048477,GO:0005794,GO:0016325,GO:2000370,GO:0032050,GO:0017137,GO:0007314,GO:0007312,GO:0007310,GO:0030100,GO:0050658,GO:0005829,GO:0005856,GO:0008298,GO:0005515,GO:2000302,GO:0003729	CG6605-PD						PF09730,PF09730						11~38,124~151,220~247,46~73								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly528.13	Protein bicaudal D	GO:0008103,GO:0030154,GO:0007293,GO:0007294,GO:0007309,GO:0051028,GO:0048488,GO:0005737,GO:0070727,GO:0045502,GO:0030727,GO:0030669,GO:0048477,GO:0005794,GO:0016325,GO:2000370,GO:0032050,GO:0017137,GO:0007314,GO:0007312,GO:0007310,GO:0030100,GO:0050658,GO:0005829,GO:0005856,GO:0008298,GO:0005515,GO:2000302,GO:0003729	CG6605-PD						PF09730						83~103,168~216									
aly528.14	Muskelin	GO:0005737,GO:0001726,GO:0031532,GO:0005829,GO:0001952,GO:0007160,GO:0008360,GO:0003674,GO:0005938	CG8811-PB				SM00667		PF13415,PF06588	PS50896			G3DSA:2.60.120.260,G3DSA:2.120.10.80	SSF49785,SSF50965,SSF50965									
aly528.15	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	GO:0047453,GO:0052855,GO:0046496,GO:0005524	CG10424-PA	MF_01965				TIGR00196	PF01256	PS51383		PS01049	G3DSA:3.40.1190.20	SSF53613									
aly528.16	Protein FAM91A1		CG7600-PA						PF14648,PF14648,PF14647														
aly528.17	Protein FAM91A1		CG7600-PA						PF14648														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly528.18	BAG family molecular chaperone regulator 2	GO:0019538,GO:0006457,GO:0042802,GO:0051082	CG7945-PA												34~61								
aly528.19	Ras-related protein Rab-23	GO:0008589,GO:0006968,GO:0055037,GO:0097094,GO:0021513,GO:0007165,GO:0010008,GO:0005737,GO:0031982,GO:0006886,GO:0005776,GO:0000045,GO:0001843,GO:0043025,GO:0005525,GO:0042384,GO:0003924,GO:0006913,GO:0032482,GO:0045335,GO:0001738,GO:0005886,GO:0042992,GO:0070062,GO:0042733,GO:0016192,GO:0030670,GO:0007224,GO:0015031,GO:0045861,GO:0045202	CG2108-PA				SM00176,SM00174,SM00173,SM00175	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly528.2	Esterase FE4	GO:0005575,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135,PF00135			PS00941	G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474									
aly528.20	Ubiquitin carboxyl-terminal hydrolase 14	GO:0007268,GO:0050920,GO:0045202,GO:0005875,GO:0005737,GO:0070062,GO:0016023,GO:0043161,GO:0005634,GO:0006511,GO:0016579,GO:0061136,GO:0009986,GO:1903070,GO:0004866,GO:0005886,GO:0010951,GO:0000502,GO:0004843,GO:0070628,GO:0016567,GO:0004197	CG5384-PB				SM00213		PF00443	PS50053,PS50235		PS00972,PS00973	G3DSA:3.10.20.90	SSF54001,SSF54236									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly528.21	DC-STAMP domain-containing protein 1	GO:0016021,GO:0035045,GO:0035042,GO:0035041,GO:0001669,GO:0007338,GO:0046872,GO:0008270	CG11281-PB						PF07782														
aly528.22	Unknown		n/a						PF13499	PS50222,PS50222		PS00018	G3DSA:1.10.238.10	SSF47473									
aly528.23	Protein wech	GO:0016203,GO:0030674,GO:0030154,GO:0005622,GO:0008270,GO:0005927,GO:0033632,GO:0002168	CG42396-PA				SM00336		PF00643,PF01436,PF01436,PF01436,PF01436	PS51125,PS50119,PS51125,PS51125,PS51125,PS50119,PS51125			G3DSA:2.120.10.30,G3DSA:4.10.45.10	SSF57845,SSF101898									
aly528.24	DNA replication licensing factor MCM4	GO:0042555,GO:0005634,GO:0006270,GO:0042023,GO:0007052,GO:0006260,GO:0003677,GO:0003678,GO:0043138,GO:0032508,GO:0005524	CG1616-PA				SM00350,SM00382		PF00493,PF14551	PS50051	PR01657,PR01657,PR01657,PR01657,PR01657,PR01660,PR01660,PR01660,PR01660,PR01660	PS00847	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:2.40.50.140,G3DSA:2.40.50.140,G3DSA:2.20.28.10,G3DSA:3.30.1640.10	SSF52540,SSF50249	821~841		REACT_152,REACT_383,REACT_1538							
aly528.25	Abhydrolase domain-containing protein 4	GO:0016787,GO:0005811,GO:0005777,GO:0052689,GO:0016042,GO:0004301	CG1882-PA						PF00561		PR00111,PR00111,PR00111		G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly528.26	Bardet-Biedl syndrome 2 protein homolog	GO:0005737,GO:0036064,GO:0042384,GO:0046907,GO:0060271,GO:0070121,GO:0070170,GO:0007368,GO:0007369,GO:0035058,GO:0031514,GO:0051877,GO:0032402,GO:0016020,GO:1903441,GO:0034464	n/a						PF14781,PF14782,PF14783				G3DSA:2.130.10.10	SSF50978	336~356								
aly528.27	SUMO-activating enzyme subunit 1	GO:0051092,GO:0007346,GO:0019948,GO:0005634,GO:0008022,GO:0031510,GO:0008641,GO:0019950,GO:0005515,GO:0022008,GO:0016925	CG12276-PA						PF00899		PR01849,PR01849		G3DSA:3.40.50.720	SSF69572									
aly528.28	Bardet-Biedl syndrome 2 protein	GO:0008104,GO:0060170,GO:0021766,GO:0010629,GO:0042311,GO:0045444,GO:0038108,GO:0021987,GO:0036064,GO:0031514,GO:0016020,GO:0043001,GO:0032402,GO:1903441,GO:0042384,GO:0035058,GO:0060271,GO:0021756,GO:0007601,GO:0014824,GO:0001103,GO:0007288,GO:0006996,GO:0030534,GO:0051216,GO:0040015,GO:0048854,GO:0005829,GO:0060296,GO:0040018,GO:0033365,GO:0045494,GO:0034464	n/a						PF14782														
aly528.29	Origin recognition complex subunit 1	GO:0008283,GO:0006342,GO:0005634,GO:0006270,GO:0006277,GO:0017111,GO:0006261,GO:0003677,GO:0022008,GO:0003682,GO:0005524,GO:0005664	CG10667-PA				SM00382,SM00439		PF00004,PF01426	PS51038			G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540									
aly528.3	Venom carboxylesterase-6	GO:0005811,GO:0052689,GO:0005576	CG2505-PA						PF00135				G3DSA:3.40.50.1820	SSF53474	256~276								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly528.30	Protein AATF	GO:0005730,GO:0048477,GO:0005634,GO:0003674,GO:0022008,GO:0043069	CG11188-PA						PF08164,PF13339														
aly528.31	Gonadotropin-releasing hormone II receptor	GO:0004930,GO:0070328,GO:0097004,GO:0016500,GO:0016021,GO:0005886,GO:0033500,GO:0016042,GO:0055088,GO:0097003,GO:0005887,GO:0008188,GO:0007186	CG11325-PC						PF00001,PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly528.32	Excitatory amino acid transporter	GO:0089711,GO:0015501,GO:0042995,GO:0017153,GO:0043195,GO:0015813,GO:0005313,GO:0015810,GO:0031594,GO:0006835,GO:0043005,GO:0007268,GO:0008340,GO:0005886,GO:0014853,GO:0008345,GO:0016021,GO:0015183	CG3747-PB						PF00375		PR00173,PR00173,PR00173,PR00173,PR00173,PR00173	PS00714	G3DSA:1.10.3860.10	SSF118215	460~460		REACT_19419,REACT_15518						
aly528.33	STAGA complex 65 subunit gamma	GO:0043966,GO:0003713,GO:0005634,GO:0004402,GO:0030914,GO:0006355,GO:0006351,GO:0051457	n/a																				
aly528.34	Cyclin-dependent kinases regulatory subunit	GO:0006468,GO:0045842,GO:0035186,GO:0004674,GO:0051301,GO:0007488,GO:0051225,GO:0016538,GO:0008054,GO:0005515,GO:0007057,GO:0004693,GO:0007144,GO:0007143,GO:0007049	CG3738-PA				SM01084		PF01111		PR00296,PR00296,PR00296,PR00296	PS00945	G3DSA:3.30.170.10	SSF55637									
aly528.35	Zinc finger protein 891	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG17328-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57716									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly528.36	Glutathione S-transferase 1, isoform D	GO:0005737,GO:0004364,GO:0004602,GO:0006749,GO:0018833	CG4421-PA						PF00043,PF13417	PS50405,PS50404			G3DSA:3.40.30.10,G3DSA:1.20.1050.10	SSF47616,SSF52833									
aly528.37	HemK methyltransferase family member 2	GO:0043234,GO:0006479,GO:0030307,GO:0008276,GO:0003676,GO:0032259	CG9960-PA					TIGR00537	PF05175			PS00092	G3DSA:3.40.50.150	SSF53335									
aly528.38	SNAPIN protein homolog	GO:0008021,GO:0005515,GO:0016079,GO:0006886,GO:0016082,GO:0032844,GO:0007269,GO:0031083	CG9958-PA						PF14712						46~77								
aly528.39	Leucine-rich repeat-containing protein 49	GO:0005737,GO:0046331,GO:0005874,GO:0005515	CG13708-PA				SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52075	950~953								
aly528.4	Aldehyde dehydrogenase, dimeric NADP-preferring	GO:0008106,GO:0004030,GO:0005783,GO:0051384,GO:0001666,GO:0016491,GO:0005737,GO:0005615,GO:0005811,GO:0016620,GO:0005654,GO:0008284,GO:0004028,GO:0004029,GO:0007584,GO:0051591,GO:0008152,GO:0005886,GO:0055114,GO:0043231,GO:0007568,GO:0006081,GO:0005829,GO:0042493,GO:0018479	CG11140-PQ						PF00171			PS00687,PS00070	G3DSA:3.40.605.10,G3DSA:3.40.309.10	SSF53720									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly528.40	LanC-like protein 3	GO:0005575,GO:0003824,GO:0004930,GO:0007186	CG2061-PA						PF05147		PR01950,PR01950,PR01950,PR01950,PR01950,PR01951,PR01951,PR01951,PR01951,PR01951,PR01951,PR01951			SSF158745									
aly528.41	Glutamate receptor	GO:0043235,GO:0071683,GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0071229,GO:0045211,GO:0030054,GO:0050907,GO:0004970	CG10633-PA										G3DSA:1.10.287.70,G3DSA:3.40.190.10	SSF53850									
aly528.42	FAS-associated factor 1	GO:1902043,GO:0002814,GO:0031072,GO:0030155,GO:0042176,GO:0031265,GO:0003674,GO:0010942,GO:0061060,GO:0008219,GO:0005737,GO:0007253,GO:0043161,GO:0005634,GO:0005635,GO:0043065,GO:0048471,GO:0045859,GO:0019887,GO:0034098,GO:0006915,GO:0031334,GO:0051059,GO:0019901,GO:0031625,GO:0005829,GO:0043130,GO:0045861	CG8400-PA				SM00594		PF00789,PF14560,PF14555				G3DSA:1.10.8.10,G3DSA:3.10.20.90,G3DSA:3.10.20.90,G3DSA:3.10.20.90	SSF54236,SSF54236,SSF54236	476~503,507~541								
aly528.43	Thrombospondin-3b	GO:0043234,GO:0016203,GO:0007517,GO:0031012,GO:0005576,GO:0005509,GO:0007155,GO:0005927,GO:0008201,GO:0033627	CG11326-PA				SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00179,SM00179,SM00179,SM00179		PF05735,PF07645,PF07645,PF02412,PF02412,PF02412,PF02412,PF02412,PF02412	PS51234,PS51234,PS51234,PS51234,PS51234,PS51234,PS51234,PS51234,PS51234		PS01187,PS01187	G3DSA:2.10.25.10,G3DSA:4.10.1080.10,G3DSA:4.10.1080.10,G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.10.25.10	SSF57184,SSF103647,SSF103647,SSF49899			REACT_16888						
aly528.44	Transient receptor potential cation channel trpm	GO:0098655,GO:0070838,GO:0097682,GO:0043052,GO:0005261,GO:0034703,GO:0016049,GO:0046873,GO:0055069,GO:0010960,GO:0055085,GO:0007005	CG44240-PE						PF00520,PF16519				G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.20.5.1010		1240~1260,864~884								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly528.45	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG13935-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly528.46	Cuticle protein 8	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG13935-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly528.47	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly528.48	Unknown		n/a																				
aly528.49	Unknown		n/a										G3DSA:2.40.128.20	SSF50814									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly528.5	Ras-like GTP-binding protein Rho1	GO:0035147,GO:0016318,GO:0045199,GO:0007369,GO:0035277,GO:0007370,GO:0030589,GO:0005886,GO:0035149,GO:0000281,GO:0010004,GO:0007164,GO:0007165,GO:0008045,GO:0070593,GO:0007411,GO:0007298,GO:0001745,GO:0035317,GO:0008354,GO:0005737,GO:0007254,GO:0007435,GO:0030950,GO:0031532,GO:0007368,GO:0016020,GO:0045179,GO:0007349,GO:0007601,GO:0051493,GO:0003924,GO:0071902,GO:0016476,GO:0070451,GO:0005525,GO:0016203,GO:0005856,GO:0071896,GO:0005938,GO:0030239,GO:0035159,GO:0034613,GO:0051017,GO:0042060,GO:0045184,GO:0019900,GO:0042249,GO:0007173,GO:0030036,GO:0090254,GO:0035298,GO:0046664,GO:0007010,GO:0007405,GO:0007264,GO:0001737,GO:0001736,GO:0008347,GO:0046663,GO:0035099,GO:0007424,GO:0007015,GO:0006897,GO:0050770,GO:0007377,GO:0007422,GO:0007395,GO:0016055,GO:0030866,GO:0007391,GO:0090090,GO:0006974,GO:0048813,GO:0090251,GO:0090303,GO:1903475,GO:0005515,GO:0035006,GO:0070252,GO:0007480,GO:0051489,GO:0007374	CG8416-PB				SM00173,SM00176,SM00175,SM00174	TIGR00231	PF00071	PS51420	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly528.6	Polynucleotide 5'-hydroxyl-kinase NOL9	GO:0051731,GO:0005730,GO:0005634,GO:0005524,GO:0000448,GO:0006396,GO:0006364	CG8414-PA						PF16575						6~6								
aly528.7	ATP synthase subunit alpha, mitochondrial	GO:0019915,GO:0045261,GO:0015986,GO:0015992,GO:0040007,GO:0046933,GO:0000275,GO:0046034,GO:0015991,GO:0005811,GO:0005739,GO:0005743,GO:0022900,GO:1902769,GO:0046961,GO:0007286,GO:0006909,GO:0008553,GO:0005875,GO:0005524	CG3612-PA	MF_01346		PIRSF039088		TIGR00962	PF02874,PF00006,PF00306			PS00152	G3DSA:1.20.150.20,G3DSA:3.40.50.300,G3DSA:2.40.30.20	SSF52540,SSF47917,SSF50615		00195+3.6.3.14,00190+3.6.3.14		PWY-7219					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly528.8	PX domain-containing protein kinase-like protein	GO:0005737,GO:0043234,GO:0006468,GO:0043271,GO:0035091,GO:0005634,GO:0005886,GO:0008022,GO:0005815,GO:0003779,GO:0032780,GO:0006954,GO:0004672,GO:0050804,GO:0005524	CG8726-PB				SM00312		PF00787	PS50195,PS51082			G3DSA:1.10.510.10,G3DSA:3.30.1520.10	SSF56112,SSF64268	327~347								
aly528.9	Transcriptional regulator ATRX homolog	GO:0005722,GO:0051276,GO:0007399,GO:0006281,GO:0006336,GO:0005524,GO:0005634,GO:0003677,GO:0007411,GO:0005700,GO:0004386,GO:0042585,GO:0006351,GO:0016887,GO:0070868,GO:0003678,GO:0046328,GO:0097193,GO:0000775,GO:0008347	CG4548-PA				SM00490		PF00271	PS51194			G3DSA:3.40.50.300	SSF52540	253~273								
aly5284.1	Pyridoxal phosphate phosphatase PHOSPHO2	GO:0016311,GO:0033883,GO:0046872,GO:0016791,GO:0008152	CG12237-PA			PIRSF031051		TIGR01488,TIGR01489	PF06888				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF56784									
aly5284.2	GrpE protein homolog, mitochondrial	GO:0006457,GO:0006626,GO:0051087,GO:0005739,GO:0051082,GO:0005759,GO:0022008,GO:0000774,GO:0042803	CG6155-PA	MF_01151					PF01025,PF01025			PS01071	G3DSA:3.90.20.20,G3DSA:3.90.20.20,G3DSA:2.30.22.10	SSF58014,SSF51064	57~98								
aly5284.3	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	GO:0008026,GO:0005730,GO:0071011,GO:0071013,GO:0000398,GO:0003724,GO:0004004,GO:0003676,GO:0005681,GO:0022008,GO:0008380,GO:0005524,GO:0006397	CG11107-PA				SM00847		PF04408,PF07717					SSF52540									
aly5284.4	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	GO:0008026,GO:0005730,GO:0071011,GO:0071013,GO:0000398,GO:0003724,GO:0004004,GO:0003676,GO:0005681,GO:0022008,GO:0008380,GO:0005524,GO:0006397	CG11107-PA				SM00490,SM00487		PF00271,PF00270	PS51194,PS51192			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5284.5	Unknown		n/a																				
aly5284.6	Unknown		n/a												9~29								
aly529.1	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653,PS00572	G3DSA:3.20.20.80	SSF51445									
aly529.10	Villin-like protein quail	GO:0005737,GO:0007300,GO:0007010,GO:0007015,GO:0051017,GO:0003779,GO:0007303,GO:0005884,GO:0051693,GO:0035317,GO:0005509	CG6433-PC				SM00153,SM00262,SM00262,SM00262,SM00262,SM00262,SM00262		PF00626,PF00626,PF02209	PS51089	PR00597,PR00597,PR00597,PR00597,PR00597,PR00597,PR00597		G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:1.10.950.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10	SSF55753,SSF55753,SSF55753,SSF55753,SSF55753,SSF55753,SSF47050,SSF55753										
aly529.11	Unknown		n/a																				
aly529.12	Elongation factor Ts, mitochondrial	GO:0003746,GO:0006414,GO:0005739,GO:0005622	CG6412-PA	MF_00050					PF00889			PS01127	G3DSA:3.30.479.20,G3DSA:3.30.479.20,G3DSA:1.10.8.10	SSF46934,SSF54713,SSF54713									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly529.13	Dynein heavy chain 7, axonemal	GO:0009331,GO:0036159,GO:0016887,GO:0005929,GO:0003341,GO:0004368,GO:0005874,GO:0005875,GO:0042623,GO:0005858,GO:0000166,GO:0005509,GO:0006072,GO:0003774,GO:0005524,GO:0007605,GO:0001539,GO:0008152,GO:0055114,GO:0036156,GO:0007018,GO:0003777	CG5526-PB						PF12774,PF03028,PF03028,PF08393,PF12780,PF12781,PF12775,PF12777				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540	2745~2786,840~860,671~691								
aly529.14	Unknown		n/a						PF03221,PF05225	PS51253,PS50960				SSF46689									
aly529.15	Unknown		n/a																				
aly529.16	Unknown	GO:0034508,GO:0000776	n/a						PF07778														
aly529.17	Protein EMSY	GO:0070822,GO:0006281,GO:0005634,GO:0006355,GO:0006351,GO:0005875,GO:0016568	CG15356-PA						PF03735	PS51138				SSF158639	117~137								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly529.18	Aspartate aminotransferase, mitochondrial	GO:0005811,GO:0019899,GO:0030170,GO:0016597,GO:0007416,GO:0070062,GO:0005743,GO:0043209,GO:0006520,GO:0006536,GO:0005739,GO:0004069,GO:0019551,GO:0005759,GO:0044822,GO:0042803,GO:0015908,GO:0009986,GO:0003824,GO:0045213,GO:0016212,GO:0005886,GO:0043204,GO:0043234,GO:0043648,GO:0045471,GO:0031406,GO:0080130,GO:0006103,GO:0019550,GO:0006537,GO:0005543,GO:0006531,GO:0006532,GO:0006533,GO:0006107	CG4233-PB						PF00155		PR00799,PR00799,PR00799,PR00799	PS00105	G3DSA:3.40.640.10	SSF53383		00360+2.6.1.1,00350+2.6.1.1,00400+2.6.1.1,00250+2.6.1.1,00401+2.6.1.1,00950+2.6.1.1,00960+2.6.1.1,00710+2.6.1.1,00270+2.6.1.1,00330+2.6.1.1	REACT_13	PWY-5913,PWY-6318,PWY-7383,PWY-6643,PWY-6642,PWY-6638,PWY-7117,PWY-7115					
aly529.19	WD repeat and FYVE domain-containing protein 2	GO:0046872,GO:0005515	CG5168-PA				SM00320,SM00320,SM00320,SM00320,SM00064		PF00400,PF01363	PS50082,PS50294,PS50178		PS00678	G3DSA:2.130.10.10,G3DSA:3.30.40.10	SSF50978,SSF57903									
aly529.2	Lactase-phlorizin hydrolase	GO:0017042,GO:0005903,GO:0044281,GO:0042594,GO:0010040,GO:0044245,GO:0010045,GO:0001666,GO:0016020,GO:0016740,GO:0010288,GO:0016324,GO:0007584,GO:0045471,GO:0005887,GO:0005886,GO:0043627,GO:0009744,GO:0000016,GO:0005975,GO:0042493,GO:0004553	CG9701-PA						PF00232,PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653,PS00572,PS00572,PS00653	G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF51445,SSF51445									
aly529.20	Peritrophin-48	GO:0006030,GO:0005576,GO:0008061,GO:0016490	CG43896-PC				SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00494,SM00494		PF01607,PF01607,PF01607,PF01607,PF01607	PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625,SSF57625,SSF57625,SSF57625,SSF57625									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly529.21	Myosin-VIIa	GO:0032027,GO:0008586,GO:0005902,GO:0031477,GO:0035317,GO:0005737,GO:0042623,GO:0045179,GO:0008407,GO:0003779,GO:0048800,GO:0016459,GO:0003774,GO:0005524,GO:0007605,GO:0030898,GO:0030048,GO:0008152,GO:0035293,GO:0007469,GO:0007015,GO:0007423,GO:0016461	CG7595-PA				SM00242,SM00015,SM00015,SM00015,SM00015,SM00139,SM00139,SM00295,SM00295,SM00326		PF00612,PF00612,PF00612,PF00063,PF00373,PF00373,PF00784,PF00784	PS50057,PS50002,PS51016,PS51016,PS50096,PS50096,PS50096,PS50057,PS51456,PS50096	PR00193,PR00193,PR00193,PR00193,PR00193,PR00193		G3DSA:3.10.20.90,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:2.30.30.40,G3DSA:1.20.80.10,G3DSA:1.20.80.10,G3DSA:2.30.29.30	SSF47031,SSF52540,SSF50044,SSF54236,SSF54236,SSF50729,SSF52540,SSF47031	888~918,2160~2161								
aly529.22	Suppressor of hairless protein	GO:0007616,GO:0008586,GO:0001077,GO:0003677,GO:0001078,GO:0005737,GO:0043565,GO:0007219,GO:0007252,GO:0000122,GO:0008356,GO:0005634,GO:0001709,GO:0007451,GO:0042688,GO:0006366,GO:0016360,GO:0042683,GO:1900087,GO:0048190,GO:0017053,GO:0046331,GO:0045892,GO:0045893,GO:0043234,GO:0003700,GO:0005700,GO:0006355,GO:0045944,GO:0005515,GO:0030097,GO:0000978,GO:0000980	CG3497-PA						PF09271,PF09270				G3DSA:2.80.10.50,G3DSA:2.60.40.10,G3DSA:2.60.40.1450	SSF49417,SSF81296,SSF110217									
aly529.23	DNA repair protein complementing XP-G cells homolog	GO:0000014,GO:0006284,GO:0004519,GO:0005634,GO:0016788,GO:0006289,GO:0070914,GO:0046872,GO:0003697	CG10890-PC				SM00484,SM00279,SM00485		PF00752,PF00867		PR00853,PR00853,PR00853,PR00853,PR00853,PR00853,PR00066,PR00066,PR00066,PR00066	PS00841,PS00842	G3DSA:3.40.50.1010,G3DSA:3.40.50.1010,G3DSA:1.10.150.20	SSF47807,SSF47807,SSF88723,SSF88723	346~366,95~115								
aly529.24	Transmembrane 9 superfamily member 2	GO:0070062,GO:0016021,GO:0006810,GO:0005887,GO:0005768,GO:0010008	CG9318-PA						PF02990														

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly529.25	Venom serine carboxypeptidase	GO:0006508,GO:0033227,GO:0004185,GO:0005576	CG4572-PA						PF00450		PR00724,PR00724,PR00724,PR00724	PS00131,PS00560	G3DSA:3.40.50.1820	SSF53474									
aly529.26	Venom serine carboxypeptidase	GO:0006508,GO:0033227,GO:0004185,GO:0005576	CG4572-PA						PF00450		PR00724,PR00724,PR00724,PR00724	PS00131,PS00560	G3DSA:3.40.50.1820	SSF53474									
aly529.27	Venom serine carboxypeptidase	GO:0006508,GO:0033227,GO:0004185,GO:0005576	CG4572-PA						PF00450		PR00724,PR00724,PR00724,PR00724	PS00560,PS00131	G3DSA:3.40.50.1820	SSF53474									
aly529.28	Serine carboxypeptidase-like 33	GO:0005576,GO:0004185	n/a						PF00450			PS00560	G3DSA:3.40.50.1820	SSF53474									
aly529.29	Venom serine carboxypeptidase	GO:0006508,GO:0033227,GO:0004185,GO:0005576	CG4572-PA						PF00450		PR00724,PR00724		G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly529.3	Lactase-phlorizin hydrolase	GO:0017042,GO:0005903,GO:0044281,GO:0042594,GO:0010040,GO:0044245,GO:0010045,GO:0001666,GO:0016020,GO:0016740,GO:0010288,GO:0016324,GO:0007584,GO:0045471,GO:0005887,GO:0005886,GO:0043627,GO:0009744,GO:0000016,GO:0005975,GO:0042493,GO:0004553	CG9701-PA						PF00232,PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00572,PS00572	G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF51445,SSF51445									
aly529.30	Vitellogenic carboxypeptidase	GO:0006508,GO:0033227,GO:0004185,GO:0005576	CG4572-PA						PF00450		PR00724,PR00724,PR00724	PS00131	G3DSA:3.40.50.1820	SSF53474									
aly529.31	Cyclic nucleotide-gated cation channel beta-3	GO:0030553,GO:0042391,GO:0050896,GO:0009187,GO:1902495,GO:0005249,GO:0071805,GO:0005221,GO:0006812,GO:0005223,GO:0005222,GO:0007601,GO:0001750,GO:0019935,GO:0005887,GO:0005886,GO:0055085,GO:0017071	CG17922-PA				SM00100		PF00520,PF00027	PS50042		PS00889,PS00888	G3DSA:2.60.120.10,G3DSA:1.10.287.630,G3DSA:1.10.287.70	SSF81324,SSF51206									
aly529.32	Tetratricopeptide repeat protein 25	GO:0005575,GO:0008150,GO:0003674,GO:0005515	CG13502-PA				SM00028,SM00028,SM00028		PF13414,PF00515	PS50293,PS50005,PS50005,PS50005			G3DSA:1.25.40.10	SSF48452	311~331								
aly529.33	Unknown	GO:0005549	n/a										G3DSA:1.10.238.20										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly529.34	Histone-lysine N-methyltransferase SETD2	GO:0034728,GO:0018024,GO:0042054,GO:0097198,GO:0006298,GO:0001763,GO:0008270,GO:0060977,GO:0060039,GO:0000228,GO:0001525,GO:0048864,GO:0006325,GO:0003712,GO:0005654,GO:0016458,GO:0006368,GO:0001843,GO:0005694,GO:0048701,GO:0048332,GO:0008134,GO:0010793,GO:0060669,GO:0035441,G	CG4976-PA				SM00570,SM00456,SM00317,SM00508		PF00856,PF08236,PF00397	PS50280,PS51215,PS50020,PS50868			G3DSA:2.20.70.10,G3DSA:2.170.270.10	SSF82199,SSF51045	503~523,1463~1464,1265~1292	00310+2.1.1.43							
aly529.35	Signal peptidase complex subunit 2	GO:0005787,GO:0008233,GO:0012505,GO:0016021,GO:0006465	CG1751-PA						PF06703														
aly529.36	Glycerol-3-phosphate dehydrogenase, mitochondrial	GO:0052591,GO:0019563,GO:0044281,GO:0009331,GO:0006127,GO:0005811,GO:0007629,GO:0004368,GO:0005743,GO:0006071,GO:0005739,GO:0035264,GO:0006072,GO:0022008,GO:0006094,GO:0043010,GO:0044255,GO:0005509	CG8256-PC				SM00054,SM00054		PF13499,PF01266,PF16901	PS50222,PS50222	PR01001,PR01001,PR01001,PR01001,PR01001,PR01001	PS00977,PS00018,PS00978	G3DSA:1.10.238.10,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF47473,SSF54373,SSF51905,SSF51905		00564+1.1.5.3		PWY-4261,PWY-6118,PWY-6952					
aly529.37	Unknown		n/a																				
aly529.38	Unknown	GO:0043565,GO:0005634,GO:0046872,GO:0005704,GO:0060968	CG5669-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly529.39	Transcription factor Sp3	GO:0030324,GO:0030224,GO:0005886,GO:0001503,GO:0001889,GO:0003677,GO:0060136,GO:0001078,GO:0005737,GO:0043565,GO:0016605,GO:0001701,GO:0001829,GO:0000122,GO:0005634,GO:0030217,GO:0005654,GO:0030851,GO:0000987,GO:0003690,GO:0046872,GO:0005794,GO:0048706,GO:0017053,GO:0030183,GO:0030218,GO:0030219,GO:0048596,GO:0045892,GO:0045893,GO:0060216,GO:0001892,GO:0001779,GO:0060968,GO:0003682,GO:0003700,GO:0005704,GO:0043353,GO:0006355,GO:0006351,GO:0000979	CG5669-PB				SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly529.4	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232,PF00232			PS00653,PS00572	G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF51445									
aly529.40	Hypodermin-B	GO:0004252,GO:0005576,GO:0006508	CG18681-PA				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly529.41	Trypsin-2 (Fragment)	GO:0007586,GO:0004252,GO:0046872,GO:0005615,GO:0006508	CG11836-PI						PF00089	PS50240	PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly529.42	Acid trehalase-like protein 1	GO:0003824,GO:0005975,GO:0016798,GO:0004555	CG16965-PC						PF03632				G3DSA:2.60.420.10,G3DSA:1.50.10.10	SSF48208	769~769								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly529.43	Unknown	GO:0016021,GO:0008146,GO:0016051	CG31743-PA						PF03567														
aly529.44	Carbohydrate sulfotransferase 11	GO:0030206,GO:0007517,GO:0016021,GO:0047756,GO:0000139,GO:0008146,GO:0008045,GO:0016051	CG31743-PA						PF03567														
aly529.45	Intraflagellar transport protein 80 homolog	GO:0005737,GO:0030992,GO:0006996,GO:0042384,GO:0035058,GO:2000051,GO:0007224,GO:0005813,GO:0050680,GO:0060349,GO:0031513,GO:0097542,GO:0072372,GO:0045880,GO:0005515,GO:0005929,GO:0002062,GO:0001649	CG9333-PB				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50294,PS50082,PS50082		PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50998,SSF50998									
aly529.46	Protein arginine N-methyltransferase 3	GO:0005737,GO:0006479,GO:0016274,GO:0019919,GO:0005840,GO:0006355,GO:0005829,GO:0008469,GO:0034969,GO:0035242,GO:0031397,GO:0008168,GO:0046872	CG6563-PA						PF06325	PS50007,PS51678			G3DSA:2.70.160.11,G3DSA:3.40.50.150	SSF57667,SSF53335	254~274,150~170								
aly529.47	Calcium/calmodulin-dependent 3',5' cyclic nucleotide phosphodiesterase 1C	GO:0060179,GO:0009187,GO:0004114,GO:0004115,GO:0004117,GO:0048101,GO:0046676,GO:0006198,GO:0046068,GO:0046069,GO:0005615,GO:0047555,GO:0046872,GO:0043025,GO:0046058,GO:0007608,GO:0032504,GO:0051592,GO:0030162,GO:0004867,GO:0030552,GO:0005516,GO:0007165	CG44007-PE				SM00471		PF08499,PF00233		PR00387,PR00387,PR00387,PR00387,PR00387,PR00387	PS00126	G3DSA:1.10.1300.10,G3DSA:1.10.1300.10	SSF109604,SSF109604		00230+3.1.4.17	REACT_15295,REACT_11061							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly529.48	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155													
aly529.49	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155		PS00233											
aly529.5	Probable G-protein coupled receptor 158	GO:0004930,GO:0002805,GO:0007377,GO:0016021,GO:0007216,GO:0008277,GO:0008066,GO:0005886,GO:0072659,GO:0007186	CG31660-PD						PF00003						217~237								
aly529.50	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155		PS00233											
aly529.51	Larval/pupal rigid cuticle protein 66	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155		PS00233											
aly529.52	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131		G3DSA:3.20.20.80	SSF51445									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly529.53	Unknown	GO:0035075,GO:0006367,GO:0035071,GO:0006357,GO:0003700,GO:0035209,GO:0005634,GO:0006366,GO:0005700,GO:0001673,GO:0001075,GO:0048812,GO:0005667,GO:0003677,GO:0005669,GO:0022008,GO:0035277,GO:0001674	CG18009-PG																				
aly529.54	Maltase 2	GO:0043169,GO:0005975,GO:0032450,GO:0003824,GO:0006006,GO:0004558	CG8696-PA				SM00642		PF00128				G3DSA:2.60.40.1180,G3DSA:3.90.400.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF51445,SSF51011										
aly529.55	Maltase A1	GO:0043169,GO:0005975,GO:0032450,GO:0003824,GO:0006006,GO:0004558	CG8696-PA				SM00642		PF00128				G3DSA:3.90.400.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:2.60.40.1180	SSF51445,SSF51011										
aly529.56	Maltase A1	GO:0043169,GO:0005975,GO:0032450,GO:0003824,GO:0006006,GO:0004558	CG8696-PA				SM00642		PF00128				G3DSA:2.60.40.1180,G3DSA:3.90.400.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF51011,SSF51445										
aly529.6	Cytosolic carboxypeptidase 6	GO:0005794,GO:0015631,GO:0036064,GO:0004181,GO:0035609,GO:0005814,GO:0008270,GO:0006508,GO:0035610,GO:0005829	CG31019-PA						PF00246				G3DSA:3.40.630.10	SSF53187									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly529.7	TATA box-binding protein-like protein 1	GO:0035209,GO:0001075,GO:0003677,GO:0001674,GO:0005737,GO:0005634,GO:0048812,GO:0006367,GO:0006366,GO:0035075,GO:0005667,GO:0035071,GO:0035277,GO:0022008,GO:0001673,GO:0009790,GO:0003700,GO:0005700,GO:0006355,GO:0006357,GO:0006352,GO:0005669	CG18009-PG						PF00352,PF00352		PR00686,PR00686,PR00686,PR00686,PR00686		G3DSA:3.30.310.10,G3DSA:3.30.310.10	SSF55945,SSF55945									
aly529.8	Rho-associated protein kinase let-502	GO:0016318,GO:0016331,GO:0032065,GO:0008335,GO:0017048,GO:0035191,GO:0007300,GO:0051020,GO:0009792,GO:0010172,GO:0007309,GO:0000022,GO:0008544,GO:0007067,GO:0005737,GO:0032231,GO:0019992,GO:0005634,GO:0000281,GO:0035317,GO:0004674,GO:0046872,GO:0048477,GO:0005524,GO:0048599,GO:0006468,GO:1901888,GO:0042067,GO:0032154,GO:0000092,GO:0045184,GO:0043292,GO:0008360,GO:0005913,GO:0030036,GO:0032956,GO:0007266,GO:0001737,GO:0001736,GO:0000910,GO:2000040,GO:0050770,GO:0005856,GO:0007302,GO:0007391,GO:0005515,GO:0042325,GO:0001932	CG9774-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly529.9	Rho-associated protein kinase 2	GO:0016318,GO:0016331,GO:0030155,GO:0005886,GO:0032065,GO:0008335,GO:0017048,GO:0035191,GO:0007300,GO:0051020,GO:0036464,GO:0007411,GO:0051893,GO:0007309,GO:0000022,GO:0008544,GO:0007067,GO:0032231,GO:0008625,GO:0048010,GO:0048511,GO:0019992,GO:0005813,GO:0005634,GO:0000281,GO:0035317,GO:0004674,GO:0010825,GO:0006939,GO:0001843,GO:0046872,GO:0005524,GO:0048599,GO:0006468,GO:0031616,GO:0051298,GO:1901888,GO:0042067,GO:0044822,GO:0051492,GO:0000092,GO:0045184,GO:0042752,GO:0008360,GO:0030036,GO:0032956,GO:0007266,GO:0048013,GO:0007264,GO:0001737,GO:0001736,GO:0000910,GO:2000040,GO:0050770,GO:0005829,GO:0007302,GO:0007391,GO:0005198,GO:0048813,GO:2000145,GO:0005515,GO:0042325,GO:0045616,GO:0001932,GO:2000114,GO:0016525	CG9774-PA				SM00220,SM00133		PF08912,PF00433,PF00069	PS50011,PS51285		PS00108,PS00107	G3DSA:3.30.60.20,G3DSA:1.10.510.10,G3DSA:2.30.29.30,G3DSA:1.20.5.730,G3DSA:3.30.200.20	SSF50729,SSF103652,SSF56112	563~618,680~714,426~509,974~1047,384~418,652~672,535~555,799~833,911~938		REACT_18266,REACT_14797							
aly5292.1	Unknown		n/a																				
aly5294.1	Unknown	GO:0005575,GO:0005089,GO:0035023,GO:0035025,GO:0007480	CG43658-PC																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5294.10	Ribosome biogenesis protein WDR12 homolog	GO:0005515,GO:0030687,GO:0042254,GO:0070545,GO:0005654,GO:0000463,GO:0000466,GO:0043021,GO:0022008	CG6724-PA	MF_03029			SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF00400,PF08154	PS50294,PS50082,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978									
aly5294.11	WD repeat-containing protein 75	GO:0005654,GO:0044822,GO:1903955,GO:1903146,GO:0005730	CG12050-PB				SM00320,SM00320,SM00320						G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF69322,SSF50978,SSF50978,SSF50978,SSF50978									
aly5294.12	Unknown	GO:0005575,GO:0003674,GO:0008150,GO:0016772	CG33510-PB				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112,SSF56112									
aly5294.13	Unknown	GO:0016772	CG9259-PA				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly5294.14	Sodium channel protein Nach	GO:0035002,GO:0016021,GO:0005272,GO:0006814	CG33508-PA						PF00858				G3DSA:1.10.287.770,G3DSA:2.60.470.10,G3DSA:2.60.470.10										
aly5294.15	Pickpocket protein 28	GO:0005272,GO:0071462,GO:0016021,GO:0009415,GO:0006814,GO:0035002,GO:0035725,GO:0042756,GO:0005886	CG15555-PA						PF00858		PR01078,PR01078,PR01078,PR01078,PR01078,PR01078,PR01078		G3DSA:2.60.470.10,G3DSA:2.60.470.10,G3DSA:1.10.287.770										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5294.16	Unknown		n/a																				
aly5294.17	Unknown	GO:0016021,GO:0016020,GO:0005272,GO:0006814	CG33508-PA						PF00858														
aly5294.18	Unknown		n/a																				
aly5294.19	Unknown	GO:0003333,GO:0016020,GO:0015171	CG9264-PD																				
aly5294.2	Rho guanine nucleotide exchange factor 10-like protein	GO:0005089,GO:0005737,GO:0007480,GO:0005575,GO:0035025,GO:0035023	CG43658-PC				SM00325		PF00621	PS50010			G3DSA:1.20.900.10	SSF48065,SSF50998	332~359								
aly5294.20	Bifunctional polynucleotide phosphatase/kinase	GO:0046404,GO:0005730,GO:0019201,GO:0006281,GO:0016311,GO:0005634,GO:0016020,GO:0046939,GO:0005654,GO:0046403,GO:0042769,GO:0005524,GO:0003690,GO:0098506,GO:0006979,GO:0098504	CG9601-PA					TIGR01664,TIGR01662	PF08645,PF13671				G3DSA:3.40.50.1000,G3DSA:2.60.200.20,G3DSA:3.40.50.300	SSF52540,SSF56784,SSF49879									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5294.21	Acetyl-coenzyme A transporter 1	GO:0015295,GO:0016020,GO:0015992,GO:0008521,GO:0060395,GO:0016021,GO:0015876,GO:0000139,GO:0030509,GO:0005887,GO:0006810,GO:0005789,GO:0055085	CG9706-PA						PF13000,PF13000					SSF103473,SSF103473									
aly5294.22	Cationic amino acid transporter 4	GO:1903401,GO:0015297,GO:0015326,GO:0000064,GO:0097638,GO:0003333,GO:0016020,GO:1903352,GO:0015189,GO:0005887,GO:0015181,GO:0015171	CG13248-PA						PF13906,PF13520														
aly5294.23	Protein lap1	GO:0015031,GO:0007163,GO:0005912,GO:0005515,GO:0017016	CG10255-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364		PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058									
aly5294.24	Replication protein A 32 kDa subunit	GO:0000723,GO:0010569,GO:0016605,GO:0003697,GO:0047485,GO:0000724,GO:0035861,GO:0005634,GO:0031571,GO:0006284,GO:0006298,GO:0000781,GO:0005662,GO:0006260,GO:0006261,GO:0003677,GO:0000785,GO:0022008,GO:0006289,GO:0003684,GO:2000001	CG9273-PA						PF01336,PF08784,PF16531				G3DSA:2.40.50.140,G3DSA:1.10.10.10	SSF46785,SSF50249	338~379,177~246,254~288		REACT_152,REACT_383						
aly5294.25	Replication protein A 32 kDa subunit	GO:0000723,GO:0010569,GO:0016605,GO:0003697,GO:0047485,GO:0000724,GO:0035861,GO:0005634,GO:0031571,GO:0006284,GO:0006298,GO:0000781,GO:0005662,GO:0006260,GO:0006261,GO:0003677,GO:0000785,GO:0022008,GO:0006289,GO:0003684,GO:2000001	CG9273-PA			PIRSF036949			PF08784,PF01336				G3DSA:1.10.10.10,G3DSA:2.40.50.140	SSF46785,SSF50249			REACT_152,REACT_383						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5294.26	LDLR chaperone boca	GO:0005737,GO:0045177,GO:0016055,GO:0006888,GO:0005783,GO:0032799,GO:0006612,GO:0005788,GO:0012505,GO:0048728,GO:0048477	CG30498-PA						PF10185														
aly5294.27	Protein spinster	GO:0051124,GO:0045476,GO:0045924,GO:0007619,GO:0008582,GO:0008333,GO:0010001,GO:0007040,GO:0048488,GO:0045477,GO:0031982,GO:0016021,GO:0043067,GO:0048477,GO:0031902,GO:0090099,GO:0046624,GO:0012501,GO:0009267,GO:0005886,GO:0055085,GO:0008347,GO:0040011,GO:0003376,GO:0006897,GO:0007422,GO:0035193,GO:0005765	CG8428-PD						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly5294.28	Ovarian-specific serine/threonine-protein kinase Lok	GO:0071480,GO:0044773,GO:0072332,GO:0005737,GO:0005634,GO:0004674,GO:0004672,GO:0005524,GO:0016607,GO:0006468,GO:0006282,GO:0006919,GO:0035234,GO:0006915,GO:0007281,GO:0006974,GO:0051091,GO:0000077,GO:0008630,GO:0000075,GO:0045944,GO:0050321	CG10895-PA				SM00240,SM00220		PF01359,PF00498,PF00069	PS50006,PS50011		PS00108	G3DSA:2.60.200.20,G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112,SSF49879									
aly5294.29	Allatostatin	GO:0005179,GO:0010459,GO:0007218,GO:0005184,GO:0008016,GO:0016085,GO:0005576,GO:0045968	CG14919-PA																				
aly5294.3	Coiled-coil-helix-coiled-coil-helix domain-containing protein 10, mitochondrial	GO:0005739,GO:2000984,GO:0005758,GO:0006754,GO:0007005,GO:0006119	CG5010-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5294.30	Unknown		n/a																				
aly5294.31	RNA-binding protein with serine-rich domain 1-B	GO:0005737,GO:0016607,GO:0000184,GO:0000166,GO:0003723,GO:0003676,GO:0006397,GO:0008380,GO:0003729	CG16788-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly5294.32	Cell cycle checkpoint protein RAD17	GO:0000077,GO:0006281,GO:0005634,GO:0003689,GO:0031389,GO:0007049,GO:0005524	CG7825-PA						PF03215				G3DSA:3.40.50.300	SSF52540									
aly5294.33	NADH dehydrogenase [ubiqui] iron-sulfur protein 7, mitochondrial	GO:0006120,GO:0051539,GO:0032981,GO:0008137,GO:0000302,GO:0046872,GO:0005747,GO:0008340,GO:0048038,GO:0003954,GO:0055114	CG9172-PB	MF_01356				TIGR01957	PF01058			PS01150	G3DSA:3.40.50.700	SSF56770									
aly5294.34	Unknown	GO:0007633,GO:0007628	CG9056-PB						PF15336						1031~1064								
aly5294.35	Autism susceptibility gene 2 protein	GO:0098582,GO:0007633,GO:2000620,GO:0005634,GO:0007628,GO:0045944,GO:0051571,GO:0003682,GO:0060013	CG9056-PB												6~26								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5294.36	Vitamin K epoxide reductase complex subunit 1-like protein 1	GO:0006766,GO:0048038,GO:0042373,GO:0016021,GO:0017187,GO:0005789,GO:0034599,GO:0047057	CG33544-PA				SM00756		PF07884														
aly5294.37	Unknown	GO:0016324,GO:0005927,GO:0003674,GO:0007476,GO:0048104	CG32556-PD																				
aly5294.38	UDP-glucuronosyltransferase 2B19	GO:0016758,GO:0015020,GO:0016021,GO:0008152,GO:0005789	CG4302-PA						PF00201			PS00375	G3DSA:3.40.50.2000,G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF53756									
aly5294.39	Unknown		n/a																				
aly5294.4	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2	GO:0043565,GO:0005634,GO:0008134,GO:0005739,GO:0045944,GO:0006351,GO:1900037	CG5010-PA						PF06747														
aly5294.40	Exonuclease GOR	GO:0005737,GO:0004527,GO:0005634,GO:0003676	CG42666-PE				SM00479						G3DSA:3.30.420.10	SSF53098									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5294.41	N-terminal Xaa-Pro-Lys N-methyltransferase 1	GO:0005737,GO:0042054,GO:0007051,GO:0005634,GO:0035568,GO:0008276,GO:0007059,GO:0035573,GO:0035572,GO:0018011,GO:0035570,GO:0018016,GO:0071885	CG1675-PA			PIRSF016958			PF05891			PS01131	G3DSA:3.40.50.150	SSF53335									
aly5294.5	Transducin beta-like protein 2	GO:0005783,GO:0030968,GO:0051297,GO:0051219,GO:0019901,GO:0030176,GO:0005515,GO:0071456,GO:0042149,GO:0031369,GO:0044822	CG10191-PB				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400	PS50294,PS50082,PS50082,PS50294		PS00678	G3DSA:2.130.10.10	SSF50978									
aly5294.6	Tripartite motif-containing protein 2	GO:0005737,GO:0004842,GO:0030239,GO:0061630,GO:0048747,GO:0006941,GO:0043523,GO:0003674,GO:0008270,GO:0016874,GO:0030018,GO:0046716	CG15105-PC				SM00184		PF13639	PS50089,PS50119		PS00518	G3DSA:3.30.40.10,G3DSA:2.120.10.30	SSF57850,SSF57845,SSF63825	233~267,196~216								
aly5294.7	Cytochrome P450 CYP12A2	GO:0004497,GO:0020037,GO:0016705,GO:0005739,GO:0005506,GO:0055114,GO:0009055	CG15077-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly5294.8	Methyltransferase-like protein	GO:0005575,GO:0008757,GO:0008150	CG13929-PB			PIRSF037755			PF13489				G3DSA:3.40.50.150	SSF53335,SSF53335									
aly5294.9	Protein alan shepard	GO:0009629,GO:0042332,GO:0000166,GO:0005575,GO:0003723,GO:0003729	CG32423-PF				SM00360,SM00360		PF00076,PF00076	PS50102,PS50102	PR00961,PR00961,PR00961,PR00961		G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly53.1	40S ribosomal protein S3	GO:0005737,GO:0003906,GO:0022627,GO:0006281,GO:0005634,GO:0008534,GO:0005875,GO:0003735,GO:0006974,GO:0015935,GO:0043524,GO:0003723,GO:0007067,GO:0016363,GO:0006412,GO:0005840	CG6779-PA					TIGR01008	PF00189,PF07650	PS50823		PS00548	G3DSA:3.30.1140.32,G3DSA:3.30.300.20	SSF54821,SSF54814									
aly53.2	Neurobeachin	GO:0005737,GO:0016319,GO:0051018,GO:0043204,GO:0016021,GO:0007528,GO:0042675,GO:0008104,GO:0005488,GO:0042462,GO:0043025,GO:0007614,GO:0008355	CG44835-PQ				SM00320,SM00320,SM00320,SM01026		PF14844,PF15787,PF02138,PF06469	PS01031,PS50197			G3DSA:1.10.1540.10,G3DSA:2.130.10.10,G3DSA:2.60.120.200,G3DSA:2.30.29.40	SSF48371,SSF48371,SSF49899,SSF50729,SSF81837,SSF50978	2995~3002,1309~1329,1224~1244								
aly53.3	Unknown		n/a																				
aly53.4	Facilitated trehalose transporter Tret1-2 homolog	GO:0005355,GO:0035428,GO:0015992,GO:0016021,GO:0016020,GO:0046323,GO:0005887,GO:0005886,GO:0005351,GO:0055085	CG4797-PB						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473			REACT_15518						
aly53.5	Protein mab-21	GO:0005575,GO:0003674,GO:0008150,GO:0048568	CG4746-PA						PF03281														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly53049.1	Transcription factor E4F1	GO:0003713,GO:0009794,GO:0003676,GO:0003677,GO:0007067,GO:0051301,GO:0005737,GO:0005819,GO:0000122,GO:0040008,GO:0003714,GO:0010564,GO:0005654,GO:0006260,GO:0046872,GO:0006351,GO:0008283,GO:0016874,GO:0071850,GO:0001227,GO:0003700,GO:0016567,GO:0000977,GO:0016032,GO:0035497,GO:0008270	CG42726-PA				SM00355,SM00355,SM00355			PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60	SSF57667										
aly531.1	Orcokinin peptides type B	GO:0007218,GO:0005576,GO:0005184	n/a												364~367								
aly531.10	DNA (cytosine-5)-methyltransferase 1	GO:0034721,GO:0010628,GO:0034647,GO:0008270,GO:0003677,GO:0010216,GO:0033522,GO:0000122,GO:0005634,GO:0003886,GO:0016458,GO:0005657,GO:0006351,GO:0042127,GO:0071230,GO:0008327,GO:0051571,GO:0051573,GO:0031519,GO:0005721,GO:0007379,GO:0070544,GO:0003723,GO:0003682,GO:0016568	CG11033-PB			PIRSF037404	SM00439,SM00439	TIGR00675	PF12047,PF02008,PF01426,PF01426,PF00145	PS51058,PS51679,PS51038,PS51038	PR00105,PR00105,PR00105	PS00094	G3DSA:3.40.50.150	SSF53335		00270+2.1.1.37								
aly531.11	ESF1 homolog	GO:0005615,GO:0005730,GO:0005634,GO:0005654,GO:0006355,GO:0006351,GO:0022008,GO:0044822	CG11417-PA						PF08159						571~601,471~491								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly531.12	TP53-regulated inhibitor of apoptosis 1	GO:0043234,GO:0030330,GO:0015914,GO:1902166,GO:0090201,GO:0043066,GO:0005739,GO:0045944,GO:0005575,GO:0005758,GO:0006977,GO:0003674,GO:0097035,GO:2001140,GO:0034644,GO:0008150,GO:0048471,GO:0043154,GO:0002039	CG30109-PB						PF05254														
aly531.13	Transcription elongation factor SPT4	GO:0008023,GO:0016582,GO:0000122,GO:0005634,GO:0005705,GO:0032785,GO:0032786,GO:0005703,GO:0045944,GO:0008270,GO:0006368,GO:0003682,GO:0046982	CG12372-PA			PIRSF025023			PF06093				G3DSA:3.30.50.10	SSF63393									
aly531.14	Unknown		n/a																				
aly531.15	Nanos homolog 2	GO:0042078,GO:0008270,GO:0035282,GO:0007275,GO:0008354,GO:0005737,GO:0005634,GO:0001709,GO:0043066,GO:0045835,GO:0006402,GO:0048477,GO:1900153,GO:0016321,GO:0007281,GO:0008595,GO:0007283,GO:0007314,GO:0045892,GO:0048471,GO:0048134,GO:0030718,GO:0007280,GO:0000932,GO:0048813,GO:0003723,GO:0005515,GO:0017148,GO:0006378,GO:0003729,GO:0045495	CG5637-PA						PF05741	PS51522													
aly531.16	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	GO:1990090,GO:0006909,GO:0000902,GO:0032312,GO:0016020,GO:0005096,GO:0036010,GO:0005575,GO:0008060,GO:0008270,GO:0005515,GO:0046872,GO:0010008	CG6742-PA				SM00248,SM00248		PF12796	PS50088,PS50297			G3DSA:1.25.40.20	SSF48403									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly531.17	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 3	GO:0006909,GO:0000902,GO:0032312,GO:0005096,GO:0005575,GO:0008060,GO:0008270,GO:0046872	CG6742-PA				SM00105,SM00233		PF01412,PF00169,PF16746	PS50115,PS50003	PR00405,PR00405,PR00405		G3DSA:2.30.29.30,G3DSA:1.20.1270.60	SSF50729,SSF103657,SSF103657,SSF57863	8~28,627~627								
aly531.18	Transmembrane protein 19	GO:0003674,GO:0016021,GO:0008150	CG10171-PB						PF01940,PF01940														
aly531.19	Sialin	GO:0006865,GO:0006820,GO:0030054,GO:0005737,GO:0044267,GO:0015992,GO:0006488,GO:0016021,GO:0016020,GO:0043687,GO:0018279,GO:0015739,GO:0005351,GO:0006811,GO:0005316,GO:0005887,GO:0005886,GO:0055085,GO:0030672,GO:0015136,GO:0005764,GO:0005765	CG4330-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly531.2	Gustatory and odorant receptor 22	GO:0007608,GO:0016021,GO:0005886,GO:0008527,GO:0050911,GO:0050912,GO:0030425,GO:0004984,GO:0010037,GO:0007610,GO:0050909,GO:0043025,GO:0003031	CG13948-PA						PF08395														
aly531.20	Protein hairy	GO:0031323,GO:0061024,GO:0003677,GO:0070888,GO:0001666,GO:0001078,GO:0007435,GO:0007366,GO:0000902,GO:0000122,GO:0005634,GO:0008407,GO:0035239,GO:0008134,GO:0045892,GO:0046983,GO:0035290,GO:0007424,GO:0007399,GO:0035289,GO:0007460,GO:0007431,GO:0006355,GO:0006351,GO:0005515,GO:0000978	CG6494-PA				SM00511,SM00353		PF07527,PF00010	PS51054,PS50888			G3DSA:4.10.280.10	SSF47459,SSF158457									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly531.21	Signal recognition particle receptor subunit beta	GO:0005737,GO:0005881,GO:0005785,GO:0005047,GO:0016020,GO:0003924,GO:0006614,GO:0005789,GO:0008363,GO:0022008,GO:0007264,GO:0035293,GO:0016021,GO:0005525	CG33162-PA						PF09439	PS51417			G3DSA:3.40.50.300	SSF52540									
aly531.22	Pyridoxine-5'-phosphate oxidase	GO:0005737,GO:0070062,GO:0004733,GO:0005654,GO:0103146,GO:0010181,GO:0042823,GO:0008615,GO:0055114,GO:0016491	CG31472-PA	MF_01629		PIRSF000190		TIGR00558	PF10590,PF01243			PS01064	G3DSA:2.30.110.10	SSF50475		00750+1.4.3.5		PWY-7204,PWY-7282	UPA00190				
aly531.23	Histidine protein methyltransferase 1 homolog	GO:0008168	CG17219-PA						PF10294				G3DSA:3.40.50.150	SSF53335									
aly531.24	Proteasome activator complex subunit 3	GO:0005737,GO:0016020,GO:2000045,GO:0005730,GO:0071011,GO:0061136,GO:0005634,GO:0005705,GO:0061133,GO:0008537,GO:0000398,GO:0005703,GO:0005654,GO:2001237,GO:0004866,GO:0071013	CG1591-PA						PF02252,PF02251				G3DSA:1.20.120.180,G3DSA:1.20.5.120	SSF47216,SSF47216			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045						
aly531.25	Unknown		n/a												158~178								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly531.26	Unknown		n/a												24~60								
aly531.27	Unknown		n/a						PF13904														
aly531.28	Dynein heavy chain-like protein PF11_0240	GO:0005737,GO:0008152,GO:0007018,GO:0003777,GO:0003774,GO:0005515,GO:0016887,GO:0030286,GO:0005874,GO:0005875,GO:0005524	CG42284-PD				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF05186,PF12796	PS50088,PS50297,PS50088,PS50297,PS50297,PS50088,PS50088,PS50297,PS50088,PS50297,PS50088			G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403,SSF48403,SSF48403,SSF48403,SSF48403	512~532								
aly531.29	Unknown		n/a												43~63								
aly531.3	Charged multivesicular body protein 2b-B	GO:0015031,GO:0000815,GO:0005829,GO:0031902,GO:0007034	CG4618-PA						PF03357						21~55								
aly531.30	Unknown		n/a												57~77								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly531.31	Malate dehydrogenase, mitochondrial	GO:0044262,GO:0016615,GO:0006919,GO:0035070,GO:0035209,GO:0005811,GO:0006475,GO:0006099,GO:0005739,GO:0006108,GO:0043067,GO:0030060,GO:0005759,GO:0005975,GO:0043068	CG7998-PA						PF00056,PF02866				G3DSA:3.90.110.10,G3DSA:3.40.50.720	SSF51735,SSF56327									
aly531.32	Interferon-inducible double-stranded RNA dependent protein kinase activator A	GO:0030422,GO:0019899,GO:0031054,GO:0007417,GO:0005737,GO:0010586,GO:0016020,GO:0005654,GO:2001244,GO:0048471,GO:0070918,GO:0042802,GO:0042803,GO:0048705,GO:0006468,GO:0044822,GO:0048132,GO:0034599,GO:0070920,GO:0030718,GO:0042473,GO:0042474,GO:0035196,GO:0005622,GO:0003725,GO:0005515,GO:0016442	CG6866-PB				SM00358,SM00358,SM00358		PF16482,PF00035,PF00035	PS50137,PS50137,PS50137			G3DSA:3.30.160.20,G3DSA:3.30.160.20,G3DSA:3.30.160.20	SSF54768,SSF54768,SSF54768									
aly531.33	Unknown		n/a																				
aly531.34	Probable ATP-dependent DNA helicase HFM1	GO:0051321,GO:0003676,GO:0005524,GO:0004386	n/a						PF02889				G3DSA:1.10.3380.10	SSF158702									
aly531.35	Coiled-coil domain-containing protein 65		CG30259-PA						PF14772						394~414,3~34								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly531.36	Pro-resilin	GO:0040003,GO:0032992,GO:0005214,GO:0030023,GO:0008010,GO:0031012,GO:0005576,GO:0008061,GO:0042302	CG9036-PA						PF00379	PS51155													
aly531.37	Probable ATP-dependent DNA helicase HFM1	GO:0051321,GO:0008026,GO:0030532,GO:0000398,GO:0004386,GO:0003724,GO:0003676,GO:0005682,GO:0005524	CG5205-PA				SM00490		PF00271				G3DSA:3.40.50.300	SSF52540									
aly531.38	Probable ATP-dependent DNA helicase HFM1	GO:0000381,GO:0043231,GO:0030532,GO:0071011,GO:0005634,GO:0004004,GO:0008380,GO:0000712,GO:0003724,GO:0000398,GO:0003676,GO:0005681,GO:0007067,GO:0004386,GO:0071013,GO:0005682,GO:0005524	CG5931-PA										G3DSA:3.40.50.300		49~69								
aly531.39	Unknown		n/a						PF00531	PS50017			G3DSA:1.10.533.10	SSF47986									
aly531.4	Putative phospholipase B-like lamina ancestor	GO:0016787,GO:0007444,GO:0016042,GO:0005576,GO:0003674,GO:0002121,GO:0046843	CG10645-PC						PF04916														
aly531.40	Unknown	GO:0007113,GO:0051726,GO:0005634,GO:0003677,GO:0007348,GO:0006275,GO:0008156,GO:0042059,GO:0007307	CG3183-PA						PF07412				G3DSA:1.20.5.170	SSF111469	88~129								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly531.41	Phosphatidylinositol 4,5-bisphosphate 5 phosphatase A	GO:0005737,GO:0001726,GO:0052658,GO:0052659,GO:0016311,GO:0043198,GO:0033137,GO:0046030,GO:0019898,GO:0034485,GO:0010977,GO:0046856,GO:0005886,GO:0004445,GO:0030426,GO:0031115	CG9784-PC				SM00128		PF03372				G3DSA:3.60.10.10	SSF56219										
aly531.42	G-protein coupled receptor Mth2	GO:0004930,GO:0016021,GO:0006950,GO:0005886,GO:0008340,GO:0007186	CG17061-PB						PF00002	PS50261			G3DSA:2.170.180.11,G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321										
aly531.43	Transposon Ty3-I Gag-Pol polyprotein	GO:0006310,GO:0005737,GO:0090501,GO:0019076,GO:0000943,GO:0005634,GO:0004540,GO:0008270,GO:0004523,GO:0003887,GO:0015074,GO:0006278,GO:0004190,GO:0005524,GO:0003677,GO:0003964,GO:0008233,GO:0032197,GO:0071897,GO:0003723	n/a						PF00078	PS50878			G3DSA:3.10.10.10	SSF56672										
aly531.44	Arginine kinase	GO:0003824,GO:0016301,GO:0016310,GO:0005524,GO:0004054	CG30274-PA						PF02807,PF00217	PS51510,PS51509			G3DSA:3.30.590.10,G3DSA:1.10.135.10	SSF48034,SSF55931			REACT_13						
aly531.5	Circadian locomoter output cycles protein kaput	GO:0032922,GO:0008062,GO:0048148,GO:0007165,GO:0004871,GO:0003677,GO:0005737,GO:0000122,GO:0005634,GO:0043069,GO:0007623,GO:0007622,GO:0008134,GO:0045187,GO:0045893,GO:0009649,GO:0009266,GO:0003700,GO:0006355,GO:0045944,GO:0006351,GO:0005667,GO:0046983,GO:0046982,GO:0045475	CG42739-PG				SM00091,SM00091		PF14598	PS50888,PS50112,PS50112			G3DSA:3.30.450.20,G3DSA:4.10.280.10,G3DSA:3.30.450.20	SSF55785,SSF47459,SSF55785										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly531.6	Serine protease persephone	GO:0004252,GO:0045087,GO:0006967,GO:0050832,GO:0005576,GO:0008592,GO:0006508,GO:0008233,GO:0006952	CG6367-PA				SM00020		PF00089	PS50240	PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly531.7	NFX1-type zinc finger-containing protein 1	GO:0044822,GO:0046872	CG6204-PA				SM00438,SM00438,SM00438,SM00438,SM00438,SM00438,SM00438		PF13087,PF13086				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	698~718,819~839,302~322								
aly531.8	KRR1 small subunit processome component homolog	GO:0032040,GO:0005730,GO:0005654,GO:0003723,GO:0007275,GO:0006364	CG4258-PA			PIRSF006515	SM00322						G3DSA:3.30.1370.10	SSF54791	270~297								
aly531.9	Serine--tRNA ligase, mitochondrial	GO:0005737,GO:0006434,GO:0097056,GO:0044822,GO:0070158,GO:0004828,GO:0005739,GO:0010467,GO:0006418,GO:0005759,GO:0005524	CG4938-PB					TIGR00414	PF00587	PS50862	PR00981,PR00981,PR00981		G3DSA:3.30.930.10	SSF55681		00970+6.1.1.11	REACT_71	PWY-6281	UPA00906				
aly5319.1	Trypsin CFT-1	GO:0004252,GO:0004175,GO:0005615,GO:0006508	CG31954-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly5319.2	Trypsin CFT-1	GO:0004252,GO:0005615,GO:0006508	CG4386-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5319.3	Trypsin CFT-1	GO:0004252,GO:0004175,GO:0005615,GO:0006508	CG31954-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly5320.1	Nucleolar complex protein 3 homolog	GO:0005730,GO:0005634,GO:0005575,GO:0003674,GO:0008150,GO:0003682	CG1234-PA																				
aly5323.1	Cell surface glycoprotein 1	GO:0005618,GO:0030246,GO:0000272,GO:0005575,GO:0005576,GO:0008150,GO:0030115,GO:0003674	CG12781-PA				SM00664,SM00664		PF03067,PF03351,PF03351	PS50026,PS50836,PS51257,PS50836		PS00022,PS01186,PS00022	G3DSA:2.170.300.10		930~934								
aly5323.10	Juvenile hormone epoxide hydrolase	GO:0008096,GO:0043231,GO:0033961,GO:0016021,GO:0005789,GO:0004301,GO:0019439,GO:0006719	CG15106-PA						PF00561		PR00412,PR00412,PR00412,PR00412		G3DSA:3.40.50.1820	SSF53474									
aly5323.2	Serpin B9	GO:0009617,GO:0004867,GO:0010628,GO:0050829,GO:0005737,GO:0042270,GO:0005615,GO:0005634,GO:0016020,GO:0043066,GO:0002020,GO:0043027,GO:0006915,GO:0033668,GO:0032504,GO:0071391,GO:0002448,GO:0030162,GO:0006955,GO:0010951,GO:0070062,GO:0005829,GO:0005622,GO:0043154,GO:0045861	CG9334-PA				SM00093		PF00079			PS00284	G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:2.30.39.10,G3DSA:2.30.39.10	SSF56574									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5323.3	Phytanoyl-CoA dioxygenase, peroxisomal	GO:0031418,GO:0001561,GO:0006720,GO:0005777,GO:0005739,GO:0003824,GO:0097089,GO:0048037,GO:0048244,GO:0046872	CG14688-PB						PF05721				G3DSA:2.60.120.620	SSF51197									
aly5323.4	Probable phytanoyl-CoA dioxygenase	GO:0031418,GO:0006631,GO:0001561,GO:0005777,GO:0048244,GO:0046872	CG14688-PB						PF05721				G3DSA:2.60.120.620,G3DSA:2.60.120.620	SSF51197									
aly5323.5	Unknown		n/a																				
aly5323.6	Unknown		n/a																				
aly5323.7	Unknown	GO:0009306,GO:0005829,GO:0005811,GO:0007611,GO:0007616,GO:0003674,GO:0008355	CG8588-PF						PF16013														
aly5323.8	Juvenile hormone epoxide hydrolase	GO:0008096,GO:0043231,GO:0033961,GO:0016021,GO:0005789,GO:0004301,GO:0019439,GO:0006719	CG15102-PA			PIRSF001112			PF06441		PR00412,PR00412,PR00412,PR00412,PR00412		G3DSA:3.40.50.1820	SSF53474		00980+3.3.2.9							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5323.9	Juvenile hormone epoxide hydrolase	GO:0008096,GO:0043231,GO:0033961,GO:0016021,GO:0005789,GO:0004301,GO:0003824,GO:0019439,GO:0006719	CG15102-PA			PIRSF001112			PF06441		PR00412,PR00412,PR00412,PR00412,PR00412,PR00412		G3DSA:3.40.50.1820	SSF53474		00980+3.3.2.9							
aly533.1	Histone chaperone asf1	GO:0007517,GO:0035059,GO:0017053,GO:0000122,GO:0006325,GO:0005634,GO:0006333,GO:0005700,GO:0045746,GO:0048813,GO:0006351,GO:0005515,GO:0001103,GO:0048024,GO:0006334,GO:0016568	CG9383-PA						PF04729				G3DSA:2.60.40.1490	SSF101546									
aly533.2	Unknown		CG31342-PB																				
aly533.3	Monocarboxylate transporter 2	GO:0005737,GO:0035879,GO:0015129,GO:0008028,GO:0016021,GO:1901475,GO:0035873,GO:0050833,GO:0015293,GO:0005887,GO:0005886,GO:0005477,GO:0055085	CG11665-PA						PF07690				G3DSA:1.20.1250.20	SSF103473									
aly533.4	Monocarboxylate transporter 9	GO:0008028,GO:0016021,GO:0055085,GO:0015293,GO:0005886	CG11665-PA						PF07690,PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly534.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly534.2	Unknown		n/a																				
aly534.3	Unknown		n/a																				
aly534.4	Unknown		n/a																				
aly5343.1	Serine--pyruvate aminotransferase, mitochondrial	GO:0051384,GO:0005782,GO:0008453,GO:0019448,GO:0042853,GO:0005811,GO:0005777,GO:0005739,GO:0051591,GO:0042866,GO:0046724,GO:0009436,GO:0004760,GO:0030170,GO:0005759,GO:0016597,GO:0019265	CG3926-PA						PF00266				G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383									
aly5347.1	Unknown		n/a										G3DSA:3.40.50.720	SSF51735									
aly535.1	Cuticle protein 18.6, isoform B	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG13935-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly535.10	39S ribosomal protein L47, mitochondrial	GO:0070126,GO:0006996,GO:0070124,GO:0070125,GO:0005739,GO:0006412,GO:0003735,GO:0005743,GO:0005761,GO:0005762,GO:0032543	CG9378-PB						PF06984														
aly535.11	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase	GO:0030210,GO:0005200,GO:0005783,GO:0008587,GO:0008146,GO:0007166,GO:0007509,GO:0005874,GO:0048488,GO:0007367,GO:0008543,GO:0016021,GO:0007474,GO:0005525,GO:0048312,GO:0016787,GO:0090097,GO:0003924,GO:0006024,GO:0007283,GO:0007507,GO:0006184,GO:0000137,GO:0051258,GO:0007427,GO:0007017,GO:0016055,GO:0007428,GO:0005622,GO:0015012,GO:0006790,GO:0015016,GO:0015014,GO:0045570,GO:0060828,GO:0000139	CG8339-PA						PF12062								PWY-6558	UPA00756,UPA00862				
aly535.12	Band 7 protein AGAP004871	GO:0003674,GO:0016021,GO:0016020,GO:0006909	CG33253-PB						PF01145		PR00721,PR00721			SSF117892									
aly535.2	Cuticle protein 19	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly535.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly535.4	Unknown	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34462-PA						PF00379	PS51155													
aly535.5	Cuticle protein 8	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly535.6	Stomatin-1	GO:0003674,GO:0016021,GO:0006909	CG33253-PB				SM00244		PF01145		PR00721,PR00721,PR00721,PR00721,PR00721,PR00721,PR00721			SSF117892	195~222								
aly535.7	Stomatin-3	GO:0016021,GO:0016020	CG14644-PA						PF01145		PR00721,PR00721,PR00721,PR00721			SSF117892									
aly535.8	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG1919-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly535.9	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly53540.1	Unknown		n/a																				
aly536.1	Selenium-binding protein 1	GO:0008430,GO:0005615,GO:0005730,GO:0005829,GO:0016020,GO:0050873,GO:0015031,GO:0070062	CG7966-PA						PF05694				G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF75011,SSF75011	123~157								
aly536.10	Unknown		n/a																				
aly536.100	Unknown		n/a																				
aly536.101	RutC family protein C23G10.2	GO:0019239,GO:0006457,GO:0017148	CG15261-PA					TIGR00004	PF01042			PS01094	G3DSA:3.30.1330.40	SSF55298									
aly536.102	54S ribosomal protein c83.06c, mitochondrial	GO:0005840,GO:0042254,GO:0005739,GO:0005622,GO:0003735,GO:0005762,GO:0006412,GO:0032543	CG18767-PA					TIGR01022	PF00444					SSF57840									

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				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.103	E3 ubiquitin-protein ligase rnf146	GO:0072572,GO:0031648,GO:0090263,GO:0016874,GO:0005829,GO:0016055,GO:0051865,GO:0042787,GO:0008270,GO:0070936,GO:0004842,GO:0005634	CG8786-PC				SM00678,SM00184		PF02825,PF13920	PS50089,PS50918		PS00518	G3DSA:3.30.40.10	SSF117839,SSF57850	174~194				UPA00143				
aly536.104	Unknown	GO:0005575,GO:0003674,GO:0008150	CG17233-PC																				
aly536.105	Gamma-aminobutyric acid receptor-associated protein	GO:0015629,GO:0016236,GO:0019898,GO:0061025,GO:0000226,GO:0005874,GO:0005875,GO:0008625,GO:0031410,GO:0005776,GO:0000045,GO:0031396,GO:0048471,GO:0010506,GO:0044753,GO:0005790,GO:0008017,GO:0044297,GO:0044804,GO:0050811,GO:0005886,GO:0008340,GO:0005930,GO:0000407,GO:0000421,GO:0000422,GO:0005829,GO:0000139,GO:0005764,GO:0015031	CG32672-PA						PF02991				G3DSA:3.10.20.90	SSF54236									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.106	Nucleoprotein TPR	GO:0045840,GO:0070090,GO:0090267,GO:0031490,GO:0042405,GO:0010965,GO:0051028,GO:0000022,GO:0051301,GO:0005737,GO:0007346,GO:0072686,GO:0005719,GO:0005730,GO:0006325,GO:0005634,GO:0005635,GO:0051225,GO:0005654,GO:0005652,GO:0043021,GO:0016363,GO:0034399,GO:0090235,GO:0007067,GO:0031965,GO:0006606,GO:0090316,GO:0060236,GO:1990047,GO:0005819,GO:0009408,GO:0051233,GO:0000775,GO:0006338,GO:0005643,GO:1901673,GO:0030496,GO:0051781,GO:0045944,GO:0006351,GO:0007094,GO:0034401,GO:0034976	CG8274-PA						PF07926						739~808,894~932,1287~1356,1199~226,1491~1515,672~724,1527~1600,73~163,312~353,231~290,1372~1462,848~889,436~480,488~508,1232~1266,1100~1134,1142~1176,1968~1968,947~1088,558~618,1620~1665								
aly536.107	cAMP-dependent protein kinase type I regulatory subunit	GO:0007015,GO:0030551,GO:0008603,GO:0008103,GO:0030552,GO:2000253,GO:0045859,GO:0007591,GO:0045471,GO:0019933,GO:0005952,GO:0001932,GO:0007274,GO:0008355	CG42341-PV				SM00100,SM00100,SM00394		PF02197,PF00027,PF00027	PS50042,PS50042	PR00103,PR00103,PR00103,PR00103,PR00103	PS00889,PS00888,PS00888,PS00889	G3DSA:2.60.120.10,G3DSA:2.60.120.10	SSF51206,SSF47391,SSF51206									
aly536.108	ATP-dependent DNA helicase Q4	GO:0002164,GO:0000785,GO:0008270,GO:0007307,GO:0003678,GO:0007275,GO:0051301,GO:0005737,GO:0006302,GO:0005634,GO:0016020,GO:0006260,GO:0045740,GO:0048477,GO:0003697,GO:0005524,GO:0008284,GO:0006284,GO:0043140,GO:0006281,GO:0032508,GO:0004386,GO:0010971,GO:0036310,GO:0006310,GO:0008094,GO:0000405,GO:0036292,GO:0000733,GO:0007095	CG7487-PA				SM00490,SM00487,SM00343	TIGR00614	PF00270,PF00098,PF11719,PF00271	PS51194,PS50158,PS51192			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:4.10.60.10	SSF52540,SSF52540,SSF52540,SSF57756,SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.109	Xylosyltransferase oxt	GO:0042732,GO:0030206,GO:0030158,GO:0050650,GO:0016020,GO:0000139,GO:0015012,GO:0008375,GO:0005789,GO:0016021	CG32300-PB				SM00321		PF02485,PF12529,PF01822	PS51212						00532+2.4.2.26,00534+2.4.2.26		PWY-6557	UPA00755,UPA00756				
aly536.11	ATP-dependent RNA helicase p62	GO:0050688,GO:0019730,GO:0000398,GO:0003676,GO:0005875,GO:0005737,GO:0000381,GO:0008026,GO:0005634,GO:0016246,GO:0010501,GO:0005524,GO:0071011,GO:0071013,GO:0004004,GO:0045893,GO:0022008,GO:0005703,GO:0005700,GO:0003724,GO:0006417,GO:0003729	CG10077-PA				SM00487,SM00490		PF00271,PF00270	PS51195,PS51194,PS51192		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									
aly536.110	Protein ecdysoneless homolog	GO:0016319,GO:0008258,GO:0007591,GO:0002165,GO:0002168,GO:0005737,GO:0007458,GO:0003713,GO:0005654,GO:0006110,GO:0006366,GO:0048477,GO:0008283,GO:0007281,GO:0008362,GO:0022008,GO:0007443,GO:0007030,GO:2000045,GO:0009608,GO:0007390,GO:0006355,GO:0042810,GO:0006697,GO:0048542	CG5714-PA						PF07093														
aly536.111	Dehydrogenase/reductase SDR family member 4	GO:0016614,GO:0005777,GO:0005739,GO:0004090,GO:0008152,GO:0016491	CG10672-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.112	U6 snRNA phosphodiesterase	GO:0034477,GO:0004518,GO:0005634,GO:0008150,GO:0005515,GO:0008380,GO:0006397	CG16790-PA	MF_03040					PF09749														
aly536.113	Tether containing UBX domain for GLUT4	GO:0043231,GO:0061024,GO:0005829,GO:0033116,GO:0009898,GO:0019898,GO:0005654,GO:0042593,GO:0012505,GO:0012506,GO:0005886,GO:0048471,GO:0006886,GO:0046324	CG33722-PD						PF11470				G3DSA:3.10.20.90,G3DSA:3.10.20.90	SSF54236,SSF54236	331~351								
aly536.114	Glutamate receptor ionotropic, NMDA 2B	GO:0008021,GO:0050966,GO:0005262,GO:0007616,GO:0007612,GO:0007613,GO:0030425,GO:0008270,GO:0048266,GO:0035249,GO:0030054,GO:0016594,GO:0045471,GO:0001701,GO:0072375,GO:0004972,GO:0016021,GO:0001967,GO:0001964,GO:0001662,GO:0050975,GO:0008328,GO:0035235,GO:0006811,GO:0005234,GO:0034220,GO:0005886,GO:0060079,GO:0097481,GO:0007423,GO:0045211,GO:0060291,GO:0017146,GO:0010738	CG33513-PC				SM00918,SM00079		PF01094,PF10613,PF00060		PR00177,PR00177,PR00177,PR00177		G3DSA:3.40.50.2300,G3DSA:1.10.287.70,G3DSA:3.40.190.10,G3DSA:3.40.190.10	SSF53850,SSF53850,SSF53822	1044~1055								
aly536.115	YTH domain-containing protein 1	GO:0016070,GO:1990247,GO:0016604,GO:0005634,GO:0006376,GO:0003723,GO:0044822	CG12076-PA						PF04146	PS50882													
aly536.116	Ganglioside-induced differentiation-associated protein 1	GO:0005737,GO:0032526,GO:0000266,GO:0005634,GO:0016020,GO:0008053,GO:0005739,GO:0031307,GO:0006626	CG4623-PA						PF13417,PF00043	PS50404,PS50405			G3DSA:3.40.30.10,G3DSA:1.20.1050.10	SSF47616,SSF52833	222~242								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.117	FIT family protein CG10671	GO:0034389,GO:0008654,GO:0005789,GO:0030176,GO:0003674,GO:0019915	CG10671-PB						PF10261														
aly536.118	Chromobox protein homolog 3	GO:0005720,GO:0005819,GO:0005719,GO:0048511,GO:0005635,GO:0010369,GO:0005654,GO:0000779,GO:0045892,GO:0019904,GO:0031618,GO:0000785,GO:0016568,GO:0006351	CG8289-PA				SM00298		PF00385	PS50013	PR00504,PR00504,PR00504		G3DSA:2.40.50.40	SSF54160									
aly536.119	Vacuolar protein sorting associated protein 8 homolog	GO:0016197,GO:0016192,GO:0006886,GO:0051020,GO:0033263,GO:0008270,GO:0005515	CG10144-PA										G3DSA:2.130.10.10	SSF50978									
aly536.12	ATP-dependent RNA helicase p62	GO:0005737,GO:0000381,GO:0003676,GO:0019730,GO:0071011,GO:0005634,GO:0050688,GO:0005703,GO:0005700,GO:0005875,GO:0045893,GO:0004004,GO:0005515,GO:0016246,GO:0006417,GO:0000398,GO:0022008,GO:0010501,GO:0071013,GO:0005524,GO:0003729	CG10279-PF				SM00487,SM00490		PF00271,PF00270	PS51195,PS51192,PS51194		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									
aly536.120	Leukocyte receptor cluster member 8 homolog		CG6700-PA						PF03399														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.121	Uncharacterized protein C16orf52 homolog A	GO:0005575,GO:0003674,GO:0008150	CG14182-PA																				
aly536.122	Opsin-2	GO:0008020,GO:0004930,GO:0009881,GO:0007604,GO:0016021,GO:0007601,GO:0018298,GO:0007602,GO:0009589,GO:0007186,GO:0016039	CG10888-PA						PF00001	PS50262	PR00577,PR00577,PR00577,PR00577,PR00577,PR00577,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00238,PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly536.123	Unknown	GO:0005575,GO:0003674,GO:0008150	CG12502-PB						PF10177														
aly536.124	Dipeptidase 1	GO:0008239,GO:0006805,GO:0035690,GO:0044281,GO:0034235,GO:0008235,GO:0030054,GO:0031225,GO:0045177,GO:0050667,GO:0070062,GO:0016999,GO:0005634,GO:0016805,GO:0043066,GO:0070573,GO:0006508,GO:0043027,GO:0030336,GO:0006749,GO:0016324,GO:0071277,GO:0005886,GO:0005615,GO:0031528,GO:0072340,GO:0072341,GO:0071732,GO:0006691,GO:0043154,GO:0019369,GO:0008270	CG6154-PC						PF01244	PS51365			G3DSA:3.20.20.140	SSF51556				PWY-7533					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.125	Unknown	GO:0005575,GO:0008150,GO:0005102,GO:0003674	CG14489-PA						PF14722														
aly536.126	Unknown		n/a						PF10545	PS51029													
aly536.127	Sodium/potassium-transporting ATPase subunit alpha	GO:0007630,GO:0051124,GO:0060439,GO:0007268,GO:0005890,GO:0050905,GO:0005737,GO:0001700,GO:0005634,GO:0019991,GO:0009612,GO:0005391,GO:0035158,GO:0035725,GO:0005886,GO:0006812,GO:0046872,GO:0015672,GO:0005524,GO:0007626,GO:0035152,GO:0007605,GO:0035159,GO:0008324,GO:0016323,GO:0008360,GO:0009266,GO:0008340,GO:0001894,GO:0008344,GO:0005918,GO:0098655,GO:0006754	CG5670-PA				SM00831	TIGR01106,TIGR01494,TIGR01494	PF00122,PF00702,PF00690,PF00689		PR00121,PR00121,PR00121,PR00121,PR00121,PR00121,PR00119,PR00119,PR00119,PR00119,PR00119,PR00119	PS00154	G3DSA:1.20.1110.10,G3DSA:1.20.1110.10,G3DSA:4.10.6.10,G3DSA:3.40.1110.10	SSF56784,SSF56784,SSF81665,SSF81665,SSF81665,SSF81653										
aly536.128	Enoyl-CoA delta isomerase 2, mitochondrial	GO:0004165,GO:0016020,GO:0005782,GO:0006635,GO:0005811,GO:0005777,GO:0000062,GO:0005654,GO:0005739,GO:0008152,GO:0050829,GO:0016863	CG13890-PA						PF00378				G3DSA:3.90.226.10	SSF52096	221~241								
aly536.129	Phosphoglycolate phosphatase	GO:0005975,GO:0016311,GO:0004725,GO:0000287,GO:0008967,GO:0098519,GO:0008152,GO:0035335,GO:0016791	CG5567-PA			PIRSF000915		TIGR01452,TIGR01460	PF13242,PF13344				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000,G3DSA:3.40.50.10410	SSF56784									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.13	Histone deacetylase Rpd3	GO:0032041,GO:0005705,GO:0035065,GO:0006099,GO:0000785,GO:0005737,GO:0070822,GO:0007517,GO:0000122,GO:0004407,GO:0005634,GO:0003714,GO:0016458,GO:0016575,GO:2001229,GO:0022904,GO:0048477,GO:0017053,GO:0008134,GO:0045879,GO:0000118,GO:0045892,GO:0008340,GO:0022008,GO:0007350,GO:0035098,GO:0016580,GO:0016581,GO:0050771,GO:0031523,GO:0070983,GO:0005700,GO:0006355,GO:0048813,GO:0006351,GO:0005515,GO:0006342,GO:0016568	CG7471-PA			PIRSF037913			PF00850		PR01270,PR01270,PR01270,PR01271,PR01271,PR01271,PR01271,PR01271		G3DSA:3.40.800.20	SSF52768										
aly536.130	TPPP family protein CG45057	GO:0005575,GO:0048812,GO:0003674	CG45057-PE						PF05517					SSF47473	3~23								
aly536.131	Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase	GO:0016787,GO:0016021,GO:0031902,GO:0005765	CG6707-PA						PF09788									PWY-6367,PWY-6368					
aly536.132	Cirhin	GO:0005730,GO:0030490,GO:0034455,GO:0005575,GO:0006355,GO:0003674,GO:0006351,GO:0005515,GO:0022008,GO:0044822	CG5018-PB				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320			PS50082,PS50294		PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF69322,SSF50998,SSF50998									
aly536.133	Unknown		n/a						PF14945														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.134	Unknown		n/a																				
aly536.135	DNA excision repair protein haywire	GO:0000381,GO:0043140,GO:0001113,GO:0004003,GO:0001111,GO:0006366,GO:1903506,GO:0006289,GO:0009411,GO:0006367,GO:0003677,GO:0000990,GO:0005675,GO:0004386,GO:0032508,GO:0005634,GO:0005524	CG8019-PB				SM00487,SM00490	TIGR00603	PF16203,PF09696,PF04851,PF13625	PS51194,PS51192	PR00851,PR00851,PR00851,PR00851,PR00851,PR00851,PR00851,PR00851,PR00851,PR00851		G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	843~846									
aly536.136	Chromodomain Y-like protein	GO:0035064,GO:0005634,GO:0003714,GO:0004402,GO:1903507,GO:0005654,GO:0006355,GO:0006351	CG14787-PA						PF00378				G3DSA:3.90.226.10	SSF52096	392~412								
aly536.137	Leukocyte receptor cluster member 1	GO:0046331	CG12818-PA				SM01083		PF10197						221~252,18~71								
aly536.138	WASH complex subunit strumpellin	GO:0015031,GO:0071203,GO:0005769	CG12272-PA						PF10266,PF10266						63~83								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.139	Peroxisomal membrane protein PMP34	GO:0005347,GO:0016020,GO:0006635,GO:0005777,GO:0044281,GO:0035350,GO:0044610,GO:0005779,GO:0005778,GO:0015230,GO:0015217,GO:0051087,GO:0080121,GO:0022857,GO:0005739,GO:0080122,GO:0015867,GO:0015908,GO:0015866,GO:0005215,GO:0006810,GO:0001561,GO:0044425,GO:0035349,GO:0043231,GO:1901679,GO:0051724,GO:0015228,GO:0043132,GO:0005740	CG32250-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly536.14	Leucine-rich repeat-containing protein 16A	GO:0017024,GO:0030032,GO:0007596,GO:0030335,GO:2000813,GO:0051638,GO:0005737,GO:0070062,GO:0030838,GO:0051496,GO:0005634,GO:0032403,GO:0016477,GO:0031941,GO:0042384,GO:0030027,GO:0031529,GO:0007015,GO:0005829,GO:1900026,GO:1902745,GO:0046415	CG1399-PF				SM00368,SM00368,SM00368,SM00368,SM00368		PF16000	PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047,SSF52047									
aly536.140	Nuclear pore complex protein Nup160 homolog	GO:0031080,GO:0005643,GO:0006406,GO:0005515,GO:0005487,GO:0007184	CG4738-PB						PF11715														
aly536.141	F-box/LRR-repeat protein 16	GO:0005737	CG32085-PA				SM00367,SM00367,SM00367,SM00367,SM00367,SM00367,SM00367						G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52047									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.142	Puromycin-sensitive aminopeptidase	GO:0004177,GO:0070062,GO:0005829,GO:1903955,GO:0008270,GO:0071456,GO:0006508,GO:0005634,GO:0008237	CG1009-PC						PF11838,PF01433		PR00756,PR00756,PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF55486,SSF63737									
aly536.143	Protein disulfide-isomerase TMX3	GO:0016021,GO:0005789,GO:0045454,GO:0005509,GO:0003756	CG5027-PA						PF00085,PF13848	PS51352		PS00194	G3DSA:3.40.30.10	SSF52833									
aly536.144	Probable ATP-dependent RNA helicase DDX20	GO:0005737,GO:0000387,GO:0071254,GO:0032797,GO:0005829,GO:0004004,GO:0004386,GO:0007528,GO:0003724,GO:0022618,GO:0007629,GO:0003676,GO:0003677,GO:0015030,GO:0005634,GO:0034719,GO:0008344,GO:0005524	CG6539-PA				SM00490,SM00487		PF00271,PF00270	PS51194,PS51192,PS51195		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									
aly536.145	SNF-related serine/threonine-protein kinase	GO:0005737,GO:0006468,GO:0005634,GO:0000287,GO:0005575,GO:0004674,GO:0030099,GO:0004672,GO:0016909,GO:0035556,GO:0005524	CG8485-PA				SM00220		PF00069	PS50011,PS50030		PS00108,PS00107	G3DSA:1.10.8.10,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly536.146	Ubiquitin-conjugating enzyme E2 variant 2	GO:0005737,GO:0061631,GO:0031625,GO:0032436,GO:0070062,GO:0042275,GO:0061630,GO:0000729,GO:0070534,GO:0043524,GO:0010976,GO:0051965,GO:0045739,GO:0006301,GO:0004842,GO:0005634,GO:0031372	CG10640-PA				SM00212		PF00179	PS50127			G3DSA:3.10.110.10	SSF54495									
aly536.147	Ubiquitin carboxyl-terminal hydrolase 36	GO:0030718,GO:0040007,GO:0005730,GO:0016579,GO:0007591,GO:0008234,GO:0036459,GO:0045824,GO:0006511,GO:0035019,GO:0042981,GO:0016578	CG5505-PD						PF00443	PS50235		PS00973,PS00972		SSF54001									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.148	Probable helicase MAGATAMA 3	GO:0009553,GO:0005634,GO:0004004,GO:0004386,GO:0009875,GO:0010183,GO:0005515,GO:0005875,GO:0005524	CG7504-PB				SM00240		PF00498,PF13087,PF13086	PS50006			G3DSA:3.40.50.300,G3DSA:2.60.200.20	SSF52540,SSF49879	761~781								
aly536.149	Potassium voltage-gated channel protein Shab	GO:0008016,GO:0071805,GO:0006813,GO:0016021,GO:0060025,GO:0051260,GO:0008076,GO:0007268,GO:0048812,GO:0005249,GO:0005886,GO:0001508,GO:0005251,GO:0008345,GO:0055085	CG43128-PM				SM00225		PF02214,PF00520		PR01494,PR01494,PR01494,PR01494,PR01494,PR01494,PR01491,PR01491,PR01491,PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR00169,PR00169		G3DSA:1.10.287.70,G3DSA:3.30.710.10	SSF54695,SSF81324	191~211								
aly536.15	Suppressor of cytokine signaling 6	GO:0050868,GO:0009968,GO:0040008,GO:0010498,GO:0017022,GO:0005622,GO:0016567,GO:0001772,GO:0035556,GO:0038202	CG8146-PB				SM00252,SM00253		PF00017,PF07525	PS50225,PS50001			G3DSA:3.30.505.10	SSF55550,SSF158235					UPA00143				
aly536.150	N-alpha-acetyltransferase 60	GO:0005737,GO:0043967,GO:0004402,GO:0000090,GO:0017196,GO:0010485,GO:0007059,GO:0004596	CG18177-PA						PF00583	PS51186			G3DSA:3.40.630.30	SSF55729									
aly536.151	Transcription factor Sox-8	GO:0003700,GO:0014029,GO:0005634,GO:0008584,GO:0006355,GO:0008301,GO:0006351,GO:0003677	CG15552-PA				SM00398		PF00505	PS50118	PR00886,PR00886,PR00886		G3DSA:1.10.30.10	SSF47095									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.152	Zinc finger CCCH domain containing protein 18	GO:0071011,GO:0005634,GO:0044822,GO:0000398,GO:0005654,GO:0022008,GO:0046872,GO:0071013	CG1677-PA				SM00356		PF00642	PS50103			G3DSA:4.10.1000.10	SSF90229	494~514								
aly536.153	Zinc finger CCCH domain containing protein 18	GO:0071011,GO:0005634,GO:0000398,GO:0022008,GO:0046872,GO:0071013	CG1677-PA												58~85								
aly536.154	Ribonucleases P/MRP protein subunit POP1	GO:0090502,GO:0090501,GO:0008033,GO:0005615,GO:0005655,GO:0000172,GO:0044822,GO:0004526,GO:0001682,GO:0016078,GO:0006396,GO:0000171	CG32763-PA						PF08170,PF06978,PF06978						656~683								
aly536.155	Unknown		n/a																				
aly536.156	Unknown		n/a																				
aly536.157	Zinc transporter ZIP11	GO:0016021,GO:0016020,GO:0030001,GO:0046873,GO:0006829,GO:0055085	CG13189-PA						PF02535														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.158	Unknown	GO:0016021,GO:0000902	CG13196-PA							PS51034													
aly536.159	Aprataxin	GO:0005730,GO:0033699,GO:0000012,GO:0071011,GO:0005634,GO:0006281,GO:0000398,GO:0005654,GO:0003824,GO:0003677,GO:0046872,GO:0003684	CG5316-PC						PF11969,PF16278	PS51084			G3DSA:3.30.428.10	SSF54197									
aly536.16	Ubiqui biosynthesis protein COQ9, mitochondrial	GO:0005743,GO:0006744,GO:0008289	CG30493-PB					TIGR02396	PF08568,PF08511										UPA00232				
aly536.160	Lariat debranching enzyme	GO:0008419,GO:0016787,GO:0005634,GO:0000375,GO:0090502,GO:0006396,GO:0006397	CG7942-PB						PF00149,PF05011				G3DSA:3.60.21.10	SSF56300									
aly536.161	Meiotic recombination protein DMC1/LIM15 homolog	GO:0016887,GO:0009994,GO:0000781,GO:0007294,GO:0007143,GO:0007276,GO:0007141,GO:0001541,GO:0009949,GO:0005634,GO:0007129,GO:0000166,GO:0005654,GO:0045003,GO:0003690,GO:0005694,GO:0003697,GO:0005524,GO:0006281,GO:0007283,GO:0000794,GO:0007286,GO:0007131,GO:0001556,GO:0006310,GO:0008094,GO:0009951,GO:0000075,GO:0048477,GO:0000150,GO:0030717,GO:0008298,GO:0005515,GO:0003684	CG7948-PA			PIRSF005856	SM00382	TIGR02238	PF08423	PS50163,PS50162			G3DSA:1.10.150.20,G3DSA:3.40.50.300	SSF47794,SSF52540	238~258								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.162	Ethanolamine-phosphate cytidylyltransferase	GO:0006646,GO:0006644,GO:0008654,GO:0005789,GO:0003824,GO:0009058,GO:0042439,GO:0044281,GO:0004306,GO:0046474	CG5547-PB					TIGR00125,TIGR00125	PF01467,PF01467				G3DSA:3.40.50.620,G3DSA:3.40.50.620	SSF52374,SSF52374									
aly536.163	MKL/myocardin-like protein 2	GO:0045844,GO:0033613,GO:0048568,GO:0030036,GO:0001077,GO:0001889,GO:0003676,GO:0007298,GO:0051302,GO:0003713,GO:0005737,GO:0007517,GO:0001701,GO:0005634,GO:0007476,GO:0048514,GO:0071456,GO:0008078,GO:0003007,GO:0001105,GO:0045893,GO:0007424,GO:0003700,GO:0048738,GO:0045944,GO:0006351,GO:0051145	CG32296-PH				SM00513,SM00707,SM00707,SM00707		PF02037,PF02755,PF02755	PS51073,PS51073,PS50800,PS51073			G3DSA:1.10.720.30	SSF68906	698~725,479~506									
aly536.164	Unknown		n/a																				
aly536.165	Heparan sulfate 2-O-sulfotransferase pipe	GO:0005794,GO:0040014,GO:0009950,GO:0005694,GO:0005634,GO:0008146,GO:0004394,GO:0007313,GO:0005515,GO:0034483,GO:0008063,GO:0016485,GO:0034481,GO:0048477,GO:0016021,GO:0030173,GO:0009880	CG9614-PL																				
aly536.166	Heparan sulfate 2-O-sulfotransferase pipe	GO:0005794,GO:0040014,GO:0009950,GO:0005694,GO:0005634,GO:0008146,GO:0004394,GO:0007313,GO:0005515,GO:0034483,GO:0008063,GO:0016485,GO:0034481,GO:0048477,GO:0016021,GO:0030173,GO:0009880	CG9614-PL						PF03567				G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.167	Glycogen-binding subunit 76A	GO:0005575,GO:0008157,GO:0008150,GO:0008599,GO:0005515	CG9619-PA						PF03370	PS51159													
aly536.168	SRSF protein kinase 3	GO:0006468,GO:0030154,GO:0007519,GO:0004674,GO:0004672,GO:0060537,GO:0005524	CG8565-PA				SM00220		PF00069,PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10	SSF56112,SSF56112	291~325								
aly536.169	Monocarboxylate transporter 7	GO:0015718,GO:0015293,GO:0034220,GO:0008028,GO:0016021,GO:0015355,GO:0005886,GO:0055085	CG8468-PC						PF07690,PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	653~658								
aly536.17	Coiled-coil domain-containing protein 93	GO:0005575,GO:0003674,GO:0008150,GO:0005769,GO:0015031	CG7773-PA						PF09762						369~403,291~350								
aly536.170	DNA replication factor Cdt1	GO:0005737,GO:0000910,GO:0000076,GO:0019730,GO:0030174,GO:0005634,GO:0042065,GO:0006261,GO:0021782,GO:0005654,GO:0042023,GO:0033262,GO:0005657,GO:0006260,GO:0005664,GO:0007307,GO:0051306,GO:0007304,GO:0003677,GO:0051298	CG8171-PA				SM01075		PF08839,PF16679					SSF46785	411~431,131~151								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.171	Pyrimidodiazepine synthase	GO:0005737,GO:0045174,GO:0004364,GO:0016782,GO:0006728,GO:0004734,GO:0006726,GO:0006749,GO:0042803	CG6776-PA						PF00043,PF13417	PS50404,PS50405	PR01625,PR01625,PR01625		G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF47616,SSF52833		00982+2.5.1.18,00053+1.8.5.1,00480+2.5.1.18+1.8.5.1,00980+2.5.1.18	REACT_11193,REACT_13433	PWY-6842,PWY-7112,PWY-6370,PWY-4061,PWY-7533,PWY-4202,PWY-2261					
aly536.172	Pyrimidodiazepine synthase	GO:0005737,GO:0045174,GO:0004364,GO:0016782,GO:0006728,GO:0004734,GO:0006726,GO:0006749,GO:0042803	CG6776-PA						PF13417,PF13410	PS50404,PS50405	PR01625,PR01625,PR01625		G3DSA:3.40.30.10,G3DSA:1.20.1050.10	SSF52833,SSF47616		00982+2.5.1.18,00053+1.8.5.1,00480+2.5.1.18+1.8.5.1,00980+2.5.1.18	REACT_11193,REACT_13433	PWY-6842,PWY-7112,PWY-6370,PWY-4061,PWY-7533,PWY-4202,PWY-2261					
aly536.173	LisH domain and HEAT repeat-containing protein KIAA1468		n/a							PS50896			G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371	108~128								
aly536.174	Centrosomal protein of 135 kDa	GO:0036064,GO:0008022,GO:0007026,GO:0005813,GO:0051297,GO:0005814,GO:0032053,GO:0046331,GO:0007099,GO:0007288,GO:0010457,GO:0008017	CG17081-PB											SSF57997	615~635,727~761,269~296,301~328,765~785,807~855,664~705,405~425,355~375,103~123,905~939,170~197,538~600,961~1037,234~261,496~530,71~91								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.175	Transmembrane protein 170A	GO:0016021	CG12341-PA						PF10190														
aly536.176	Nucleolar GTP-binding protein 2	GO:0006909,GO:0005730,GO:0005634,GO:0016020,GO:0003924,GO:0042254,GO:0005654,GO:0008152,GO:0001745,GO:0044822,GO:0005525	CG6501-PA						PF08153,PF01926	PS51721	PR00326,PR00326		G3DSA:3.40.50.300,G3DSA:1.10.1580.10	SSF52540									
aly536.177	Craniofacial development protein 1	GO:0042127,GO:0008360,GO:0019894,GO:2000270,GO:0007155,GO:0007275,GO:0000777	CG40218-PA						PF07572	PS51279													
aly536.178	Breast cancer anti-estrogen resistance protein 1	GO:0016337,GO:0015629,GO:0007596,GO:0008286,GO:0048011,GO:0048008,GO:0004871,GO:0060326,GO:0005925,GO:0007414,GO:0051301,GO:0005737,GO:0001726,GO:0005730,GO:0042981,GO:0030335,GO:0016477,GO:0007186,GO:0035729,GO:0050851,GO:0050852,GO:0050853,GO:0008283,GO:0030027,GO:0019901,GO:0001558,GO:0007173,GO:0005886,GO:0007155,GO:0048010,GO:0048012,GO:0030168,GO:0030011,GO:0007015,GO:0007016,GO:0010595,GO:0005829,GO:0007229	CG1212-PD				SM00326		PF14604,PF12026,PF08824	PS50002	PR00452,PR00452,PR00452,PR00452		G3DSA:2.30.30.40	SSF50044	198~218								
aly536.179	Unknown		CG32813-PH				SM00717,SM00717		PF13873,PF13873						75~95,340~372								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.18	Unknown		n/a																				
aly536.180	N-alpha-acetyltransferase 10	GO:0005737,GO:0022626,GO:0008080,GO:0005730,GO:0017198,GO:0005634,GO:0016020,GO:0031415,GO:0006474,GO:0006475,GO:0005622,GO:0005575,GO:1990189,GO:0022008,GO:0043022,GO:0048477,GO:0018002,GO:0004596,GO:1990190	CG11989-PA						PF00583	PS51186			G3DSA:3.40.630.30	SSF55729									
aly536.181	Unknown		CG6674-PA						PF15264						184~204								
aly536.182	BTB/POZ domain-containing protein 3	GO:0048813,GO:0005829,GO:0005634,GO:0021987,GO:0005515	CG8398-PA				SM00225		PF00651,PF07707	PS50097			G3DSA:3.30.710.10	SSF54695									
aly536.183	Unknown		n/a												52~72								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.184	Ataxin-1	GO:0008022,GO:0051168,GO:0034046,GO:0042405,GO:0003677,GO:0008542,GO:0005737,GO:0000122,GO:0005634,GO:0043569,GO:0007474,GO:0005654,GO:0016363,GO:0042802,GO:0006351,GO:0048286,GO:0060252,GO:0008266,GO:0045892,GO:0060079,GO:0008344,GO:0043621,GO:0042326,GO:0043231,GO:0045944,GO:0003723,GO:0005515,GO:0003682,GO:0045494	CG4547-PB				SM00536		PF08517	PS51148			G3DSA:2.170.16.10	SSF102031										
aly536.185	Anamorsin homolog	GO:0005737,GO:0006915,GO:0051536,GO:0051537,GO:0030707,GO:0016226,GO:0005575,GO:0043066,GO:0003674,GO:0005758,GO:0046872,GO:0009055	CG4180-PA						PF05093,PF13847				G3DSA:3.40.50.150	SSF53335									
aly536.186	Unknown		CG42495-PA											SSF103481									
aly536.187	Unknown		n/a																				
aly536.188	Dual specificity protein phosphatase 22	GO:0005737,GO:0002710,GO:0000122,GO:0050868,GO:0008138,GO:0008283,GO:0042127,GO:0006470,GO:0005634,GO:0006915,GO:0050860,GO:0000188,GO:0005575,GO:0046330,GO:0004725,GO:0007275,GO:0007179	CG10089-PD						PF00782	PS50056,PS50054			G3DSA:3.90.190.10	SSF52799									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.189	Unknown		n/a																				
aly536.19	Sperm-associated antigen 6	GO:0005737,GO:0015630,GO:0021591,GO:0097228,GO:0005643,GO:0005634,GO:0006606,GO:0008320,GO:0007283,GO:1990716,GO:0007288,GO:0005874,GO:0030317	CG8548-PA				SM00185,SM00185,SM00185,SM00185,SM00185,SM00185		PF00514,PF00514	PS50176			G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371										
aly536.190	Transmembrane protein 184B	GO:0050832,GO:0016021,GO:0030246,GO:0008039	CG12004-PC						PF03619														
aly536.191	Cell division cycle protein 27 homolog	GO:0005737,GO:0000278,GO:0071011,GO:0005813,GO:0005634,GO:0009987,GO:0090302,GO:0000398,GO:0007091,GO:0005654,GO:0000793,GO:0008054,GO:0005515,GO:0070979,GO:0007067,GO:0022008,GO:0005876,GO:0005680	CG8610-PA				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF12895,PF13181,PF13414,PF13414,PF13174	PS50005,PS50005,PS50005,PS50005,PS50005,PS50293,PS50005,PS50005,PS50005,PS50293,PS50005			G3DSA:1.25.40.120,G3DSA:1.25.40.120	SSF48452,SSF48452,SSF48452										
aly536.192	Nuclear receptor coactivator 5	GO:0015629,GO:0046627,GO:0006355,GO:0071011,GO:0005615,GO:0005634,GO:0003988,GO:0000166,GO:0005654,GO:0042593,GO:0006351,GO:0003676,GO:0003682,GO:0044822,GO:0003729	CG8614-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330,G3DSA:3.40.50.800	SSF54928,SSF52954										
aly536.193	Mpv17-like protein 2	GO:0005743,GO:0016021,GO:0005779	CG1662-PA						PF04117,PF04117														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.194	Unknown	GO:0022008	CG34109-PC						PF04087,PF04087														
aly536.195	Sodium/hydrogen exchanger 3	GO:0051384,GO:0007623,GO:0070062,GO:0016324,GO:0006885,GO:0016021,GO:0006898,GO:0006873,GO:0006814,GO:0035725,GO:0030165,GO:0005886,GO:0031988,GO:0015385,GO:0031526,GO:0055085,GO:0002028	CG9256-PG					TIGR00840	PF00999		PR01084,PR01084,PR01084,PR01084						REACT_15518						
aly536.196	Protein phosphatase 1 regulatory inhibitor subunit 16B	GO:0051489,GO:0014066,GO:0007476,GO:0005634,GO:0017020,GO:0008599,GO:1902309,GO:0008157,GO:0005515,GO:0005886,GO:1903589,GO:0048471,GO:0042995,GO:0061028,GO:0035307	CG6896-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796	PS50088,PS50297,PS50088,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20	SSF48403										
aly536.197	Peptide methionine sulfoxide reductase	GO:0008113,GO:0035071,GO:0000096,GO:0048102,GO:0048812,GO:0008340,GO:0034599,GO:0006979,GO:0055114,GO:0030091	CG7266-PG	MF_01401				TIGR00401	PF01625				G3DSA:3.30.1060.10	SSF55068									
aly536.198	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.199	Palmitoyl-protein thioesterase 1	GO:0008021,GO:0006898,GO:0030308,GO:0030149,GO:0050803,GO:0006907,GO:0030425,GO:0030424,GO:0002084,GO:0007042,GO:0048260,GO:0031579,GO:0051186,GO:0051181,GO:0005615,GO:0008306,GO:0005634,GO:0016020,GO:0016042,GO:0043066,GO:0043025,GO:0048666,GO:0005794,GO:0007625,GO:0032429,GO:0007601,GO:0043202,GO:0030163,GO:0007269,GO:0044257,GO:0008340,GO:0008474,GO:0008344,GO:0070062,GO:0006897,GO:0007420,GO:0007399,GO:0005829,GO:0045121,GO:0005764,GO:0048549,GO:0005576,GO:0016290,GO:0015031,GO:0043524,GO:0050896	CG12108-PA						PF02089,PF02089		PR00414,PR00414,PR00414		G3DSA:3.40.50.1820	SSF53474									
aly536.2	E3 ubiquitin-protein ligase sina	GO:0016874,GO:0005634,GO:0016567,GO:0006511,GO:0008270,GO:0004842,GO:0007275	CG2681-PA						PF03145				G3DSA:3.30.40.10,G3DSA:3.90.890.10	SSF49599					UPA00143				
aly536.20	60S ribosomal protein L14	GO:0022626,GO:0005840,GO:0022625,GO:0051297,GO:0003735,GO:0007052,GO:0043524,GO:0000022,GO:0006412,GO:0051298	CG6253-PA						PF01929				G3DSA:2.30.30.30	SSF50104									
aly536.200	Unknown	GO:0008080	CG13759-PA						PF00583				G3DSA:3.40.630.30	SSF55729,SSF55729									
aly536.201	Unknown		n/a												91~111								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.202	Dorsal root ganglia homeobox protein	GO:0043565,GO:0009593,GO:0016048,GO:0007399,GO:0003700,GO:0050954,GO:0005634,GO:0021516,GO:0021559,GO:0006355,GO:0001764,GO:0006351,GO:0007409,GO:0003677,GO:0030182,GO:0007411	CG11294-PA				SM00389		PF00046	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689									
aly536.203	Chitooligosaccharidolytic beta-N-acetylglucosaminidase	GO:0005975,GO:0005615,GO:0032504,GO:0016231,GO:0000272,GO:0004563,GO:0005886,GO:0006032,GO:0044130	CG1787-PA						PF14845,PF00728		PR00738,PR00738,PR00738,PR00738,PR00738,PR00738,PR00738		G3DSA:3.30.379.10,G3DSA:3.20.20.80	SSF55545,SSF51445		00604+3.2.1.52,00520+3.2.1.52,00511+3.2.1.52,00603+3.2.1.52,00513+3.2.1.52,00531+3.2.1.52		PWY-6902					
aly536.204	Protein FAM195A		CG7841-PA						PF14799														
aly536.205	Unknown		n/a																				
aly536.206	Mpv17-like protein	GO:0003674,GO:0016021,GO:0005778,GO:0008150,GO:0005777	CG12355-PB						PF04117														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.207	Rab11 family-interacting protein 4A	GO:0055038,GO:0030306,GO:0030139,GO:0005875,GO:0043565,GO:0031532,GO:0005813,GO:0007476,GO:0005509,GO:0016360,GO:0048471,GO:0048592,GO:0042803,GO:0048190,GO:0008017,GO:0017137,GO:0032154,GO:0000910,GO:0007017,GO:0000915,GO:0051726,GO:0003700,GO:0030496,GO:0032456,GO:0005768	CG33991-PJ						PF09457	PS51511				SSF144270	460~487,243~263,389~416,290~352									
aly536.208	Fas-binding factor 1	GO:0042384,GO:0005813,GO:0005814,GO:0000922,GO:0090162,GO:0043297,GO:0030054,GO:0097539	CG5964-PA												652~672,684~726,577~604,517~537,797~817,617~644,473~493,730~775,542~562									
aly536.209	Ubiquitin domain-containing protein UBFD1	GO:0044822,GO:0005515	n/a				SM00213		PF00240	PS50053			G3DSA:3.10.20.90	SSF54236									
aly536.21	Intraflagellar transport protein 172 homolog	GO:0036064,GO:0042384,GO:0035058,GO:0060271,GO:0030992,GO:0007018,GO:0048793,GO:0031513,GO:0030990,GO:0060041,GO:0005515,GO:0005929,GO:0005871,GO:0032006,GO:0005930,GO:0045494	CG13809-PB										G3DSA:2.130.10.10	SSF50978									
aly536.210	Unknown		CG2211-PA											SSF51197	1~21								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.211	Polycomb protein SUZ12	GO:0008284,GO:0042054,GO:0035064,GO:0040029,GO:0031491,GO:0046976,GO:0007517,GO:0000122,GO:0006325,GO:0005634,GO:0010467,GO:0005654,GO:0016574,GO:2001229,GO:0016571,GO:0045814,GO:0046872,GO:0006351,GO:0048666,GO:0008283,GO:0045596,GO:0001739,GO:0022008,GO:0035098,GO:0000979,GO:0005704,GO:0005730,GO:0035097,GO:0048813,GO:0003723,GO:0005515,GO:0003682	CG8013-PB						PF09733						645~668									
aly536.212	Unknown		n/a																				
aly536.213	Methyltransferase-like protein 22	GO:0005575,GO:0008150,GO:0005634,GO:0003674,GO:0008168	CG10584-PA						PF10294				G3DSA:3.40.50.150	SSF53335									
aly536.214	Protein disulfide-isomerase	GO:0005737,GO:0012505,GO:0005811,GO:0006457,GO:0005783,GO:0060187,GO:1902175,GO:0015035,GO:0005635,GO:0034976,GO:0005788,GO:0045169,GO:0006662,GO:0005615,GO:0003756,GO:0005791,GO:0048471,GO:0019511,GO:0043025,GO:0045454,GO:0070732	CG6988-PA					TIGR01130,TIGR01126,TIGR01126	PF13848,PF00085,PF00085	PS51352,PS51352	PR00421,PR00421,PR00421	PS00194,PS00194	G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10,G3DSA:3.40.30.10	SSF52833,SSF52833,SSF52833,SSF52833									
aly536.215	TOM1-like protein 2	GO:0070062,GO:0006886,GO:0005622,GO:0019901,GO:0030276,GO:0007165,GO:0045839	CG3529-PB			PIRSF036948	SM00288		PF03127,PF00790	PS50179,PS50909			G3DSA:1.20.58.160,G3DSA:1.25.40.90	SSF89009,SSF48464	251~271								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.216	Leucine-rich repeat-containing protein 48	GO:0005737,GO:0008599,GO:0000164,GO:0005929	CG13125-PA				SM00365,SM00365,SM00365		PF13855	PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52075	189~209								
aly536.217	Leucine-rich repeat-containing protein 48	GO:0006470,GO:0008599	CG40440-PA																				
aly536.218	Protein FAM49A	GO:0005622	CG32066-PC						PF07159,PF00378				G3DSA:3.90.226.10	SSF52096									
aly536.219	Protein FAM135A		CG32333-PC						PF12394,PF05057				G3DSA:3.40.50.1820	SSF53474									
aly536.22	Intraflagellar transport protein 172 homolog	GO:0036064,GO:0042384,GO:0035058,GO:0030992,GO:0007018,GO:0042073,GO:0031513,GO:0030990,GO:0005515,GO:0005929,GO:0007275,GO:0005871,GO:0005930	CG13809-PB										G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10										
aly536.220	Brevican core protein	GO:0007155,GO:0005540,GO:0030246,GO:0005578	CG9134-PB				SM00034		PF00059	PS50041		PS00615	G3DSA:3.10.100.10	SSF56436									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.221	Unknown		n/a																				
aly536.222	Unknown		n/a																				
aly536.223	Unknown		n/a												350~370								
aly536.224	DNA-directed RNA polymerase III subunit RPC7-like	GO:0022008,GO:0006384,GO:0000790,GO:0006359,GO:0005666	CG33051-PA						PF11705														
aly536.225	Unknown		n/a																				
aly536.226	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.227	Helicase sen1	GO:0016180,GO:0008033,GO:0043144,GO:0031124,GO:0032508,GO:0033682,GO:0000790,GO:0004004,GO:0017116,GO:0032575,GO:0006364,GO:0006369,GO:0035649,GO:1903623,GO:0005634,GO:0005875,GO:0005524	CG7504-PB						PF13086				G3DSA:3.40.50.300	SSF52540										
aly536.228	Unknown		n/a																				
aly536.229	Unknown		n/a																				
aly536.23	Intraflagellar transport protein 172 homolog	GO:0036064,GO:0030990,GO:0035058,GO:0030992,GO:0007018,GO:0042073,GO:0031513,GO:0042384,GO:0005929,GO:0007275,GO:0005871,GO:0005930	CG13809-PB												229~249								
aly536.24	Intraflagellar transport protein 172 homolog	GO:0036064,GO:0030990,GO:0035058,GO:0030992,GO:0005929,GO:0007018,GO:0042073,GO:0031513,GO:0042384,GO:0003677,GO:0007275,GO:0005871,GO:0005930	CG13809-PB						PF02944,PF10545	PS51031													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.25	Protein piccolo	GO:0007416,GO:0030426,GO:0030425,GO:0030424,GO:0031594,GO:0003674,GO:0045202,GO:0030133,GO:0030054,GO:0048788,GO:0048786,GO:0005544,GO:0097470,GO:0005509,GO:0043005,GO:0005522,GO:0048471,GO:0043025,GO:0016080,GO:2000809,GO:0060077,GO:0043195,GO:0044316,GO:0044317,GO:0007010,GO:0001956,GO:0005802,GO:0005515	CG43955-PD				SM00239,SM00239,SM00228		PF00168,PF00168,PF00595	PS50106,PS50089,PS50004			G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:2.30.42.10,G3DSA:3.30.40.10	SSF57903,SSF50156,SSF49562,SSF49562									
aly536.26	Unknown	GO:0001956,GO:0048786,GO:0003674,GO:2000809	CG43955-PD																				
aly536.27	Transcription initiation factor IIA subunit 1	GO:0001094,GO:0051123,GO:0017025,GO:0005634,GO:0005672,GO:0006357,GO:0045944,GO:0006367,GO:0006366,GO:0001128,GO:0001129	CG5930-PA						PF03153,PF03153				G3DSA:2.30.18.10,G3DSA:1.10.287.100	SSF50784,SSF47396									
aly536.28	Activating transcription factor of chaperone	GO:0043565,GO:0035074,GO:0035073,GO:0042594,GO:0006641,GO:0003700,GO:0005634,GO:0007552,GO:0007591,GO:0005991,GO:0006355,GO:0006986,GO:0045944,GO:0006351,GO:0001102,GO:0046982,GO:0001105,GO:0000980	CG8669-PA				SM00338		PF00170	PS50217		PS00036	G3DSA:1.20.5.170	SSF57959									
aly536.29	DNA polymerase delta small subunit	GO:0006974,GO:0005634,GO:0003887,GO:0007052,GO:0006260,GO:0003677,GO:0043625,GO:0005875	CG12018-PA						PF04042								REACT_152,REACT_383,REACT_22172						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.3	Unknown		n/a																				
aly536.30	Meiosis-specific with OB domain-containing protein	GO:0043234,GO:0005737,GO:0008310,GO:0000724,GO:0000712,GO:0005634,GO:0009566,GO:0007129,GO:0090305,GO:0005515,GO:0007144,GO:0003682,GO:0005694,GO:0003697,GO:0007140,GO:0007141	CG15329-PA										G3DSA:2.40.50.140	SSF50249									
aly536.31	Unknown		n/a																				
aly536.32	Dynein intermediate chain 3, ciliary	GO:0005737,GO:0042623,GO:0007605,GO:0005929,GO:0007018,GO:0005875,GO:0005515,GO:0005868,GO:0030286,GO:0005874,GO:0003774	CG6053-PC				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320			PS50294,PS50082			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978	507~527,550~570									
aly536.33	Ecto-NOX disulfide-thiol exchanger 1	GO:0005615,GO:0000166,GO:0048511,GO:0003676,GO:0005886,GO:0003729,GO:0016491	CG10948-PC				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928	363~397,270~300,474~508									
aly536.34	DNA-directed RNA polymerase III subunit RPC8	GO:0006139,GO:0006386,GO:0006385,GO:0051607,GO:0005813,GO:0005829,GO:0005666,GO:0032481,GO:0005654,GO:0010467,GO:0003677,GO:0003899,GO:0022008,GO:0006384,GO:0006383,GO:0045087,GO:0043231	CG7339-PB					TIGR00448	PF08292,PF03876				G3DSA:3.30.1490.120	SSF88798,SSF50249									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.35	Integral membrane protein GPR155	GO:0070062,GO:0016021,GO:0050890,GO:0005622,GO:0035556,GO:0055085	CG7510-PB				SM00049		PF03547,PF00610	PS50186			G3DSA:1.10.10.10	SSF46785									
aly536.36	Unknown		n/a																				
aly536.37	Probable ATP-dependent RNA helicase DDX5	GO:0008026,GO:0050681,GO:0009299,GO:0003676,GO:2001014,GO:0072332,GO:0036002,GO:0001701,GO:0000381,GO:0070062,GO:0005730,GO:0005634,GO:0016020,GO:0003713,GO:0003712,GO:0030529,GO:0005654,GO:0045667,GO:0010501,GO:0044822,GO:0005524,GO:0007623,GO:0030331,GO:0071013,GO:0033148,GO:0004004,GO:0045893,GO:0043517,GO:0060765,GO:0000122,GO:0008380,GO:0003724,GO:0045944,GO:0006397	CG10777-PB				SM00490,SM00487		PF00270,PF00271	PS51192,PS51195,PS51194		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	371~391								
aly536.38	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.39	3-phosphoinositide-dependent protein kinase 1	GO:0051124,GO:0030307,GO:0030154,GO:0008286,GO:0030036,GO:0031594,GO:0007166,GO:0005737,GO:0007476,GO:0004674,GO:0043066,GO:0004672,GO:0048477,GO:0005524,GO:0006468,GO:0046620,GO:0006915,GO:0007548,GO:0006974,GO:0045471,GO:0007283,GO:0001558,GO:0005886,GO:0007292,GO:0045793,GO:0005829	CG1210-PD				SM00220		PF00069,PF14593	PS50011		PS00108,PS00107	G3DSA:1.10.510.10,G3DSA:2.30.29.30,G3DSA:2.30.29.30,G3DSA:3.30.200.20	SSF50729,SSF50729,SSF56112,SSF56112										
aly536.4	Unknown		n/a																				
aly536.40	Protein Tube	GO:0005737,GO:0019732,GO:0004871,GO:0009950,GO:0009620,GO:0005829,GO:0008063,GO:0035172,GO:0006952,GO:0019904,GO:0005515,GO:0005886,GO:0048262,GO:0030097,GO:0007352,GO:0007275	CG10520-PC						PF14786				G3DSA:1.10.533.10	SSF47986									
aly536.41	Unknown	GO:0003674,GO:0005615,GO:0032504,GO:0004867	CG42648-PA						PF16053														
aly536.42	IQ domain-containing protein K		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.43	Serine protease 42	GO:0005737,GO:0004252,GO:0007281,GO:0046658,GO:0007283,GO:0005576,GO:0006508	CG4998-PB				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly536.44	Unknown		n/a																				
aly536.45	Unknown		n/a																				
aly536.46	Unknown		n/a																				
aly536.47	Unknown		n/a																				
aly536.48	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.49	Unknown		n/a																				
aly536.5	Unknown		n/a																				
aly536.50	Unknown		n/a																				
aly536.51	Unknown		n/a																				
aly536.52	Unknown		n/a																				
aly536.53	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.54	Unknown		n/a																				
aly536.55	Unknown		CG13044-PA																				
aly536.56	Unknown		n/a																				
aly536.57	Unknown		n/a																				
aly536.58	Unknown		n/a																				
aly536.59	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.6	ADP-ribosylation factor-like protein 4A	GO:0005737,GO:0005730,GO:0005634,GO:0003924,GO:0050873,GO:0005622,GO:0005575,GO:0008150,GO:0005886,GO:0007264,GO:0005525	CG2219-PB				SM00175,SM00178,SM00177	TIGR00231	PF00025	PS51417	PR00328,PR00328		G3DSA:3.40.50.300	SSF52540									
aly536.60	Unknown		n/a								PR01217,PR01217,PR01217,PR01217,PR01217												
aly536.61	Unknown		n/a																				
aly536.62	Unknown		n/a																				
aly536.63	Unknown		n/a																				
aly536.64	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.65	Unknown		n/a																				
aly536.66	Unknown		n/a							PS51257													
aly536.67	Unknown		n/a																				
aly536.68	Unknown	GO:0005575,GO:0003674,GO:0008150	CG32603-PA																				
aly536.69	Unknown		n/a																				
aly536.7	Unknown		n/a												178~198								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.70	Unknown		n/a																				
aly536.71	Unknown		n/a																				
aly536.72	Unknown		n/a																				
aly536.73	Gamma-glutamyl hydrolase A	GO:0005615,GO:0005618,GO:0008242,GO:0006541,GO:0005575,GO:0008150,GO:0006508,GO:0034722	CG32155-PA						PF07722	PS51275			G3DSA:3.40.50.880	SSF52317		00790+3.4.19.9		PWY-2161B,PWY-6842,PWY-4061,PWY-7112					
aly536.74	COP9 signalosome complex subunit 1	GO:0005737,GO:0051726,GO:0050821,GO:0008277,GO:0046331,GO:0007095,GO:0022008,GO:0008180	CG3889-PA				SM00088		PF01399,PF10602				G3DSA:1.10.10.10	SSF46785	383~403								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.75	DIS3-like exonuclease 2	GO:0004540,GO:0000176,GO:1990074,GO:0051306,GO:0007067,GO:0051301,GO:0005737,GO:0010587,GO:0000287,GO:0006364,GO:0006402,GO:0008859,GO:0008285,GO:0019827,GO:0008266,GO:0090503,GO:0000291,GO:0090501,GO:0016075,GO:0000932,GO:0000177,GO:0000175,GO:0034427	CG16940-PC				SM00955		PF00773			PS01175		SSF50249,SSF50249									
aly536.76	Multifunctional methyltransferase subunit TRM112-like protein	GO:0043234,GO:0070062,GO:0018364,GO:0005575,GO:0008276,GO:0003674,GO:0008150	CG12975-PA						PF03966				G3DSA:2.20.25.10	SSF158997									
aly536.77	Cytochrome b-c1 complex subunit 2, mitochondrial	GO:0004222,GO:0070062,GO:0005750,GO:0043209,GO:0005811,GO:0008121,GO:0006122,GO:0005739,GO:0005743,GO:0003824,GO:0009060,GO:0044237,GO:0022904,GO:0046872,GO:0044281,GO:0005875,GO:0006119	CG4169-PA						PF05193,PF00675				G3DSA:3.30.830.10,G3DSA:3.30.830.10	SSF63411,SSF63411,SSF63411									
aly536.78	ATPase family AAA domain-containing protein 5	GO:0005634,GO:0017111,GO:0000166,GO:0006974,GO:0022008,GO:0005524	CG16838-PA				SM00382		PF13401				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	207~227								
aly536.79	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.8	Unknown		n/a																				
aly536.80	Equilibrative nucleoside transporter 4	GO:0016021,GO:0008504,GO:0005337,GO:0015395,GO:0015858	CG11010-PA						PF01733,PF01733					SSF103473,SSF103473			REACT_1698,REACT_15518						
aly536.81	Farnesoate epoxidase	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005506,GO:0055114,GO:0009055	CG8733-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly536.82	Purine nucleoside phosphorylase	GO:0005737,GO:0005856,GO:0006139,GO:0004731,GO:0009116,GO:0043101	CG16758-PH			PIRSF000477		TIGR01700,TIGR01697	PF01048				G3DSA:3.40.50.1580	SSF53167		00230+2.4.2.1,00760+2.4.2.1,00240+2.4.2.1		PWY-6644,PWY-7179-1,PWY-7179,PWY-6609,PWY-6608,PWY-5695,PWY-6620,PWY-6627,PWY-4202,PWY-6611	UPA00606				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.83	Epimerase family protein SDR39U1	GO:0003824,GO:0016491,GO:0044237,GO:0050662	CG8768-PA					TIGR01777	PF08338,PF01370				G3DSA:3.40.50.720	SSF51735									
aly536.84	tRNA-splicing endonuclease subunit Sen34	GO:0090502,GO:0005654,GO:0090501,GO:0005730,GO:0000213,GO:0016829,GO:0000214,GO:0005575,GO:0003674,GO:0003676,GO:0008150,GO:0005634,GO:0000379,GO:0006397	CG33260-PC			PIRSF017250			PF01974				G3DSA:3.40.1350.10	SSF53032	79~99			PWY-6689					
aly536.85	Programmed cell death protein 5	GO:0005737,GO:0005575,GO:0045089,GO:0070062,GO:0008285,GO:1903645,GO:1903638,GO:0090200,GO:0043065,GO:0071560,GO:0010698,GO:0010628,GO:0003674,GO:0003677,GO:0050829,GO:0043280,GO:0005634,GO:0008201	CG13072-PA			PIRSF015730			PF01984				G3DSA:1.10.8.140	SSF46950	30~50								
aly536.86	Lipase 1	GO:0004806,GO:0006629,GO:0007586,GO:0016788,GO:0016042,GO:0048812,GO:0005576	CG31871-PA			PIRSF000862			PF04083				G3DSA:3.40.50.1820	SSF53474									
aly536.87	Lipase 1	GO:0004806,GO:0006629,GO:0007586,GO:0016788,GO:0016042,GO:0048812,GO:0005576	CG31871-PA			PIRSF000862			PF04083				G3DSA:3.40.50.1820	SSF53474									
aly536.88	Lipase 3	GO:0048812,GO:0004806,GO:0006629,GO:0016788,GO:0016042	CG31871-PA			PIRSF000862			PF04083				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.89	BAI1-associated protein 3	GO:0008021,GO:0016082,GO:0007269,GO:0005515	CG32381-PB				SM00239,SM00239		PF00168,PF00168,PF00168	PS51259,PS50004,PS50004	PR00360,PR00360		G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562,SSF49562									
aly536.9	Unknown		n/a						PF13863						134~154								
aly536.90	Unknown		n/a																				
aly536.91	Unknown		n/a																				
aly536.92	Unknown	GO:0003674,GO:0016021,GO:0008150	CG10596-PC												455~478								
aly536.93	Probable prefoldin subunit 4	GO:0006457,GO:0051087,GO:0016272,GO:0051082,GO:0006458	CG10635-PA			PIRSF016477			PF01920				G3DSA:1.10.287.370	SSF46579	28~62,78~119								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly536.94	Sodium/hydrogen exchanger 8	GO:0006885,GO:0016021,GO:0006814,GO:0051453,GO:0006811,GO:0015386,GO:0015385,GO:0000139,GO:0055085	CG12178-PB					TIGR00840	PF00999		PR01084,PR01084,PR01084,PR01084						REACT_15518						
aly536.95	Acyl-protein thioesterase 1	GO:0005737,GO:0098734,GO:0006631,GO:0008474,GO:0052689	CG18815-PE						PF02230				G3DSA:3.40.50.1820	SSF53474									
aly536.96	Unknown		CG5056-PA																				
aly536.97	Unknown		n/a																				
aly536.98	UBA-like domain-containing protein 2		n/a						PF14555	PS51257			G3DSA:1.10.8.10	SSF46934									
aly536.99	Putative RNA exonuclease NEF-sp	GO:0070062,GO:0005730,GO:0004527,GO:0000166,GO:0003723,GO:0003676	CG8368-PB				SM00479		PF00929				G3DSA:3.30.420.10	SSF53098									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5360.1	Unknown		n/a																				
aly5360.2	Unknown		n/a																				
aly5360.3	Unknown	GO:0006633,GO:0005835,GO:0016788,GO:0004312,GO:0008270,GO:0055114,GO:0016491	CG17374-PC						PF00975				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474									
aly5360.4	Fatty acid synthase	GO:0006633,GO:0047451,GO:0004320,GO:0042587,GO:0008144,GO:0008270,GO:0001649,GO:0016491,GO:0005737,GO:0070062,GO:0016295,GO:0005835,GO:0016020,GO:0071353,GO:0005739,GO:0030879,GO:0005794,GO:0044822,GO:0004315,GO:0016788,GO:0003824,GO:0047117,GO:0008152,GO:0005886,GO:0055114,GO:0006084,GO:0042470,GO:0004312,GO:0004313,GO:0016296,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319	CG17374-PC				SM00825,SM00827		PF16197,PF00698,PF00109				G3DSA:3.40.47.10,G3DSA:3.40.47.10,G3DSA:3.40.366.10,G3DSA:3.40.366.10	SSF53901,SSF52151,SSF52151,SSF53901,SSF55048									
aly5365.1	Transmembrane protein fend	GO:0016021,GO:0005886,GO:0008045	CG12664-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly537.1	Unknown		n/a																				
aly537.10	Scolexin B	GO:0004252,GO:0005576,GO:0006508	CG12387-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10	SSF50494									
aly537.11	Progestin and adipoQ receptor family member 4	GO:0016021,GO:0046331,GO:0004872	CG33203-PF						PF03006														
aly537.12	Progestin and adipoQ receptor family member 4	GO:0016021,GO:0046331,GO:0004872	CG33203-PF						PF03006														
aly537.13	Serine/threonine-protein kinase Doa	GO:0005783,GO:0042051,GO:0048102,GO:0005875,GO:0007417,GO:0005737,GO:0000381,GO:0005634,GO:0000165,GO:0008407,GO:0046777,GO:0004674,GO:0001964,GO:0004712,GO:0004713,GO:0004672,GO:0048477,GO:0005524,GO:0048749,GO:0031987,GO:0006468,GO:0035071,GO:0009306,GO:0007601,GO:2000255,GO:0008362,GO:0007350,GO:0007548,GO:0007399,GO:0048854,GO:0005829,GO:0030717,GO:0045494	CG42320-PP				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112	149~169									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly537.14	NADP-dependent malic enzyme	GO:0005737,GO:0046872,GO:0004473,GO:0051287,GO:0004471,GO:0008948,GO:0030431,GO:0008340,GO:0010941,GO:0006108,GO:0055114	CG10120-PB				SM00919		PF03949,PF00390		PR00072,PR00072,PR00072,PR00072,PR00072,PR00072	PS00331	G3DSA:3.40.50.10380,G3DSA:3.40.50.720	SSF53223,SSF51735		00620+1.1.1.38							
aly537.15	Translation initiation factor eIF-2B subunit alpha	GO:0005737,GO:0051716,GO:0019509,GO:0005851,GO:0006446,GO:0005085,GO:0044237,GO:0046331,GO:0046523,GO:0005886,GO:0014003,GO:0030234,GO:0006413,GO:0005829,GO:0003743	CG7883-PA						PF01008				G3DSA:3.40.50.10470	SSF100950		00270+5.3.1.23		PWY-7174,PWY-4361	UPA00904				
aly537.16	Tyrosine-protein kinase Fps85D	GO:0016020,GO:0030154,GO:0019898,GO:0007169,GO:0007411,GO:0005737,GO:0038083,GO:0005543,GO:0004715,GO:0004713,GO:0016477,GO:0005524,GO:0042127,GO:0006468,GO:0045087,GO:0051017,GO:0008594,GO:0005912,GO:0005886,GO:0046664,GO:0031234,GO:0007394,GO:0007391,GO:0005102	CG8874-PA				SM00055		PF00611	PS51741				SSF103657	16~36,309~329								
aly537.17	Eukaryotic translation initiation factor 4B	GO:0006446,GO:0044267,GO:0008286,GO:0000288,GO:0046427,GO:0006412,GO:0008283,GO:0005829,GO:0044822,GO:0000166,GO:0010467,GO:0003723,GO:0000289,GO:0003729,GO:0006413,GO:0016281,GO:0003743	CG10837-PB				SM00360		PF14259	PS50102			G3DSA:3.30.70.330	SSF54928	357~390								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly537.18	Unknown	GO:0003700,GO:0006355,GO:0043565	n/a						PF07716	PS50217			G3DSA:1.20.5.170	SSF57959	490~553								
aly537.19	Transmembrane and ubiquitin-like domain-containing protein 2	GO:0016021,GO:0005515	n/a						PF00240	PS50053			G3DSA:3.10.20.90	SSF54236									
aly537.2	Modifier of mdg4	GO:0016311,GO:0000785,GO:0003677,GO:0007060,GO:0008354,GO:0007141,GO:0005730,GO:0006325,GO:0010032,GO:0005634,GO:0046872,GO:0048477,GO:0042803,GO:0006915,GO:0000794,GO:0005886,GO:0001672,GO:0008195,GO:0005704,GO:0005700,GO:0006355,GO:0006351,GO:0005515,GO:0031208,GO:0003682,G	CG32491-PT				SM00225		PF04500,PF04500,PF00651	PS50097			G3DSA:3.30.710.10	SSF54695									
aly537.20	60S ribosomal protein L15	GO:0003735,GO:0005622,GO:0022625,GO:0006412,GO:0005840	CG17420-PI						PF00827			PS01194	G3DSA:3.40.1120.10	SSF54189									
aly537.21	Double-strand-break repair protein rad21 homolog	GO:0034991,GO:0071168,GO:0010628,GO:0000785,GO:0007064,GO:0000228,GO:0007067,GO:0051301,GO:0005737,GO:0005634,GO:0016020,GO:0008278,GO:0005654,GO:0006366,GO:0006281,GO:0006915,GO:0016322,GO:0006289,GO:0007052,GO:0000794,GO:0007059,GO:0000775,GO:0005721,GO:0005705,GO:0001228,GO:0006357,GO:0045944,GO:0005515	CG17436-PA						PF04825														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly537.22	Unknown		n/a																				
aly537.23	ATP synthase lipid-binding protein, mitochondrial	GO:0045263,GO:0015986,GO:0015992,GO:0015991,GO:0016021,GO:0000276,GO:0008289,GO:0031966,GO:0008553,GO:0015078	CG1746-PA	MF_01396					PF00137		PR00124,PR00124,PR00124	PS00605	G3DSA:1.20.20.10	SSF81333									
aly537.24	Juxtaposed with another zinc finger protein 1	GO:0006629,GO:0017053,GO:0000122,GO:0005634,GO:0003714,GO:0006351,GO:0003676,GO:0046872	CG12054-PA				SM00355,SM00355					PS00028	G3DSA:3.30.160.60										
aly537.25	Vacuolar protein sorting associated protein 16 homolog	GO:0005737,GO:0016197,GO:0008057,GO:0030897,GO:0006886,GO:0008333,GO:0000046,GO:0005765,GO:0031902,GO:0035542,GO:0033263,GO:0003674,GO:0007041,GO:0005768,GO:0005829,GO:0007033	CG8454-PA			PIRSF007949			PF04840,PF04841					SSF50978,SSF50978									
aly537.26	Chaoptin	GO:0035996,GO:0016028,GO:0042052,GO:0050896,GO:0007601,GO:0046658,GO:0005886,GO:0007156	CG7896-PA				SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00369,SM00082,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364		PF13855,PF13855,PF13855,PF13855,PF13855,PF13855	PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52047,SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly537.27	Coiled-coil domain-containing protein 113	GO:0005737,GO:0005654,GO:0043234,GO:0034451,GO:0042384	CG13693-PA						PF13870						267~287,330~350,38~58,157~177,383~403								
aly537.28	Unknown		n/a						PF04500														
aly537.29	Unknown		n/a																				
aly537.3	Pyrethroid hydrolase Ces2a	GO:0005575,GO:0008150,GO:0004772,GO:0052689,GO:0006486	CG5397-PA						PF00135				G3DSA:3.40.50.1820	SSF53474,SSF53474									
aly537.30	Unknown		n/a																				
aly537.31	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly537.4	Unknown		n/a																				
aly537.5	Glutathione S-transferase 1	GO:0005737,GO:0004364,GO:0003676,GO:0007095,GO:0022008,GO:0043295	CG33546-PB						PF00043,PF02798	PS50404,PS50405			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF52833,SSF47616									
aly537.6	Mucin-1	GO:1902166,GO:0090240,GO:0016266,GO:0010944,GO:0036003,GO:0044267,GO:0070062,GO:0005615,GO:0003712,GO:0043618,GO:0033629,GO:0005796,GO:0016324,GO:0043687,GO:0000790,GO:0006977,GO:0005887,GO:0006978,GO:0031982,GO:0006493,GO:0000978,GO:0002039	n/a																				
aly537.7	F-box/LRR-repeat protein 2	GO:0005737,GO:0016567,GO:0004842,GO:0016020,GO:0031146,GO:0006464,GO:0006513,GO:0019903,GO:0019005,GO:0016032,GO:0006508,GO:0014066,GO:0010506,GO:0036312	CG9003-PB				SM00256		PF12937	PS50181			G3DSA:3.80.10.10	SSF52047									
aly537.8	Phenylalanine-tRNA ligase beta subunit	GO:0004826,GO:0006450,GO:0006432,GO:0009328,GO:0000287,GO:0003723,GO:0002161,GO:0005524	CG5706-PA				SM00873,SM00874	TIGR00471	PF03484,PF03483	PS51483			G3DSA:3.30.56.20,G3DSA:3.50.40.10,G3DSA:3.30.930.10	SSF55681,SSF46955,SSF56037,SSF46955		00970+6.1.1.20							
aly537.9	AN1-type zinc finger protein 5	GO:0005737,GO:0048705,GO:0001701,GO:0001944,GO:0048745,GO:0005575,GO:0048008,GO:0008150,GO:0008270,GO:0003016,GO:0003677,GO:0003674,GO:0010761,GO:0060324	CG45050-PG				SM00154		PF01428	PS51039			G3DSA:4.10.1110.10	SSF118310									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly53846.1	Unknown		n/a																				
aly5386.1	Unknown	GO:0008455,GO:0005797,GO:0006487,GO:0016021,GO:0009312,GO:0008375	CG7921-PA																				
aly53877.1	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00572	G3DSA:3.20.20.80	SSF51445									
aly54.1	Unknown		n/a																				
aly54.10	Calcineurin subunit B type 2	GO:0008021,GO:0007126,GO:0016192,GO:0006470,GO:0030241,GO:0050790,GO:0004723,GO:0008597,GO:0045214,GO:0005509,GO:0005515,GO:0005516,GO:0007269,GO:0005955,GO:0030431	CG11217-PA				SM00054,SM00054,SM00054,SM00054		PF13499,PF13499	PS50222,PS50222,PS50222,PS50222		PS00018,PS00018,PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									
aly54.11	39S ribosomal protein L14, mitochondrial	GO:0003735,GO:0005739,GO:0005840,GO:0005762,GO:0006412	CG14048-PA	MF_01367					PF00238				G3DSA:2.40.150.20	SSF50193									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly54.12	Visual system homeobox 2	GO:0005737,GO:0043565,GO:0045165,GO:0000122,GO:0003700,GO:0005634,GO:0007601,GO:0008285,GO:0008284,GO:0006355,GO:0045944,GO:0006351,GO:0001748,GO:0003677,GO:0060040,GO:0050896	CG15781-PA				SM00389		PF00046,PF03826	PS51496,PS50071,PS50803		PS00027	G3DSA:1.10.10.60	SSF46689									
aly54.13	Unknown		n/a																				
aly54.14	Unknown		n/a						PF15860														
aly54.15	Unknown		n/a																				
aly54.16	Early 94 kDa protein		n/a												22~42								
aly54.17	Early 94 kDa protein		n/a												22~49								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly54.18	Early 94 kDa protein		n/a												29~49								
aly54.19	Unknown	GO:0007605	CG14636-PA																				
aly54.2	Potassium voltage-gated channel protein eag	GO:0051259,GO:0042391,GO:0005887,GO:0007619,GO:0006813,GO:0000155,GO:0008016,GO:0042066,GO:0008076,GO:0007629,GO:0007611,GO:0048150,GO:0022843,GO:0005249,GO:0000160,GO:0071805,GO:0005886,GO:0005622,GO:0055085,GO:0007612,GO:0007608	CG10952-PB				SM00086,SM00100	TIGR00229	PF13426,PF00520,PF00027	PS50113,PS50112,PS50042	PR01464,PR01464,PR01464,PR01464,PR01464,PR01464,PR01464,PR01464,PR01464,PR01464,PR01463,PR01463,PR01463,PR01463,PR01463,PR01463,PR01463		G3DSA:3.30.450.20,G3DSA:1.10.287.630,G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:2.60.120.10	SSF81324,SSF81324,SSF55785,SSF51206									
aly54.20	Unknown		n/a						PF16043														
aly54.21	Reticulocyte-binding protein 2 homolog a	GO:0016021,GO:0016020,GO:0016337,GO:0008201,GO:0005886	n/a												76~347								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly54.22	V-type proton ATPase catalytic subunit A	GO:0016197,GO:0033180,GO:0015992,GO:0007446,GO:0015991,GO:0046034,GO:0033181,GO:0048388,GO:0000221,GO:0046961,GO:0005886,GO:0005524	CG3762-PA	MF_00309				TIGR01042	PF02874,PF00306,PF00006,PF16886			PS00152	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.1140.10	SSF50615,SSF47917,SSF52540		00195+3.6.3.14,00190+3.6.3.14		PWY-7219					
aly54.23	tRNA 2'-phosphotransferase 1	GO:0016772,GO:0006388,GO:0000215,GO:0008665	CG33057-PA						PF01885					SSF56399									
aly54.24	Speckle targeted PIP5K1A-regulated poly(A) polymerase	GO:0016607,GO:0016180,GO:0016779,GO:0046872,GO:0005730,GO:0004652,GO:0050265,GO:0003723,GO:0006378,GO:0006379,GO:0005524,GO:0003730	CG7163-PA						PF03828				G3DSA:3.30.70.330,G3DSA:3.30.460.10	SSF81631,SSF81301,SSF54928									
aly54.25	Poly(A) RNA polymerase cid11	GO:0016779,GO:0005829,GO:0004652,GO:0003723,GO:0046872,GO:0005634,GO:0005524,GO:0006397	CG7163-PA						PF03828,PF01909				G3DSA:3.30.460.10	SSF81631,SSF81301									
aly54.26	Iron/zinc purple acid phosphatase-like protein	GO:0046872,GO:0003993,GO:0005576	CG1637-PD						PF14008				G3DSA:3.60.21.10	SSF56300									
aly54.27	Iron/zinc purple acid phosphatase-like protein	GO:0046872,GO:0003993,GO:0005576	CG1637-PD						PF14008,PF00149,PF16656				G3DSA:2.60.40.380,G3DSA:3.60.21.10	SSF49363,SSF56300									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly54.28	Unknown		n/a																				
aly54.29	Interferon regulatory factor 2-binding protein-like A	GO:0005634,GO:0046872	CG11138-PD						PF11261				G3DSA:3.30.40.10	SSF57850									
aly54.3	Unknown		n/a																				
aly54.30	Unknown	GO:0003676	n/a				SM00980,SM00692		PF05485	PS50950				SSF57716									
aly54.31	Probable RNA directed DNA polymerase from transposon X-element	GO:0003964,GO:0006278,GO:0006313	n/a						PF00078	PS50878													
aly54.32	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly54.33	Ribosome-recycling factor, mitochondrial	GO:0006412,GO:0005739	CG4447-PA						PF01765				G3DSA:3.30.1360.40	SSF55194									
aly54.34	Poly(A) RNA polymerase, mitochondrial	GO:0002134,GO:0071044,GO:0006351,GO:0043231,GO:0044822,GO:0000287,GO:0030145,GO:0005739,GO:0004652,GO:0005524,GO:0006378,GO:0042802,GO:0042803	CG11418-PA						PF03828				G3DSA:3.30.460.10	SSF81301,SSF81631									
aly54.35	Thyroid adenoma-associated protein homolog	GO:0005488	CG15618-PB						PF10350,PF10350					SSF48371,SSF48371,SSF48371									
aly54.36	Unknown		n/a																				
aly54.37	Unknown		n/a												164~184								
aly54.38	23 kDa integral membrane protein	GO:0016021	CG30160-PA			PIRSF002419			PF00335		PR00259,PR00259			SSF48652									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly54.39	Leukocyte surface antigen CD53	GO:0070062,GO:0016021,GO:0003674,GO:0001772,GO:0005911,GO:0005886,GO:0008150,GO:1901741	CG12846-PA						PF00335		PR00259,PR00259,PR00259	PS00421	G3DSA:1.10.1450.10	SSF48652									
aly54.4	Protein stoned A	GO:0008021,GO:0007269,GO:0016079,GO:0030054,GO:0009612,GO:0030139,GO:0007629,GO:0005515,GO:0005886,GO:0048488,GO:0048489	CG12500-PC																				
aly54.40	Ninjurin-1	GO:0007399,GO:0016021,GO:0001954,GO:0042246,GO:1990384,GO:0007155,GO:0007411	CG6449-PB						PF04923														
aly54.41	Eukaryotic translation initiation factor 5	GO:0005829,GO:0005525,GO:0006413,GO:0022008,GO:0003743	CG9177-PF				SM00653,SM00515		PF02020,PF01873	PS51363			G3DSA:1.25.40.180,G3DSA:3.30.30.50	SSF75689,SSF48371,SSF100966									
aly54.42	Unknown		n/a																				
aly54.43	Mitochondrial import inner membrane translocase subunit TIM44	GO:0015450,GO:0006626,GO:0051087,GO:0005739,GO:0030150,GO:0005743,GO:0005759,GO:0005744,GO:0071456,GO:0015031,GO:0005524	CG11779-PA				SM00978		PF04280					SSF54427	56~83								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly54.44	Echinoderm microtubule-associated protein-like 2	GO:0005737,GO:0008022,GO:0007017,GO:0031115,GO:0071683,GO:0007605,GO:0008017,GO:0015631,GO:0005102,GO:0035011,GO:0003824,GO:0005819,GO:0010968,GO:0005515,GO:0035556,GO:0005874,GO:0008344	CG42247-PG				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400	PS50082,PS50294,PS50082			G3DSA:2.130.10.10	SSF50978										
aly54.45	Echinoderm microtubule-associated protein-like 1	GO:0015631,GO:0005829,GO:0007017,GO:0007420,GO:0071683,GO:0007605,GO:0008017,GO:0007405,GO:0035011,GO:0007052,GO:0000226,GO:0005515,GO:0035556,GO:0005874,GO:0008344,GO:0048471	CG42247-PG				SM00320,SM00320		PF03451				G3DSA:2.130.10.10	SSF50978										
aly54.46	Unknown		n/a																				
aly54.47	Unknown		n/a						PF12017														
aly54.5	Protein stoned-B	GO:0008021,GO:0016183,GO:0007269,GO:0006901,GO:0016021,GO:0005886,GO:1900242,GO:0030139,GO:0030054,GO:0005515,GO:0007268,GO:0030131,GO:0030135,GO:0006886,GO:0048488,GO:0048489	CG12473-PE						PF00928	PS51070,PS51072			G3DSA:2.60.40.1170	SSF49447,SSF49447										
aly54.6	Tigger transposable element-derived protein 6	GO:0005634,GO:0003677	n/a						PF03184,PF05225	PS51253				SSF46689										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly54.7	Unknown		n/a																				
aly54.8	Unknown		CG15894-PB												372~399								
aly54.9	Elongation factor 1-gamma	GO:0005737,GO:0005853,GO:0035071,GO:0005634,GO:0005811,GO:0005875,GO:0048102,GO:0003746,GO:0006414,GO:0005829	CG11901-PB						PF00043,PF02798,PF00647	PS50405,PS50404,PS50040			G3DSA:1.20.1050.10,G3DSA:3.30.70.1010,G3DSA:3.40.30.10	SSF89942,SSF52833,SSF47616									
aly540.1	Unknown		n/a						PF01753	PS50865				SSF144232	39~59								
aly540.2	Unknown		n/a				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly540.3	Unknown		n/a						PF16012,PF16012,PF16012,PF16012						1136~1142								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5411.1	Tyrosine-protein kinase PR2	GO:0006468,GO:0035071,GO:0018108,GO:0005575,GO:0048102,GO:0004715,GO:0004713,GO:0005524	CG43741-PE				SM00219		PF07714	PS50011	PR00109,PR00109,PR00109,PR00109,PR00109	PS00109,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:2.30.30.40	SSF50044,SSF56112									
aly5411.2	Unknown		n/a																				
aly5411.3	Neuronal calcium sensor 2	GO:0005509	CG7646-PA				SM00054,SM00054,SM00054		PF13499,PF13833	PS50222,PS50222,PS50222	PR00450,PR00450,PR00450,PR00450,PR00450,PR00450	PS00018,PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly5411.4	Neurocalcin homolog	GO:0042326,GO:0005509	CG7641-PA				SM00054,SM00054,SM00054		PF00036,PF13499	PS50222,PS50222,PS50222,PS50222	PR00450,PR00450,PR00450,PR00450,PR00450,PR00450	PS00018,PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly5411.5	Zinc finger protein 408	GO:0043565,GO:0000278,GO:0005634,GO:0007349,GO:0005654,GO:0006355,GO:0000785,GO:0045893,GO:0005515,GO:0003677,GO:0000976,GO:0046872,GO:0042802,GO:0006351	CG12701-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12171	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly5411.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5411.7	Unknown		n/a																				
aly5411.8	Unknown		n/a																				
aly5412.1	Homeobox protein OTX1 B	GO:0046552,GO:0042052,GO:0042051,GO:0035288,GO:0007419,GO:0010628,GO:0003677,GO:0035284,GO:0007417,GO:0043565,GO:0001700,GO:0000122,GO:0005634,GO:0060875,GO:0042803,GO:0045871,GO:0045872,GO:0042463,GO:0007628,GO:0007389,GO:0045893,GO:0008056,GO:0045315,GO:0061541,GO:0007355,GO:0042472,GO:0007420,GO:0007399,GO:0003700,GO:0006355,GO:0001077,GO:0045944,GO:0003406,GO:0048816,GO:0046982	CG12154-PF						PF00046	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689										
aly5412.10	Unknown		n/a										G3DSA:2.120.10.30,G3DSA:2.120.10.30	SSF101898									
aly5412.11	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5412.12	Unknown		n/a																				
aly5412.13	Unknown		n/a																				
aly5412.2	Thioredoxin-related transmembrane protein 1	GO:0006457,GO:0005783,GO:0005730,GO:0016021,GO:0005789,GO:0003756,GO:0045454,GO:0034976,GO:0015036	CG5554-PB						PF00085	PS51352		PS00194	G3DSA:3.40.30.10	SSF52833									
aly5412.3	Serine/threonine-protein kinase MRCK alpha	GO:0031032,GO:0005083,GO:0030426,GO:0030424,GO:0008064,GO:0000226,GO:0035556,GO:0042641,GO:0005737,GO:0070062,GO:0019992,GO:0000287,GO:0004674,GO:0004672,GO:0016477,GO:0042802,GO:0006468,GO:0031252,GO:0008039,GO:0008154,GO:0005911,GO:0031532,GO:0005524,GO:0007097	CG4012-PA				SM00220,SM00133,SM00285,SM00109		PF00069,PF00433,PF00780,PF15796,PF00130	PS51285,PS50081,PS50108,PS50011	PR00008,PR00008,PR00008,PR00008	PS00479,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.20.5.340,G3DSA:3.30.60.20	SSF57889,SSF50729,SSF56112	918~959,699~719,770~821,484~504,558~585,728~766,512~539,600~669									
aly5412.4	Protein lines	GO:0007362,GO:0005737,GO:0007440,GO:0048617,GO:0009880,GO:0009946,GO:0007442,GO:0005634,GO:0016055,GO:0035220,GO:0045944,GO:0006351,GO:0035277,GO:0008293,GO:0008544,GO:0048619,GO:0007367	CG11770-PA						PF14695,PF14694														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5412.5	Dr1-associated corepressor	GO:0017055,GO:0017054,GO:0003714,GO:0043565,GO:0005634,GO:0000122,GO:0005622,GO:0001075,GO:0045944,GO:0006351,GO:0046982,GO:0008134	CG10318-PA						PF00808				G3DSA:1.10.20.10	SSF47113									
aly5412.6	Dr1-associated corepressor	GO:0017055,GO:0017054,GO:0003714,GO:0043565,GO:0005634,GO:0000122,GO:0005622,GO:0001075,GO:0045944,GO:0006351,GO:0046982,GO:0008134	CG10318-PA						PF00808				G3DSA:1.10.20.10	SSF47113									
aly5412.7	Puff-specific protein Bx42	GO:0001700,GO:0035214,GO:0000974,GO:0071011,GO:0005634,GO:0000398,GO:0000790,GO:0005515,GO:0003677,GO:0071013	CG8264-PA						PF02731						297~317								
aly5412.8	Thioredoxin-2	GO:0050832,GO:0006662,GO:0005634,GO:0005623,GO:0006974,GO:0008340,GO:0045454,GO:0015035,GO:0006979,GO:0015036	CG31884-PB					TIGR01068	PF00085	PS51352	PR00421,PR00421,PR00421		G3DSA:3.40.30.10	SSF52833	19~39								
aly5412.9	Prostamide/prostaglandin F synthase	GO:0001516,GO:0005829,GO:0016616	n/a						PF13911				G3DSA:3.40.30.10	SSF52833									
aly542.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly542.2	RNA-binding protein 26	GO:0007346,GO:0006397,GO:1900364,GO:0005634,GO:0010923,GO:0045879,GO:0000166,GO:0010628,GO:0003723,GO:0046833,GO:0046872,GO:0003729	CG10084-PC						PF14605					SSF54928	18~38								
aly542.3	RNA-binding protein 26	GO:0007346,GO:0006397,GO:1900364,GO:0005634,GO:0010923,GO:0045879,GO:0000166,GO:0010628,GO:0003723,GO:0046833,GO:0046872,GO:0003729	CG10084-PC				SM00360		PF13893,PF01480				G3DSA:3.30.70.330,G3DSA:1.20.1390.10	SSF54928	519~546,603~637								
aly542.4	Unknown		n/a												95~99								
aly543.1	Unknown		n/a																				
aly5434.1	Unknown		n/a																				
aly5434.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5434.3	E3 ubiquitin-protein ligase RFWD2	GO:0032436,GO:0008270,GO:0051568,GO:0005925,GO:0061630,GO:0005875,GO:0005737,GO:0010212,GO:0005813,GO:0005634,GO:0004402,GO:0005654,GO:0005671,GO:0016573,GO:0046872,GO:0016607,GO:0022008,GO:0016874,GO:0006338,GO:0044545,GO:0000139,GO:0048188,GO:0007095,GO:0044666,GO:0044665	CG17437-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00184		PF00097,PF00400	PS50082,PS50089,PS50082,PS50294	PR00320,PR00320,PR00320	PS00518	G3DSA:3.30.40.10,G3DSA:2.130.10.10	SSF57850,SSF50978									
aly5434.4	Bromodomain and WD repeat-containing protein 1	GO:0005737,GO:0006909,GO:0046427,GO:0005730,GO:0005634,GO:0008360,GO:0006357,GO:0005515,GO:0007095,GO:0007010,GO:0006351	CG31132-PA				SM00297,SM00320,SM00320,SM00320,SM00320,SM00320		PF00439,PF00439,PF00400,PF00400	PS50014,PS50082,PS50082,PS50014,PS50082,PS50082,PS50082,PS50294	PR00503,PR00503,PR00503,PR00503	PS00678	G3DSA:1.20.920.10,G3DSA:2.130.10.10,G3DSA:1.20.920.10	SSF47370,SSF50978,SSF47370									
aly5434.5	Unknown		n/a						PF06936						87~134								
aly5434.6	Unknown		n/a																				
aly5434.7	RNA-binding protein Musashi homolog Rbp6	GO:0005737,GO:0019827,GO:0048864,GO:0042078,GO:0000900,GO:0003727,GO:0005634,GO:0001709,GO:0000166,GO:0008266,GO:0005844,GO:0022416,GO:0003723,GO:0003676,GO:0071456,GO:0006417,GO:0017148,GO:0006397,GO:0045182,GO:0003729	CG5099-PB				SM00360,SM00360		PF00076,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5465.1	Irregular chiasm C-roughest protein	GO:0048749,GO:0016202,GO:0045177,GO:0001745,GO:0007409,GO:0046667,GO:0016021,GO:0030165,GO:0046331,GO:0005913,GO:0005515,GO:0005886,GO:0007520,GO:0046666,GO:0007156,GO:0042802	CG4125-PA				SM00408,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409,SM00409		PF08205,PF13927,PF07679,PF07679	PS50835,PS50835,PS50835,PS50835,PS51257			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF48726	1~21								
aly54796.1	Protein sel-1 homolog 1	GO:0007219,GO:0016021,GO:0030970,GO:0005789,GO:0005886,GO:0034976	CG10221-PA				SM00671,SM00671,SM00671		PF08238,PF08238,PF08238				G3DSA:1.25.40.10	SSF81901	128~137								
aly5481.1	Probable 4-coumarate--CoA ligase 3	GO:0016207,GO:0046627,GO:0009062,GO:0019433,GO:0004467,GO:0071616,GO:0009698,GO:0005524	CG9009-PA						PF00501,PF00501,PF00501,PF13193,PF13193			PS00455,PS00455	G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.40.50.980,G3DSA:3.30.300.30,G3DSA:3.30.300.30,G3DSA:3.40.50.980	SSF56801,SSF56801	950~959								
aly5490.1	Acetyl-CoA carboxylase 1	GO:0006633,GO:0005737,GO:0006084,GO:0000902,GO:0051289,GO:0005829,GO:0005811,GO:0042493,GO:0009374,GO:0019900,GO:0014070,GO:0003989,GO:0004075,GO:0046872,GO:0005524,GO:2001295	CG11198-PA						PF01039	PS50980,PS50989			G3DSA:3.90.226.10,G3DSA:3.90.226.10,G3DSA:3.90.226.10,G3DSA:3.90.226.10	SSF52096,SSF52096,SSF52096	727~727,629~656,706~715	00253+6.4.1.2,00620+6.4.1.2,00640+6.4.1.2,00061+6.4.1.2,00254+6.4.1.2,00720+6.4.1.2		PWY-7388,PWY-5789,PWY-5743,PWY-5744,PWY-6722,PWY-6679,PWY-4381	UPA00655				
aly55.1	Unknown		n/a											SSF56672									
aly55.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly55.3	Transcription factor collier	GO:0035203,GO:0035288,GO:0035289,GO:0003677,GO:0035287,GO:0007389,GO:0001700,GO:0005634,GO:0007476,GO:0007474,GO:0035291,GO:0046872,GO:0006351,GO:0046427,GO:0016204,GO:0045087,GO:0007350,GO:0007526,GO:0003700,GO:0009608,GO:0006355,GO:0048813,GO:0045944,GO:0048814,GO:0046983,GO:0042694	CG10197-PC				SM00429		PF01833,PF16422,PF16423			PS01345	G3DSA:2.60.40.10	SSF81296										
aly55.4	Trypsin-3	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG8299-PA				SM00020		PF00089	PS50240	PR00722,PR00722	PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly55.5	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0060179,GO:0009744,GO:0016021,GO:0070328,GO:0005783,GO:0017105,GO:0019216,GO:0046872,GO:0031410,GO:0016717,GO:0005811,GO:0006631,GO:0042593,GO:0042811,GO:0048047,GO:0004768,GO:0010506,GO:0006723,GO:0055114	CG5887-PA								PR00075,PR00075,PR00075	PS00476						PWY-5987,PWY-5996					
aly55.6	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0006631,GO:0016021,GO:0006629,GO:0017105,GO:0016717,GO:0046872,GO:0042811,GO:0004768,GO:0006723,GO:0055114	CG5925-PA								PR00075,PR00075												
aly55.7	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0006631,GO:0016021,GO:0006629,GO:0017105,GO:0006723,GO:0046872,GO:0042811,GO:0004768,GO:0016717,GO:0055114	CG5925-PA						PF00487		PR00075,PR00075,PR00075,PR00075,PR00075,PR00075,PR00075	PS00476						PWY-5987,PWY-5996					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly55014.1	Unknown	GO:0005575,GO:0008150,GO:0003674	CG12781-PA																				
aly551.1	Ankyrin repeat and zinc finger domain-containing protein 1	GO:0046872,GO:0016020,GO:0005515	n/a				SM00248			PS50088,PS50297			G3DSA:1.25.40.20	SSF48403									
aly551.2	Kin of IRRE-like protein 3	GO:0072102,GO:0048812,GO:0021740,GO:0043198,GO:0016021,GO:0030424,GO:0005576,GO:0001764,GO:0005886,GO:0030097,GO:0002121	CG43462-PC				SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408		PF13895,PF13895,PF08205	PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726									
aly5543.1	A disintegrin and metalloproteinase with thrombospondin motifs 17	GO:0004222,GO:0072499,GO:0016021,GO:0030426,GO:0030424,GO:0004872,GO:0005886,GO:0007411,GO:0031290,GO:0005578,GO:0008270	CG32227-PA				SM00209		PF00090	PS50092			G3DSA:2.20.100.10	SSF82895,SSF49854									
aly5543.10	Esterase FE4	GO:0005575,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135			PS00122,PS00941	G3DSA:3.40.50.1820	SSF53474									
aly5543.11	Unknown	GO:0046872	n/a									PS00028			147~150								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5543.12	Probable tyrosyl-DNA phosphodiesterase	GO:0005737,GO:0006281,GO:0005634,GO:0008081,GO:0045197,GO:0017005,GO:0004527,GO:0007417	CG8825-PA						PF06087				G3DSA:3.30.870.10,G3DSA:3.30.870.20	SSF56024,SSF56024									
aly5543.13	Uncharacterized protein C9orf117 homolog		CG17122-PA												187~207,34~71,276~327,73~107,140~167,230~261								
aly5543.2	Unknown		n/a										G3DSA:3.60.10.10	SSF56219	10~30								
aly5543.3	Unknown		CG14568-PA						PF16042														
aly5543.4	Unknown		n/a																				
aly5543.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5543.6	Unknown		CG14568-PA						PF16042,PF16042														
aly5543.7	Esterase B1	GO:0052689	CG6018-PA						PF00135			PS00122,PS00941	G3DSA:3.40.50.1820	SSF53474,SSF53474	338~343,374~374								
aly5543.8	Esterase B1	GO:0052689	CG6018-PA						PF00135			PS00122,PS00941	G3DSA:3.40.50.1820	SSF53474									
aly5543.9	Juvenile hormone esterase	GO:0004453,GO:0052689	CG6018-PA						PF00135,PF00135,PF00135,PF00135			PS00122,PS00941,PS00941,PS00122	G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474,SSF53474										
aly5547.1	Unknown		n/a						PF02194														
aly5547.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5547.3	ATP-binding cassette sub-family A member 12	GO:0005319,GO:0006869,GO:0017127,GO:0032940,GO:0061436,GO:0034040,GO:0034191,GO:0005737,GO:0042626,GO:0097209,GO:0016021,GO:2000010,GO:0045055,GO:0043129,GO:0005524,GO:0033700,GO:0019725,GO:0005548,GO:0035627,GO:0005215,GO:0006810,GO:0055088,GO:0005887,GO:0005886,GO:0072659,GO:0055085,GO:0010875,GO:0043190,GO:0031424,GO:0005829,GO:0005743,GO:0033344,GO:0048286,GO:0005102	CG34120-PE				SM00382,SM00382		PF00005,PF00005,PF12698,PF12698	PS50893,PS50893			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	3748~3748								
aly5547.4	TNF receptor-associated factor 2	GO:0035631,GO:0012506,GO:0019901,GO:0033209,GO:0034351,GO:0019899,GO:0051023,GO:0003674,GO:0007165,GO:0046328,GO:0043507,GO:0002726,GO:0042981,GO:0005737,GO:0007250,GO:0043623,GO:0008270,GO:0043066,GO:0070534,GO:0042802,GO:0043123,GO:1990604,GO:1903265,GO:0032743,GO:2001238,GO:0006915,GO:0051291,GO:0005174,GO:0046625,GO:0006952,GO:0019903,GO:0004842,GO:0009898,GO:0005164,GO:0016874,GO:1903721,GO:0051092,GO:0051091,GO:0031625,GO:0031996,GO:0090073,GO:0005829,GO:0045121,GO:0000151,GO:0030163,GO:0071732,GO:0051865,GO:0097300,GO:0070207,GO:0097057,GO:0005938	CG4394-PA							PS50144			G3DSA:2.60.210.10	SSF49599,SSF49599	182~202,241~286,217~237								
aly5547.5	Unknown		n/a												22~45								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5547.6	NEDD8 ultimate buster 1	GO:0005737,GO:0032436,GO:0005730,GO:0005634,GO:0016567,GO:0006511,GO:0022008	CG15445-PA				SM00165,SM00165			PS50053,PS50030			G3DSA:3.10.20.90,G3DSA:1.10.8.10,G3DSA:1.10.8.10	SSF54236,SSF46934,SSF46934	279~306								
aly5547.7	Unknown		n/a																				
aly5553.1	Facilitated trehalose transporter Tret1	GO:0015574,GO:0015771,GO:0005215,GO:0016021,GO:0016020,GO:0015749,GO:0005886,GO:0015145,GO:0055085	CG33282-PB						PF00083	PS50850		PS00216,PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly5553.10	Zinc finger protein 500	GO:0003700,GO:0005634,GO:0006351,GO:0003677,GO:0046872,GO:0008270	CG6654-PA				SM00355,SM00355			PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667									
aly5553.11	Unknown		n/a						PF00089	PS50240			G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5553.2	Agrin	GO:0043547,GO:2000541,GO:1903277,GO:0008582,GO:0030154,GO:0035374,GO:0031012,GO:0042030,GO:0007009,GO:0002162,GO:0045202,GO:0044325,GO:0043087,GO:0007275,GO:0030054,GO:0005737,GO:0032092,GO:0030548,GO:0070062,GO:0016021,GO:0051491,GO:0007268,GO:0005509,GO:0061098,GO:0010469,GO:0005796,GO:1903407,GO:0009986,GO:0007528,GO:0043395,GO:0045213,GO:0004866,GO:0005886,GO:0055117,GO:0005615,GO:0005605,GO:0005604,GO:0086036,GO:0033691,GO:0045887,GO:0005576,GO:0045944,GO:0043113,GO:0001934,GO:0043525	CG32354-PA				SM00280,SM00280,SM00280,SM00280,SM00280,SM00280,SM00280,SM00280		PF07648,PF07648,PF07648,PF07648,PF07648,PF07648,PF07648,PF00050	PS51465,PS51465,PS51465,PS51465,PS51465,PS51465,PS51465,PS51465			G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30	SSF100895,SSF100895,SSF100895,SSF100895,SSF100895,SSF100895,SSF100895,SSF100895									
aly5553.3	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0005215,GO:0016021,GO:0016020,GO:0008643,GO:0005886,GO:0055085	CG30035-PA						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20	SSF103473									
aly5553.4	Facilitated trehalose transporter Tret1-1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0016020,GO:0008643,GO:0005886,GO:0055085	CG30035-PA						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly5553.5	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0005351,GO:0055085	CG1380-PA						PF00083	PS50850		PS00217	G3DSA:1.20.1250.20	SSF103473									
aly5553.6	Facilitated trehalose transporter Tret1-2 homolog	GO:0005355,GO:0022891,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850,PS51257			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5553.7	DNA-directed RNA polymerase II subunit RPB1	GO:0007015,GO:0005214,GO:0003677,GO:0006366,GO:0007160,GO:0016324,GO:0005665,GO:0003383,GO:0003899,GO:0016476,GO:0046872	CG15013-PB				SM00241		PF00100	PS51034													
aly5553.8	Guanine nucleotide exchange factor MSS4 homolog	GO:0016192,GO:0005829,GO:0016020,GO:0005085,GO:0008270,GO:0015031,GO:0007264	CG7787-PA						PF04421				G3DSA:2.170.150.10	SSF51316									
aly5553.9	Protein FAM192A	GO:0005634	CG14480-PA						PF10187						45~65								
aly5556.1	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0035006,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG1102-PC						PF00089	PS50240		PS00135	G3DSA:2.40.10.10	SSF50494									
aly5556.2	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG4920-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly5556.3	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0035006,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG1102-PC				SM00020,SM00680		PF12032,PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5558.1	Unknown		n/a												27~47								
aly55634.1	Serine/threonine kinase SAD 1	GO:0006468,GO:0046872,GO:0006487,GO:0007416,GO:0034613,GO:0018105,GO:0008088,GO:0030424,GO:0007528,GO:0004674,GO:0050321,GO:0007163,GO:0030054,GO:0030516,GO:0050808,GO:0007411,GO:0030425,GO:0005622,GO:0048489,GO:0005524,GO:0045202	CG6114-PA																				
aly5565.1	Glutamate receptor 1	GO:0045211,GO:0032281,GO:0008328,GO:0035235,GO:0006812,GO:0005230,GO:0015277,GO:0005234,GO:0035249,GO:0034220,GO:0030425,GO:0005886,GO:0016021,GO:0030054,GO:0004971	CG8442-PA				SM00079,SM00918		PF00060,PF10613,PF01094				G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.190.10,G3DSA:1.10.287.70	SSF53822,SSF53822,SSF53850,SSF53850									
aly55650.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly55680.1	Dynactin subunit 1	GO:0016330,GO:0051383,GO:0042052,GO:0042051,GO:0035371,GO:0045198,GO:0030286,GO:0031616,GO:0007067,GO:0005874,GO:0051028,GO:0005876,GO:0034501,GO:0005737,GO:0005818,GO:0005813,GO:0045502,GO:0001709,GO:0007018,GO:0005739,GO:0051225,GO:0048477,GO:0003774,GO:0003777,GO:0051299,GO:0047497,GO:0090316,GO:0031122,GO:0035011,GO:0007052,GO:0010970,GO:0048491,GO:0005869,GO:0001754,GO:0022008,GO:0001751,GO:0000776,GO:0051642,GO:0008090,GO:0005828,GO:0030496,GO:0051256,GO:0006886	CG9206-PA												55~138,3~51								
aly55752.1	Asparagine--tRNA ligase, cytoplasmic	GO:0005737,GO:0006421,GO:0003676,GO:0005524,GO:0004816	CG10687-PA						PF00152				G3DSA:3.30.930.10	SSF55681			REACT_71						
aly5578.1	Succinate dehydrogenase [ubiqui] iron-sulfur subunit, mitochondrial	GO:0046872,GO:0051538,GO:0051539,GO:0051537,GO:0006121,GO:0005743,GO:0006099,GO:0008177,GO:0048039,GO:0005749,GO:0005875,GO:0009055	CG3283-PA					TIGR00384	PF13534,PF13085	PS51085		PS00197,PS00198	G3DSA:3.10.20.30,G3DSA:1.10.1060.10	SSF46548,SSF54292		00720+1.3.5.1,00190+1.3.5.1,00020+1.3.5.1,00650+1.3.5.1		PWY-561,PWY-4302,PWY-3781,PWY-7279,PWY-6969,PWY-6728,PWY-7254,PWY-5690					
aly558.1	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016335,GO:0016021,GO:0016020,GO:0051017,GO:0035220,GO:0005886,GO:0006508	CG4316-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly558.2	Unknown		n/a																				
aly558.3	Unknown		n/a												87~107,37~57								
aly558.4	Phosphoglycolate phosphatase 2	GO:0004674,GO:0006468,GO:0016791,GO:0008967,GO:0009507	CG15739-PA			PIRSF000915		TIGR01460	PF13344,PF13242				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000,G3DSA:3.40.50.10410	SSF56784									
aly558.5	Phosphoglycolate phosphatase 2	GO:0004674,GO:0006468,GO:0016791,GO:0008967,GO:0009507	CG15739-PA			PIRSF000915		TIGR01460	PF13242,PF13344				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000,G3DSA:3.40.50.10410	SSF56784									
aly558.6	Unknown		n/a																				
aly558.7	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly558.8	Unknown		n/a																				
aly558.9	Unknown		n/a																				
aly5582.1	Oxysterol-binding protein-related protein 6	GO:0005794,GO:0007030,GO:0097038,GO:0005783,GO:0006869,GO:0008142,GO:0006886,GO:0031965,GO:0008289,GO:0007291,GO:0005886,GO:0005829	CG6708-PA				SM00233		PF01237,PF15409	PS50003		PS01013	G3DSA:2.30.29.30	SSF144000,SSF50729	228~262								
aly5582.2	Probable aminopeptidase NPEPL1	GO:0005737,GO:0004177,GO:0005634,GO:0030145,GO:0006508,GO:0008235	CG7340-PF										G3DSA:3.40.50.10590										
aly5582.3	Probable aminopeptidase NPEPL1	GO:0005737,GO:0004177,GO:0019538,GO:0005634,GO:0030145,GO:0006508,GO:0008235	CG7340-PF						PF00883		PR00481,PR00481,PR00481,PR00481,PR00481	PS00631	G3DSA:3.40.630.10	SSF53187		00480+3.4.11.1		PWY-5988,PWY-6018					
aly5582.4	Coactosin-like protein	GO:0005737,GO:0005856,GO:0070062,GO:0050832,GO:0031965,GO:0019899,GO:0005622,GO:0003779,GO:0019370	CG6891-PA				SM00102		PF00241	PS51263			G3DSA:3.40.20.10	SSF55753									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5582.5	TP53-regulating kinase	GO:0005737,GO:0016787,GO:0006468,GO:0016020,GO:0008033,GO:0040018,GO:0000408,GO:0032008,GO:0030307,GO:0004674,GO:0004713,GO:0004672,GO:0005634,GO:0002039,GO:0005829,GO:0005524,GO:0070525	CG10673-PA					TIGR03724	PF06293	PS50011		PS00109	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly5582.6	39S ribosomal protein L39, mitochondrial	GO:0006435,GO:0004829,GO:0000166,GO:0003735,GO:0031047,GO:0005762,GO:0006417,GO:0006412	CG17166-PA										G3DSA:3.30.54.20,G3DSA:3.10.20.30	SSF55186									
aly5582.7	Unknown		n/a																				
aly5582.8	Origin recognition complex subunit 5	GO:0006342,GO:0006270,GO:0017111,GO:0000166,GO:0007052,GO:0046331,GO:0006260,GO:0006261,GO:0003677,GO:0007076,GO:0005524,GO:0005664	CG7833-PA						PF13191,PF14630				G3DSA:3.40.50.300	SSF52540	1~21								
aly5582.9	Unknown		n/a												34~54								
aly5583.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5583.2	SH3 and multiple ankyrin repeat domains protein 3	GO:0008022,GO:0048170,GO:2000463,GO:0060170,GO:0097107,GO:0042297,GO:0005886,GO:0007612,GO:0017124,GO:0061001,GO:1900452,GO:1900451,GO:0030054,GO:0005737,GO:0032232,GO:0050885,GO:0000165,GO:0035640,GO:0035641,GO:0060999,GO:0007416,GO:0043005,GO:0051835,GO:0060997,GO:0042802,GO:0071625,GO:0040011,GO:0035176,GO:0044309,GO:0035255,GO:0007613,GO:0045211,GO:0021773,GO:0014069,GO:0030160,GO:0060076,GO:2000822,GO:2000969,GO:2000821,GO:0097481,GO:0001838,GO:0030534,GO:1900273,GO:0045794,GO:0043197,GO:1900271,GO:0060291,GO:0048854,GO:0060292,GO:0097114,GO:0097117,GO:0097110,GO:0005515,GO:0097113,GO:0051968,GO:0008270	CG30483-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00228,SM00326		PF12796,PF13637,PF16511,PF07653,PF00595	PS50297,PS50088,PS50088,PS50106,PS50002,PS50088			G3DSA:1.25.40.20,G3DSA:2.30.42.10,G3DSA:2.30.30.40	SSF48403,SSF50044,SSF50156									
aly5583.3	Unknown		n/a																				
aly5593.1	Unknown		n/a																				
aly5593.2	Unknown	GO:0003676	n/a						PF03184														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5593.3	Unknown		n/a																				
aly5593.4	Unknown		n/a																				
aly5593.5	Unknown	GO:0003677	n/a						PF13412				G3DSA:1.10.10.60										
aly560.1	Unknown		n/a																				
aly560.2	WD repeat-containing protein 48 homolog	GO:0005515	CG9062-PC				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF11816	PS50082,PS50294,PS50082,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678	G3DSA:2.130.10.10	SSF50978									
aly560.3	Elongation factor Tu, mitochondrial	GO:0042645,GO:0070062,GO:0044822,GO:0016020,GO:0003924,GO:0005739,GO:0003746,GO:0006414,GO:0006412,GO:0005525	CG12736-PA					TIGR00231	PF00009,PF03143,PF03144	PS51722	PR00315,PR00315,PR00315,PR00315,PR00315	PS00301	G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:3.40.50.300	SSF50447,SSF52540,SSF50465									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly560.4	Uncharacterized protein C17orf104 homolog		n/a						PF15189,PF15189						480~500,379~399								
aly560.5	Photoreceptor-specific nuclear receptor	GO:0016319,GO:0043565,GO:0031103,GO:0020037,GO:0003700,GO:0005634,GO:0048842,GO:0016322,GO:0003707,GO:0006355,GO:0008270,GO:0043401,GO:0007411,GO:0022008,GO:0048526,GO:0004879,GO:0006351	CG16801-PC				SM00399		PF00105	PS51030	PR00047,PR00047,PR00047,PR00047	PS00031	G3DSA:3.30.50.10	SSF57716			REACT_71						
aly560.6	Photoreceptor-specific nuclear receptor	GO:0016319,GO:0007165,GO:0008270,GO:0043401,GO:0007411,GO:0004879,GO:0042462,GO:0043565,GO:0030522,GO:0045872,GO:0000122,GO:0005634,GO:0048842,GO:0005654,GO:0010467,GO:0006367,GO:0006366,GO:0008285,GO:0031103,GO:0020037,GO:0007601,GO:0016322,GO:0007602,GO:0022008,GO:0003700,GO:0003707,GO:0006355,GO:0045944,GO:0005667,GO:0048526,GO:0060041	CG16801-PC				SM00430		PF00104		PR00398,PR00398,PR00398		G3DSA:1.10.565.10	SSF48508			REACT_71						
aly560.7	Unknown		n/a																				
aly560.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly56085.1	Gamma-taxilin	GO:0051726,GO:0010564,GO:0005829,GO:0031965,GO:0006355,GO:0019905,GO:0006351,GO:0030500,GO:0046982,GO:0007049	CG5886-PA						PF09728						7~36,67~94								
aly5609.1	Tau-tubulin kinase 1	GO:0005737,GO:0006468,GO:0005819,GO:0008360,GO:0004674,GO:0018105,GO:0021762,GO:0004672,GO:0005524	CG11533-PD				SM00220		PF00069	PS50011		PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly5612.1	Unknown		n/a																				
aly5612.2	Glucose-1-phosphatase	GO:0008877,GO:0042597,GO:0003993	n/a						PF00328			PS00778	G3DSA:3.40.50.1240,G3DSA:3.40.50.1240,G3DSA:3.40.50.1240	SSF53254									
aly5612.3	Glucose-1-phosphatase	GO:0008877,GO:0016311,GO:0016158,GO:0030288,GO:0006006,GO:0003993	n/a						PF00328			PS00616,PS00778	G3DSA:3.40.50.1240,G3DSA:3.40.50.1240,G3DSA:3.40.50.1240	SSF53254									
aly5612.4	Vacuolar protein sorting associated protein 37A	GO:0005737,GO:0016197,GO:0019082,GO:0043231,GO:0005813,GO:0043162,GO:0000813,GO:0075733,GO:0005654,GO:0061024,GO:0019058,GO:0003674,GO:0016032,GO:0015031,GO:0019068,GO:0031902,GO:0010008	CG17828-PA						PF07200	PS51314													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly56179.1	Elongation factor 1-alpha (Fragment)	GO:0005737,GO:0005853,GO:0005829,GO:0005811,GO:0003924,GO:0006412,GO:0008340,GO:0003746,GO:0006414,GO:0005875,GO:0005525	CG8280-PA						PF03144				G3DSA:2.40.30.10	SSF50447									
aly5623.1	Suppressor of cytokine signaling 7	GO:0005737,GO:0008286,GO:0040008,GO:0043231,GO:0009968,GO:0005730,GO:0005634,GO:0017124,GO:0017022,GO:0021819,GO:0016567,GO:0005886,GO:0045444,GO:0035556,GO:0021942,GO:0038202	CG8146-PB				SM00969,SM00252,SM00253		PF00017,PF07525	PS50001,PS50225			G3DSA:3.30.505.10	SSF158235,SSF55550	390~410				UPA00143				
aly5623.2	Mediator of RNA polymerase II transcription subunit 23	GO:0005634,GO:0001104,GO:0006355,GO:0006351,GO:0006367,GO:0006366,GO:0016592	CG3695-PA						PF11573														
aly5623.3	Unknown		n/a																				
aly5623.4	Unknown		n/a												101~137								
aly5623.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5623.6	Unknown		n/a																				
aly5623.7	Unknown		n/a																				
aly5623.8	Unknown		n/a												5~43								
aly5627.1	Unknown		n/a																				
aly563.1	Ethanolaminephosphotransferase 1	GO:0006646,GO:0006644,GO:0016780,GO:0008654,GO:0016021,GO:0016020,GO:0008414,GO:0005789,GO:1903955,GO:0044281,GO:0004307,GO:0046474,GO:0046872	CG33116-PA						PF01066			PS00379											
aly563.10	Trypsin-5	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG12350-PA						PF00089	PS50240			G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly563.11	Inactive dipeptidyl peptidase 10	GO:0072659,GO:0016021,GO:0016020,GO:0008239,GO:1901379,GO:0005886,GO:0006508,GO:0090004,GO:0015459,GO:0008236	CG11319-PB						PF00930				G3DSA:2.140.10.30	SSF82171	217~219								
aly563.12	PiggyBac transposable element-derived protein 2		n/a						PF13843														
aly563.2	Eyes absent homolog 4	GO:0009996,GO:0042051,GO:0007498,GO:0006470,GO:0008584,GO:0007419,GO:0010628,GO:0009416,GO:0001746,GO:0007411,GO:0001744,GO:0007275,GO:0005737,GO:0007435,GO:0007455,GO:0005634,GO:0008406,GO:0030707,GO:0046872,GO:0008134,GO:0048749,GO:0016787,GO:0006281,GO:0007605,GO:0072499,GO:0045087,GO:0007280,GO:0007283,GO:0007526,GO:0042474,GO:0030946,GO:0004725,GO:0004721,GO:0006355,GO:0045944,GO:0006351,GO:0016568	CG9554-PA					TIGR01658							655~655								
aly563.3	Intraflagellar transport protein 52 homolog	GO:0008022,GO:0050680,GO:0042073,GO:0030990,GO:0005929,GO:0005871,GO:0072372,GO:0031514,GO:0005814,GO:0001947,GO:0001841,GO:0030992,GO:0032391,GO:0042384,GO:0060271,GO:0044292,GO:0006996,GO:0042733,GO:0070613,GO:0009953,GO:0007224,GO:0007018,GO:0097542,GO:0097546	CG9595-PA						PF09822					SSF52317									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly563.4	Trypsin	GO:0007586,GO:0004252,GO:0008236,GO:0005576,GO:0006508	CG4812-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494	178~198,154~174								
aly563.5	Nucleolar protein 4-like		CG17341-PB																				
aly563.6	Nucleolar protein 4	GO:0005634,GO:0005730	CG16879-PB																				
aly563.7	Unknown		CG15601-PA				SM00595		PF10545	PS51029													
aly563.8	Nucleolar protein 4	GO:0005634,GO:0005730	CG16879-PB																				
aly563.9	Zinc finger protein 180	GO:0045931,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF12874,PF12874,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57716,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly56312.1	Exosome complex component RRP4	GO:0030307,GO:0071049,GO:0008312,GO:0005737,GO:0000288,GO:0005730,GO:0005634,GO:0010467,GO:0006364,GO:0005652,GO:0010468,GO:0034475,GO:0071051,GO:0071035,GO:0071034,GO:0071038,GO:0000467,GO:0043928,GO:0000178,GO:0005829,GO:0000176,GO:0000177,GO:0000175,GO:0034427,GO:0003723,GO:0006397	CG3931-PB											SSF50249,SSF110324									
aly5635.1	Cysteine proteinase 3	GO:0005773,GO:0005811,GO:0005875,GO:0004197,GO:0006508,GO:0008234	CG8947-PA				SM00645,SM00848		PF00112,PF08246		PR00705,PR00705,PR00705	PS00640,PS00139,PS00639	G3DSA:3.90.70.10,G3DSA:3.90.70.10	SSF54001,SSF54001									
aly5635.2	Cysteine proteinase 3	GO:0005773,GO:0005811,GO:0005875,GO:0004197,GO:0006508,GO:0008234	CG8947-PA				SM00848,SM00645		PF00112,PF08246	PS51257	PR00705,PR00705,PR00705	PS00640,PS00639,PS00139	G3DSA:3.90.70.10	SSF54001									
aly5635.3	Pancreatic lipase-related protein 2	GO:0009395,GO:0006629,GO:0047714,GO:0004806,GO:0005615,GO:0016042,GO:0005575,GO:0005509,GO:0019376,GO:0004620,GO:0016298,GO:0047372	CG4582-PA						PF00151				G3DSA:3.40.50.1820	SSF53474									
aly5635.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly56404.1	Unknown		n/a																				
aly56576.1	Zinc finger protein 317	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG7372-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028		SSF57667,SSF57667,SSF57667									
aly56599.1	Desumoylating isopeptidase 2	GO:0005737,GO:0008233	CG7222-PA						PF05903														
aly566.1	Nephrin	GO:0061321,GO:0007286,GO:0030036,GO:0007520,GO:0001745,GO:0072015,GO:0007254,GO:0007523,GO:0070062,GO:0097206,GO:0030838,GO:0007519,GO:0007156,GO:0007588,GO:0032836,GO:0005917,GO:0036059,GO:0017022,GO:0005887,GO:0005886,GO:0007155,GO:0007157,GO:0042995,GO:0036057,GO:0044062,GO:0005622,GO:0005515	CG33141-PB				SM00409		PF07679	PS50835			G3DSA:2.60.40.10	SSF48726									
aly56635.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5673.1	Solute carrier family 25 member 44	GO:0005743,GO:0005740,GO:0016021,GO:0022857,GO:0055085	CG5805-PA						PF00153,PF00153	PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly5673.2	Calmodulin-like protein 4	GO:0005509	CG17272-PA										G3DSA:1.10.238.10	SSF47473									
aly5673.3	Unknown	GO:0016021	CG17270-PA						PF03694														
aly5673.4	Unknown		n/a																				
aly569.1	CDK-activating kinase assembly factor MAT1	GO:0032806,GO:0051301,GO:0005634,GO:0000990,GO:0008270,GO:0006367,GO:0005675,GO:0004693,GO:0008353,GO:0007049	CG7614-PA			PIRSF003338	SM00184	TIGR00570	PF17121,PF06391	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850	143~186								
aly569.2	Uncharacterized protein C2orf47 homolog, mitochondrial	GO:0008150,GO:0005739,GO:0005515	CG3776-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly569.3	Unknown		n/a																				
aly569.4	Unknown		n/a																				
aly569.5	Structure-specific endonuclease subunit SLX4	GO:0043234,GO:0008283,GO:0045132,GO:0006281,GO:0007712,GO:0005634,GO:0017108,GO:0000715,GO:0006260,GO:0033557,GO:0005515,GO:0035825,GO:0007095,GO:0007131	CG8601-PE						PF09494														
aly569.6	Protein IMPACT-A	GO:0006417,GO:0005515	n/a				SM00591		PF05773,PF01205	PS50908			G3DSA:3.30.230.30,G3DSA:3.10.110.10	SSF54211,SSF54495	3~23,162~182								
aly569.7	Paired box pox-neuro protein	GO:0030154,GO:0007399,GO:0007423,GO:0007480,GO:0003700,GO:0005634,GO:0009415,GO:0007476,GO:0006355,GO:0048800,GO:0006351,GO:0003677,GO:0008343,GO:0008049	CG8246-PA				SM00351		PF00292	PS51057			G3DSA:1.10.10.10	SSF46689									
aly569.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5692.1	RING finger protein 113A	GO:0022008,GO:0046872,GO:0005634,GO:0030182,GO:0008270	CG4973-PA				SM00356,SM00184		PF00642,PF13920	PS50089,PS50103		PS00518	G3DSA:4.10.1000.10,G3DSA:3.30.40.10	SSF57850,SSF90229									
aly5692.2	Cysteine dioxygenase type 1	GO:0046439,GO:0005506,GO:0017172,GO:0042412,GO:0055114	CG5493-PA						PF05995,PF05995				G3DSA:2.60.120.10,G3DSA:2.60.120.10	SSF51182,SSF51182		00430+1.13.11.20,00270+1.13.11.20		PWY-5331	UPA00012				
aly5692.3	Unknown		n/a																				
aly5692.4	Unknown		n/a																				
aly5692.5	Unknown		n/a																				
aly5692.6	Unknown	GO:0006030,GO:0005576,GO:0008061	n/a							PS50940			G3DSA:2.170.140.10	SSF57625									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5692.7	Unknown	GO:0006030,GO:0005576,GO:0008061	n/a										G3DSA:2.170.140.10	SSF57625									
aly56959.1	Cytosolic beta-glucosidase	GO:0005975,GO:0005829,GO:0008422,GO:0004565,GO:0004553,GO:0017042,GO:0046477	CG9701-PA						PF00232			PS00572	G3DSA:3.20.20.80	SSF51445									
aly570.1	Protein NEDD1	GO:0000242,GO:0000086,GO:0005886,GO:0008274,GO:0007067,GO:0051301,GO:0000278,GO:0005737,GO:0036064,GO:0045177,GO:0005730,GO:0005813,GO:0005814,GO:0000922,GO:0005654,GO:0051298,GO:0051297,GO:0007052,GO:0007057,GO:0045450,GO:0006996,GO:0051726,GO:0005829,GO:0005515,GO:0043015	CG10346-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320			PS50294			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978	483~503									
aly570.2	Nucleoporin seh1	GO:0043234,GO:0051445,GO:0007346,GO:0017056,GO:0031080,GO:0005643,GO:0048477,GO:0005635,GO:0006999,GO:0007080,GO:0051301,GO:0015031,GO:0051028,GO:0035859,GO:0051315,GO:0007184,GO:0000777	CG8722-PB				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400	PS50294,PS50082,PS50082,PS50294		PS00678	G3DSA:2.130.10.10	SSF50978										
aly570.3	Serine/threonine-protein kinase SIK3	GO:0005737,GO:0006468,GO:0000287,GO:0055088,GO:0004674,GO:0042594,GO:0004672,GO:0005524	CG42856-PB				SM00220		PF00069,PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:3.30.200.20	SSF56112,SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly570.4	Unknown		n/a																				
aly570.5	Lipase 3	GO:0006629,GO:0016788,GO:0016042	CG18301-PA						PF04083				G3DSA:3.40.50.1820	SSF53474									
aly570.6	Homeobox protein TGIF2	GO:0043565,GO:0006351,GO:0038092,GO:0010470,GO:0045666,GO:0000122,GO:0003700,GO:0005813,GO:0005634,GO:0003714,GO:0005654,GO:0006355,GO:0007283,GO:0001077,GO:0045893,GO:0005515,GO:0003677,GO:0042826,GO:0060041	CG8821-PB				SM00389		PF05920	PS50071			G3DSA:1.10.10.60	SSF46689									
aly570.7	Unknown		n/a												33~66								
aly570.8	DNA repair protein RAD52 homolog	GO:0006310,GO:0043234,GO:0000724,GO:0005634,GO:0000150,GO:0006974,GO:0010792,GO:0003677,GO:0034599,GO:2000819,GO:0042802	n/a						PF04098					SSF54768									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly570.9	Unknown		n/a																				
aly571.1	Unknown	GO:0008080	CG10659-PA						PF00583	PS51186			G3DSA:3.40.630.30	SSF55729									
aly571.2	Glia maturation factor beta	GO:0003779,GO:0034316,GO:0042063,GO:0005622	CG5869-PA			PIRSF001788	SM00102		PF00241	PS51263			G3DSA:3.40.20.10	SSF55753									
aly5714.1	GTPase-activating protein CdGAPr	GO:0043547,GO:0005096,GO:0005622,GO:0005575,GO:0007165,GO:0005100,GO:0007266,GO:0031290	CG10538-PA				SM00324		PF00620	PS50238			G3DSA:1.10.555.10	SSF48350			REACT_11044						
aly5715.1	Zinc finger protein 771	GO:0031936,GO:0043565,GO:0005634,GO:0005700,GO:0006355,GO:0045892,GO:0006351,GO:0005515,GO:0003677,GO:0000785,GO:0046872,GO:0043035	CG8573-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly5715.2	Transport and Golgi organization protein 2	GO:0009306,GO:0005794,GO:0005829,GO:0003674,GO:0007030	CG11176-PB						PF05742														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5715.3	Clathrin heavy chain	GO:0008021,GO:0033227,GO:0008103,GO:0007594,GO:0005886,GO:0035002,GO:0007291,GO:0005905,GO:0030130,GO:0030132,GO:0030135,GO:0030136,GO:0016183,GO:0031410,GO:0006886,GO:0005811,GO:0071439,GO:0005198,GO:0045747,GO:0035159,GO:0048471,GO:0045451,GO:0048749,GO:0030141,GO:0032051,GO:0030129,GO:0005938,GO:0007269,GO:0007268,GO:0046667,GO:0030125,GO:0006897,GO:0016192,GO:0016079,GO:0005802,GO:0030198,GO:0005515,GO:0045807,GO:0040008,GO:0033363	CG9012-PG			PIRSF002290	SM00299,SM00299,SM00299,SM00299,SM00299,SM00299,SM00299		PF09268,PF01394,PF01394,PF01394,PF00637,PF00637,PF00637,PF00637,PF00637,PF00637,PF13838	PS50236,PS50236,PS50236,PS50236,PS50236,PS50236,PS50236			G3DSA:2.130.10.110,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.30	SSF50989,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371	1624~1624,1030~1050		REACT_11123							
aly5715.4	Ubiquitin fusion degradation protein 1 homolog	GO:0006508,GO:0006511,GO:0098586,GO:0032436,GO:0000502	CG6233-PA						PF03152														
aly5715.5	Ras-related protein Rab-35	GO:1990090,GO:0016020,GO:0006909,GO:0048227,GO:0005905,GO:0031175,GO:0045202,GO:0010008,GO:0006888,GO:0031982,GO:0006886,GO:0005811,GO:0000281,GO:0005739,GO:0005546,GO:0043025,GO:0005525,GO:0016197,GO:0019882,GO:0003924,GO:0031253,GO:0032482,GO:0045334,GO:0005886,GO:0045171,GO:0070062,GO:0000910,GO:0042470,GO:0016192,GO:0036010,GO:0019003,GO:0032456,GO:0015031,GO:0007165	CG9575-PA				SM00173,SM00175,SM00176,SM00174	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly5715.6	Actin-related protein 2/3 complex subunit 4	GO:0005737,GO:0019899,GO:0005200,GO:0006909,GO:0000902,GO:0030031,GO:0030866,GO:0042060,GO:0003779,GO:0008360,GO:0005885,GO:0034314,GO:0030041,GO:0042995,GO:0070062	CG5972-PA			PIRSF039100			PF05856				G3DSA:3.30.1460.20	SSF69645									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly57167.1	Probable C-mannosyltransferase DPY19L1	GO:0005637,GO:0016021,GO:0016020,GO:0018406,GO:0000030	n/a						PF10034														
aly5719.1	Myotubularin-related protein 13	GO:0008023,GO:0016311,GO:0019208,GO:0032968,GO:0042552,GO:0043547,GO:0019992,GO:0005634,GO:0016020,GO:0051262,GO:0005774,GO:0055037,GO:0000278,GO:0008138,GO:0017137,GO:0017112,GO:0032483,GO:0019902,GO:0005938,GO:0036313,GO:0030674,GO:0035091,GO:0030866,GO:0032456,GO:0003682	CG6939-PA				SM00799,SM00800,SM00801		PF03456,PF02141	PS50946,PS50947,PS50211													
aly5719.2	Fez family zinc finger protein 2	GO:0021902,GO:0008285,GO:0016358,GO:0045666,GO:0003676,GO:0007411,GO:0007413,GO:1902667,GO:0050767,GO:0005634,GO:0045665,GO:0021853,GO:0046872,GO:0021797,GO:0007626,GO:0048664,GO:0021542,GO:0045892,GO:0019827,GO:0001227,GO:0001228,GO:0006357,GO:0000977,GO:0000978,GO:0003682	CG31670-PC				SM00355,SM00355,SM00355,SM00355		PF13912,PF13912,PF12874	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										
aly5719.3	Putative Ras-related protein Rab-33	GO:0008021,GO:0016192,GO:0055037,GO:0003924,GO:0031982,GO:0005622,GO:0032482,GO:0045202,GO:0005886,GO:0015031,GO:0007264,GO:0043025,GO:0005525	CG8287-PA				SM00174,SM00176,SM00175,SM00173	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5719.4	E3 ubiquitin-protein ligase UBR1	GO:0005737,GO:0071233,GO:0070728,GO:0016874,GO:0005829,GO:0061630,GO:0000151,GO:0016567,GO:0008270,GO:0032007,GO:0000502,GO:0004842,GO:0071596,GO:0030163	CG9086-PA				SM00396		PF02207,PF02617	PS51157			G3DSA:3.30.1390.10	SSF46785,SSF54736	964~984								
aly5719.5	NADH dehydrogenase [ubiqui] complex I, assembly factor 7 homolog	GO:0005575,GO:0008150,GO:0003674,GO:0005739,GO:0032981	CG17726-PA						PF02636					SSF53335									
aly5719.6	RNA-binding protein 28	GO:0005730,GO:0044822,GO:0000166,GO:0005575,GO:0003674,GO:0003676,GO:0008150,GO:0022008,GO:0006397,GO:0008380,GO:0005681,GO:0003729	CG4806-PA				SM00360,SM00360,SM00360,SM00360		PF00076,PF00076,PF00076,PF00076	PS50102,PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928,SSF54928	701~721								
aly5719.7	Unknown	GO:0005575,GO:0003674,GO:0008150	CG3082-PB						PF05705				G3DSA:3.40.50.1820	SSF53474									
aly5723.1	Zinc finger protein 350	GO:0016363,GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG14711-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667	297~298								
aly5723.2	Cytochrome P450 6B6	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0070330,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA						PF00067		PR00465,PR00465,PR00465,PR00465,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly57279.1	Unknown		n/a																				
aly5729.1	Serine protease 46	GO:0004252,GO:0016021,GO:0005576,GO:0006508	CG40160-PA						PF00089	PS50240			G3DSA:2.40.10.10	SSF50494									
aly5729.10	Telomerase Cajal body protein 1	GO:0005737,GO:0032203,GO:0030576,GO:0019001,GO:0003723,GO:0005515,GO:0034512,GO:0015030,GO:0005697,GO:0051973	CG9226-PB				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400	PS50082,PS50082,PS50294		PS00678	G3DSA:2.130.10.10	SSF50978									
aly5729.11	Elongation of very long chain fatty acids protein 1	GO:0007111,GO:0007110,GO:0034625,GO:0007112,GO:0000915,GO:0000212,GO:0016021,GO:0016020,GO:0030497,GO:0005789,GO:0009922,GO:0030148,GO:0019367,GO:0042761,GO:0051225,GO:0005783	CG6921-PB						PF01151,PF01151							00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					
aly5729.12	G-protein coupled receptor moody	GO:0004930,GO:0048149,GO:0048148,GO:0016021,GO:0019991,GO:0035095,GO:0030866,GO:0007419,GO:0060857,GO:0008366,GO:0005886,GO:0007186,GO:0005919	CG4313-PD						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly5729.13	G-protein coupled receptor moody	GO:0004930,GO:0048148,GO:0016021,GO:0008366,GO:0005886,GO:0007186	CG4313-PD						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5729.14	Unknown		n/a																				
aly5729.15	Unknown		n/a																				
aly5729.2	Sortilin-related receptor	GO:0005783,GO:0006869,GO:0030306,GO:0014910,GO:0055037,GO:0043407,GO:2001137,GO:1902997,GO:0070863,GO:0032091,GO:0031985,GO:0001540,GO:0070062,GO:0000042,GO:0045053,GO:0016021,GO:0016020,GO:0050768,GO:1902771,GO:0005509,GO:1902955,GO:0048471,GO:0030169,GO:0032460,GO:1902953,GO:0005794,GO:0034362,GO:0006622,GO:0006605,GO:1902430,GO:1901215,GO:0008203,GO:0005615,GO:0006892,GO:0006897,GO:0051604,GO:0005641,GO:0005802,GO:0005041,GO:0045732,GO:1902960,GO:1902963,GO:1902948,GO:0005768,GO:0005769,GO:1902966	CG33087-PF				SM00135,SM00135,SM00135,SM00135,SM00135,SM00135,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00060,SM00060,SM00060,SM00060,SM00602,SM00181,SM00181,SM00181		PF15902,PF15901,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00041,PF00058,PF00058	PS50068,PS50853,PS50068,PS50068,PS51120,PS50853,PS50853,PS51120,PS50068,PS50068,PS50853,PS51120,PS51120,PS50068,PS50068,PS51120,PS50068,PS50068	PR00261,PR00261,PR00261,PR00261,PR00261,PR00261,PR00261	PS01209,PS01209,PS01209,PS01209,PS01209,PS01209,PS01209,PS01209,PS01209	G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.60.40.10,G3DSA:2.130.10.140,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.60.40.10,G3DSA:2.120.10.30,G3DSA:2.60.40.10	SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF110296,SSF110296,SSF49265,SSF57424,SSF49265,SSF57424,SSF63825								
aly5729.3	Sortilin-related receptor (Fragment)	GO:0016021,GO:0006869,GO:0006897,GO:0034362,GO:0008203	n/a						PF15902				G3DSA:2.130.10.140	SSF110296									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5729.4	40S ribosomal protein S19a	GO:0003735,GO:0005622,GO:0022627,GO:0006412,GO:0005840	CG4464-PD						PF01090			PS00628		SSF46785									
aly5729.5	Protein lin-52 homolog	GO:0006351,GO:0007049,GO:0070176	n/a						PF10044														
aly5729.6	1,25-dihydroxyvitamin D(3) 24-hydroxylase, mitochondrial	GO:0007490,GO:0042369,GO:0006766,GO:0008202,GO:0042359,GO:0020037,GO:0006805,GO:0008403,GO:0016705,GO:0005739,GO:0030342,GO:0005743,GO:0001649,GO:0070561,GO:0005506,GO:0016491,GO:0044281,GO:0033280,GO:0055114,GO:0009055	CG8587-PA						PF00067			PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly5729.7	Probable cytochrome P450 301a1, mitochondrial	GO:0007490,GO:0004497,GO:0020037,GO:0016705,GO:0005739,GO:0031966,GO:0005506,GO:0055114,GO:0009055	CG8587-PA						PF00067		PR00463,PR00463,PR00463,PR00463		G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly5729.8	Probable N-acetyltransferase san	GO:0005737,GO:0031248,GO:0008280,GO:0008080,GO:0048812,GO:0006474,GO:0046331,GO:0005504,GO:0007064,GO:0007067,GO:0004596	CG12352-PA						PF00583	PS51186			G3DSA:3.40.630.30	SSF55729									
aly5729.9	Hormone-sensitive lipase	GO:0005737,GO:0016787,GO:0006642,GO:0033878,GO:0005829,GO:0005811,GO:0019433,GO:0005739,GO:0016042,GO:0006361,GO:0005901,GO:0006363,GO:0042134,GO:0008152,GO:0004806,GO:0016298,GO:0005634,GO:0008203	CG11055-PB						PF07859,PF07859,PF06350				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474					UPA00256				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly573.1	Transmembrane protease serine 2	GO:0004252,GO:0070062,GO:0016540,GO:0005044,GO:0005887,GO:0005886,GO:0006508,GO:0046598,GO:0008236	n/a						PF00089				G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly5732.1	General odorant-binding protein 1	GO:0005549,GO:0050896,GO:0006810,GO:0007608	n/a			PIRSF015604	SM00708		PF01395		PR00484,PR00484,PR00484,PR00484,PR00484,PR00484		G3DSA:1.10.238.20	SSF47565									
aly5732.2	Tafazzin homolog	GO:0035965,GO:0006644,GO:0016021,GO:0032049,GO:0032048,GO:0005739,GO:0031966,GO:0032577,GO:0007291,GO:0016746,GO:0007007,GO:0007006,GO:0031224	CG8766-PA																				
aly5732.3	Tafazzin homolog	GO:0035965,GO:0006644,GO:0016021,GO:0032049,GO:0032048,GO:0005739,GO:0031966,GO:0032577,GO:0007291,GO:0016746,GO:0008152,GO:0007007,GO:0007006,GO:0031224	CG8766-PA				SM00563		PF01553		PR00979,PR00979,PR00979,PR00979,PR00979,PR00979			SSF69593									
aly5732.4	Enhancer of mRNA-decapping protein 3	GO:0000932,GO:0005875,GO:0003723	CG6311-PB							PS51512													
aly5732.5	Endoplasmic reticulum metallopeptidase 1	GO:0005783,GO:0016021,GO:0005789,GO:0006508,GO:0008233,GO:0046872,GO:0008237,GO:0001541	CG11961-PA						PF04389				G3DSA:3.40.630.10	SSF53187									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5732.6	Pachytene checkpoint protein 2 homolog	GO:0006302,GO:0017111,GO:0007283,GO:0007131,GO:0007130,GO:0048477,GO:0005524	CG31453-PA				SM00382		PF00004				G3DSA:3.40.50.300	SSF52540,SSF52540									
aly5732.7	Guanine nucleotide-binding protein subunit beta-5	GO:0043234,GO:0031682,GO:0051087,GO:0005834,GO:0044297,GO:0005829,GO:0032794,GO:0003924,GO:0007165,GO:0004871,GO:1901386,GO:0007186	CG10763-PA			PIRSF002394	SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50082,PS50082,PS50294,PS50082	PR00319,PR00319,PR00319,PR00319,PR00320,PR00320,PR00320	PS00678,PS00678,PS00678	G3DSA:2.130.10.10	SSF50978	47~81								
aly5732.8	Basigin	GO:0016020,GO:0016337,GO:0072661,GO:0007596,GO:0002080,GO:0050900,GO:0044281,GO:0007166,GO:0002121,GO:0005925,GO:0006090,GO:0048788,GO:0048786,GO:0005739,GO:0005886,GO:0046689,GO:0022617,GO:0042383,GO:0008594,GO:0051591,GO:0045214,GO:0005887,GO:0007286,GO:0051646,GO:0051647,GO:0043434,GO:0051643,GO:0070062,GO:0042470,GO:0042475,GO:0007566,GO:0045121,GO:0044237,GO:0000139,GO:0030198,GO:0046697,GO:0005537	CG31605-PG				SM00409,SM00409,SM00408,SM00408		PF13927,PF07679	PS50835,PS50835		PS00290	G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly5732.9	Unknown		n/a																				
aly57373.1	Unknown		CG1105-PA				SM01017		PF02752,PF00339					SSF81296									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly57391.1	Unknown		n/a												67~104								
aly5745.1	Pancreatic lipase-related protein 2	GO:0009395,GO:0009791,GO:0047714,GO:0032094,GO:0005615,GO:0033993,GO:0008970,GO:0052689,GO:0016042,GO:0005575,GO:0042589,GO:0051384,GO:0005509,GO:0019376,GO:0004806,GO:0004620,GO:0016298,GO:0043434,GO:0047372	CG6283-PA						PF00151		PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly5745.2	Pancreatic lipase-related protein 2	GO:0009395,GO:0047714,GO:0004806,GO:0005615,GO:0008970,GO:0016042,GO:0005575,GO:0005509,GO:0019376,GO:0022008,GO:0016298,GO:0004620,GO:0047372	CG6277-PA						PF00151		PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly5745.3	Pancreatic lipase-related protein 2	GO:0009395,GO:0047714,GO:0004806,GO:0005615,GO:0008970,GO:0016042,GO:0005575,GO:0005509,GO:0019376,GO:0004620,GO:0016298,GO:0047372	CG6271-PA						PF00151		PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly5745.4	Pancreatic lipase-related protein 2	GO:0009395,GO:0009791,GO:0047714,GO:0032094,GO:0005615,GO:0033993,GO:0008970,GO:0016042,GO:0005575,GO:0042589,GO:0051384,GO:0005509,GO:0019376,GO:0004806,GO:0004620,GO:0016298,GO:0043434,GO:0047372	CG6283-PA						PF00151		PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly5745.5	Sodium-coupled monocarboxylate transporter 1	GO:0016020,GO:0008507,GO:0070062,GO:0015293,GO:0016324,GO:0016021,GO:0006915,GO:0006814,GO:0006810,GO:0005886,GO:0006811,GO:0055085	CG9657-PA					TIGR00813	PF00474	PS50283													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5745.6	Sodium-coupled monocarboxylate transporter 1	GO:0016020,GO:0008507,GO:0070062,GO:0015293,GO:0016324,GO:0016021,GO:0006915,GO:0006814,GO:0006810,GO:0005886,GO:0006811,GO:0055085	CG6723-PA					TIGR00813	PF00474	PS50283													
aly5745.7	Exosome complex component RRP42	GO:0005737,GO:0090503,GO:0000178,GO:0000288,GO:0005730,GO:0005634,GO:0000176,GO:0000175,GO:0006364,GO:0010467,GO:0003723,GO:0005652,GO:0006401,GO:0022008,GO:0043928,GO:0005829,GO:0006397	CG8395-PA						PF01138					SSF54211			REACT_21257						
aly5745.8	Unknown	GO:0005549	n/a						PF01395				G3DSA:1.10.238.20	SSF47565									
aly5746.1	Unknown		n/a						PF05585														
aly5746.2	Unknown		n/a																				
aly5746.3	Unknown		n/a												119~139								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly57581.1	Unknown		n/a																				
aly57581.2	Unknown		n/a																				
aly5762.1	Unknown		n/a																				
aly5762.2	Unknown		n/a																				
aly57688.1	DNA-directed RNA polymerase III subunit RPC1	GO:0006383,GO:0005634,GO:0005666,GO:0008270,GO:0032549,GO:0003899,GO:0003677,GO:0006351	CG17209-PC						PF04998					SSF64484		00240+2.7.7.6,00230+2.7.7.6	REACT_1788						
aly5769.1	Putative inorganic phosphate cotransporter	GO:0015293,GO:0016021,GO:0006817,GO:0015114,GO:0005316,GO:0022857,GO:0006820,GO:0005886,GO:0006814,GO:0055085	CG15094-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5769.2	Putative inorganic phosphate cotransporter	GO:0015293,GO:0016021,GO:0006814,GO:0015114,GO:0005316,GO:0055085	CG8791-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly5769.3	Putative inorganic phosphate cotransporter	GO:0015293,GO:0016021,GO:0006820,GO:0005316,GO:0022857,GO:0015114,GO:0005886,GO:0006814,GO:0055085	CG15096-PA						PF07690,PF07690	PS50850,PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly5769.4	Putative inorganic phosphate cotransporter	GO:0015293,GO:0016021,GO:0006814,GO:0015114,GO:0005316,GO:0055085	CG15096-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly5769.5	Putative inorganic phosphate cotransporter	GO:0015293,GO:0016021,GO:0006820,GO:0005316,GO:0022857,GO:0015114,GO:0005886,GO:0006814,GO:0055085	CG15096-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly5769.6	Putative inorganic phosphate cotransporter	GO:0015293,GO:0016021,GO:0006820,GO:0005316,GO:0022857,GO:0015114,GO:0005886,GO:0006814,GO:0055085	CG15096-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly5769.7	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly577.1	Unknown		n/a																				
aly577.10	Unknown	GO:0005615	CG11854-PB				SM00700		PF06585														
aly577.11	Neurogenic locus protein delta	GO:0016318,GO:0016330,GO:0007498,GO:0030720,GO:0008586,GO:0030707,GO:0030139,GO:0007419,GO:0045465,GO:0030718,GO:0007474,GO:0048190,GO:0007298,GO:0008356,GO:0007417,GO:0007219,GO:0031410,GO:0016021,GO:0035157,GO:0007476,GO:0007451,GO:0050768,GO:0007475,GO:0048800,GO:0005509,GO:0045468,GO:0048477,GO:0005112,GO:0008284,GO:0048749,GO:0035155,GO:0007480,GO:0042067,GO:0009986,GO:0042676,GO:0046331,GO:0005912,GO:0005886,GO:0007155,GO:0046667,GO:0036011,GO:0001736,GO:0008347,GO:0008407,GO:0007424,GO:0007015,GO:0045931,GO:0007399,GO:0007423,GO:0035003,GO:0007460,GO:0030713,GO:0007398,GO:0007464,GO:0048863,GO:0007314,GO:0005102,GO:0005768,GO:0001708,GO:0007422	CG3619-PA				SM00179,SM00179,SM00179,SM00179,SM00179,SM00179,SM00051,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181		PF07657,PF01414,PF00008,PF00008,PF00008,PF00008,PF00008,PF00008,PF12661	PS50026,PS50026,PS50026,PS50026,PS50026,PS51051,PS50026,PS50026,PS50026		PS01187,PS01186,PS00022,PS01186,PS00022,PS00022,PS01186,PS00022,PS01186,PS00022,PS00022,PS01186,PS01186,PS01186,PS01186,PS00010,PS00022,PS00022,PS01186,PS00022	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.170.300.10,G3DSA:2.10.25.10	SSF57184,SSF57184,SSF57196			REACT_299							
aly577.12	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly577.13	Serine-arginine protein 55	GO:0016607,GO:0035062,GO:0000381,GO:0005515,GO:0071011,GO:0005634,GO:0000398,GO:0000166,GO:0006376,GO:0005700,GO:0003676,GO:0048024,GO:0035327,GO:0007067,GO:0071013,GO:0003729	CG10851-PM				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly577.14	Unknown	GO:0005811,GO:0042051,GO:0006869,GO:0060361,GO:0035149,GO:0061024,GO:0030286,GO:0001745,GO:0005737,GO:0042623,GO:0031887,GO:0016021,GO:0005635,GO:0003779,GO:0048471,GO:0035239,GO:0005881,GO:0007523,GO:0051640,GO:0040011,GO:0007018,GO:0005515,GO:0007097	CG17046-PE						PF10541	PS51049					326~346,1066~1086,1245~1272								
aly577.15	Unknown	GO:0005811,GO:0042051,GO:0006869,GO:0060361,GO:0035149,GO:0061024,GO:0030286,GO:0001745,GO:0005737,GO:0042623,GO:0031887,GO:0016021,GO:0005635,GO:0003779,GO:0048471,GO:0035239,GO:0005881,GO:0007523,GO:0051640,GO:0040011,GO:0007018,GO:0005515,GO:0007097	CG17046-PE											SSF46966									
aly577.16	39S ribosomal protein L19, mitochondrial	GO:0003735,GO:0005622,GO:0006412,GO:0005762,GO:0005840	CG8039-PA						PF01245		PR00061,PR00061			SSF50104									
aly577.17	Short coiled-coil protein homolog	GO:0005829,GO:0000139	CG5934-PA						PF10224						73~107								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly577.18	Unknown		n/a																				
aly577.19	Transcription initiation factor TFIID subunit 12	GO:0000124,GO:0001129,GO:0051123,GO:0006367,GO:0001075,GO:0005634,GO:0006355,GO:0006352,GO:0005669,GO:0022008,GO:0046982,GO:0008134,GO:0042803	CG17358-PB						PF03847				G3DSA:1.10.20.10	SSF47113									
aly577.2	Repetin	GO:0005509,GO:0001533,GO:0005578	n/a																				
aly577.20	Unknown	GO:0005721,GO:0005719,GO:0010369,GO:0000792,GO:0042752,GO:0007076,GO:0048542,GO:0003682,GO:0005694,GO:0000775	CG18608-PA						PF13873														
aly577.21	Nuclear RNA export factor 1	GO:0005737,GO:0030534,GO:0016973,GO:0051168,GO:0007616,GO:0005634,GO:0005635,GO:0031965,GO:0000166,GO:0005654,GO:0003723,GO:0006378,GO:0006406	CG1664-PA							PS50177			G3DSA:3.10.450.50,G3DSA:3.80.10.10	SSF54427,SSF52058									
aly577.22	Peptidyl-prolyl cis-trans isomerase FKBP2	GO:0006457,GO:0018208,GO:0016020,GO:0005789,GO:0005528,GO:0003755	CG14715-PA						PF00254	PS50059			G3DSA:3.10.50.40	SSF54534									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly577.23	Alpha-1,3/1,6-mannosyltransferase ALG2	GO:0005811,GO:0048306,GO:0005789,GO:0005737,GO:0044267,GO:0006488,GO:0016021,GO:0016020,GO:0048471,GO:0033164,GO:0018279,GO:0043687,GO:0051592,GO:0009058,GO:0000033,GO:0004376,GO:0047485,GO:0004378,GO:0097502,GO:0033577,GO:0046982,GO:0005634	CG1291-PA						PF00534,PF13439				G3DSA:3.40.50.2000	SSF53756										
aly577.24	Activating signal cointegrator 1 complex subunit 3	GO:0006307,GO:0005794,GO:0016020,GO:0043140,GO:0008026,GO:0030532,GO:0032508,GO:0008283,GO:0044822,GO:0000398,GO:0004386,GO:0006355,GO:0003724,GO:0006351,GO:0003676,GO:0005634,GO:0005682,GO:0005524	CG5205-PA			PIRSF039073	SM00382,SM00382,SM00611,SM00611,SM00490,SM00490,SM00973,SM00973,SM00487,SM00487		PF02889,PF02889,PF00270,PF00270,PF00271,PF00271,	PS51194,PS51192,PS51194,PS51192			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:2.60.40.150,G3DSA:1.10.3380.10,G3DSA:1.10.3380.10	SSF52540,SSF46785,SSF158702,SSF81296,SSF46785,SSF158702,SSF52540,SSF52540,SSF52540									
aly577.25	Synaptobrevin	GO:0008021,GO:0006906,GO:0043195,GO:0016192,GO:0016081,GO:0016021,GO:0048786,GO:0031201,GO:0007268,GO:0005887,GO:0043005,GO:0005515,GO:0005886,GO:0007269,GO:0005484,GO:0030672,GO:0000149,GO:0030054	CG17248-PJ						PF00957	PS50892	PR00219,PR00219	PS00417	G3DSA:1.20.5.110	SSF58038	46~66								
aly577.26	Unknown		n/a																				
aly577.27	Unknown		CG13314-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly577.28	Unknown		n/a										G3DSA:3.30.60.30										
aly577.29	Unknown		n/a																				
aly577.3	Rho guanine nucleotide exchange factor 17	GO:0005089,GO:0043065,GO:0043547,GO:0051056,GO:0005085,GO:0005829,GO:0097190,GO:0030036,GO:0005575,GO:0035025,GO:0048011,GO:0007264	CG43102-PC				SM00325		PF00621	PS50010			G3DSA:1.20.900.10,G3DSA:2.130.10.10,G3DSA:2.30.29.30,G3DSA:2.30.29.30	SSF50729,SSF101898,SSF48065	1592~1619,521~541,1650~1650,865~909								
aly577.30	Neuronal PAS domain-containing protein 4	GO:0035147,GO:0007424,GO:0007427,GO:0005667,GO:0043565,GO:0003700,GO:0005634,GO:0071386,GO:0001077,GO:0006355,GO:0006357,GO:0045944,GO:0007165,GO:0004871,GO:0006366,GO:0060080,GO:0043234,GO:0046983,GO:0046982,GO:0000978	CG32474-PD				SM00091,SM00091		PF14598	PS50888,PS50112			G3DSA:3.30.450.20,G3DSA:3.30.450.20,G3DSA:4.10.280.10	SSF55785,SSF55785									
aly577.31	Unknown		n/a										G3DSA:3.30.60.30										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly577.32	Synaptobrevin	GO:0008021,GO:0006906,GO:0043195,GO:0016192,GO:0016081,GO:0016021,GO:0048786,GO:0031201,GO:0007268,GO:0005887,GO:0043005,GO:0005515,GO:0005886,GO:0007269,GO:0005484,GO:0030672,GO:0000149,GO:0030054	CG17248-PJ						PF00957	PS50892	PR00219,PR00219	PS00417	G3DSA:1.20.5.110	SSF58038	72~99								
aly577.33	Neuronal PAS domain-containing protein 4	GO:0035147,GO:0007424,GO:0007427,GO:0005667,GO:0043565,GO:0003700,GO:0005634,GO:0071386,GO:0001077,GO:0006355,GO:0006357,GO:0045944,GO:0007165,GO:0004871,GO:0006366,GO:0060080,GO:0043234,GO:0000978,GO:0046982	CG32474-PD				SM00091,SM00091		PF14598	PS50888,PS50112			G3DSA:3.30.450.20,G3DSA:3.30.450.20	SSF55785,SSF55785									
aly577.34	Mediator of RNA polymerase II transcription subunit 24	GO:0007517,GO:0006919,GO:0035209,GO:0005634,GO:0035070,GO:0048813,GO:0001104,GO:0006355,GO:0043067,GO:0006351,GO:0006367,GO:0006366,GO:0016592,GO:0043068	CG7999-PA						PF11277														
aly577.35	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A	GO:0030488,GO:0005634,GO:0046331,GO:0016429,GO:0031515	CG14544-PA			PIRSF017269			PF08704	PS51620			G3DSA:3.10.330.20,G3DSA:3.40.50.150,G3DSA:3.40.50.150	SSF53335				PWY-6829					
aly577.36	HEAT repeat-containing protein 5A	GO:0022008	CG2747-PF										G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371	1303~1327								
aly577.37	Cell differentiation protein RCD1 homolog	GO:0033147,GO:0006351,GO:0019221,GO:0005634,GO:0016020,GO:0000932,GO:2000327,GO:0006355,GO:0030014,GO:0003674,GO:0005488,GO:0017148,GO:0006417,GO:0006402,GO:0031047	CG14213-PB						PF04078				G3DSA:1.25.10.10	SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly577.38	Putative glutathione-specific gamma-glutamylcyclotransferase 2	GO:0005575,GO:0003674,GO:0008150,GO:0016746	CG2540-PA						PF04752				G3DSA:3.10.490.10	SSF110857									
aly577.39	Unknown		n/a																				
aly577.4	Unknown		CG7713-PA																				
aly577.40	RalA-binding protein 1	GO:0016020,GO:0017160,GO:0005096,GO:0006898,GO:0046578,GO:0005622,GO:0032321,GO:0030675,GO:0007165,GO:0005515,GO:0007275,GO:0043547	CG11622-PA				SM00324		PF00620	PS50238			G3DSA:1.10.555.10	SSF48350	450~470,213~233		REACT_11044						
aly577.41	RalA-binding protein 1	GO:0016020,GO:0017160,GO:0005096,GO:0006898,GO:0046578,GO:0005622,GO:0032321,GO:0030675,GO:0007165,GO:0005515,GO:0007275,GO:0043547	CG11622-PA																				
aly577.42	Golgin subfamily A member 5	GO:0005794,GO:0007030,GO:0048193,GO:0016021,GO:0031985,GO:0017137,GO:0000139,GO:0042803	CG17785-PA											SSF90257	149~204,430~450,234~310,335~397,493~513								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly577.43	Uncharacterized serpin-like protein MM_2675	GO:0035011,GO:0005615,GO:0048149,GO:0009950,GO:0002213,GO:0004867,GO:0009611,GO:0050832,GO:0005576,GO:0035006,GO:0008063,GO:0010951,GO:0004857,GO:0035009,GO:0045861	CG11331-PA				SM00093		PF00079			PS00284	G3DSA:2.30.39.10,G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574										
aly577.44	Serpin B9	GO:0016020,GO:0004867,GO:0010628,GO:0005737,GO:0042270,GO:0005615,GO:0005634,GO:0002784,GO:0043066,GO:0002020,GO:0043027,GO:0009617,GO:0071391,GO:0033668,GO:0032504,GO:0006915,GO:0002448,GO:0030162,GO:0006955,GO:0010951,GO:0070062,GO:0050832,GO:0005829,GO:0005622,GO:0043154,GO:0045861	CG9456-PB				SM00093		PF00079			PS00284	G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:2.30.39.10,G3DSA:2.30.39.10	SSF56574										
aly577.45	Serpin B6	GO:0005737,GO:0043234,GO:0005615,GO:0032504,GO:0007605,GO:0071470,GO:0008406,GO:0005622,GO:0030162,GO:0002020,GO:0004867,GO:0010951,GO:0070062	CG1342-PA				SM00093		PF00079,PF00079				G3DSA:2.30.39.10,G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574,SSF56574										
aly577.46	G2/mitotic-specific cyclin-2	GO:0005737,GO:0005819,GO:0035308,GO:0000086,GO:0005634,GO:0005816,GO:0016538,GO:0032888,GO:0005935,GO:0007067,GO:0010696,GO:0000079,GO:0051301	n/a				SM00385		PF00134				G3DSA:1.10.472.10	SSF47954										
aly577.47	Serpin B9	GO:0009617,GO:0004867,GO:0010628,GO:0005737,GO:0042270,GO:0005615,GO:0005634,GO:0016020,GO:0043066,GO:0002020,GO:0043027,GO:0006915,GO:0033668,GO:0071391,GO:0002448,GO:0030162,GO:0006955,GO:0010951,GO:0070062,GO:0005829,GO:0005622,GO:0005575,GO:0043154,GO:0045861	CG10913-PA				SM00093		PF00079				G3DSA:2.30.39.10,G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly577.48	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0022857,GO:0005886,GO:0055085	CG4797-PB						PF00083	PS50850		PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly577.49	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG4797-PB						PF00083	PS50850		PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly577.5	Protein trachealess	GO:0072175,GO:0001077,GO:0007165,GO:0004871,GO:0043565,GO:0007435,GO:0007431,GO:0005634,GO:0006366,GO:0000981,GO:0007425,GO:0046331,GO:0035277,GO:0007443,GO:0007424,GO:0003700,GO:0006355,GO:0048813,GO:0006357,GO:0045944,GO:0046983,GO:0046982	CG42865-PD				SM00353,SM00086,SM00091,SM00091	TIGR00229	PF00989,PF08447	PS50888,PS50112,PS50112			G3DSA:3.30.450.20,G3DSA:3.30.450.20	SSF55785,SSF47459,SSF55785									
aly577.50	D-tyrosyl-tRNA(Tyr) deacylase 1	GO:0005737,GO:0006450,GO:0019478,GO:0051500,GO:0005634,GO:0016788,GO:0006399,GO:0006260,GO:0002161,GO:0003677,GO:0046872	CG18643-PB					TIGR00256	PF02580				G3DSA:3.50.80.10	SSF69500									
aly577.51	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly577.52	Inhibitor of growth protein 1	GO:0070822,GO:0035064,GO:0008285,GO:0005634,GO:0006606,GO:0008270,GO:0010941,GO:0016568,GO:0007049,GO:0045893	CG7379-PA				SM00249		PF12998	PS50016		PS01359	G3DSA:3.30.40.10	SSF57903	336~350								
aly577.53	Ras association domain-containing protein 8	GO:0048749,GO:0033227,GO:0040015,GO:0007165,GO:0005912	CG5053-PA				SM00314		PF00788	PS50200				SSF54236	356~376,257~284,316~336,384~418								
aly577.54	Histone-lysine N-methyltransferase trithorax	GO:0008023,GO:0051568,GO:0008270,GO:0003677,GO:0007411,GO:0032968,GO:0005875,GO:0008354,GO:0043565,GO:0005634,GO:0007275,GO:0016571,GO:0042800,GO:0043966,GO:0048096,GO:0008157,GO:2001020,GO:0044212,GO:0003700,GO:0005700,GO:0035097,GO:0006351,GO:0003682,GO:0044665	CG8651-PD				SM00542,SM00317,SM00508		PF05965,PF00856	PS50868,PS51543,PS50280			G3DSA:2.170.270.10	SSF82199	928~948	00310+2.1.1.43							
aly577.55	Histone-lysine N-methyltransferase trithorax	GO:0008023,GO:0051568,GO:0008270,GO:0003677,GO:0007411,GO:0032968,GO:0005875,GO:0008354,GO:0043565,GO:0005634,GO:0007275,GO:0016571,GO:0042800,GO:0043966,GO:0048096,GO:0008157,GO:2001020,GO:0044212,GO:0003700,GO:0005700,GO:0035097,GO:0006351,GO:0003682,GO:0044665	CG8651-PD				SM00249,SM00249,SM00541		PF13771,PF05964	PS50016,PS51542,PS51030			G3DSA:3.30.40.10	SSF57903	49~70,626~646		REACT_71						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly577.56	Unknown		n/a												67~101								
aly577.57	RNA exonuclease 1 homolog	GO:0005654,GO:0004527,GO:0046872,GO:0003676	CG12877-PC				SM00479		PF15870	PS50103			G3DSA:3.30.420.10	SSF53098									
aly577.58	Ubiquitin-conjugating enzyme E2-17 kDa	GO:0032436,GO:1902166,GO:0061630,GO:0000209,GO:0005737,GO:0043161,GO:0005634,GO:0033503,GO:0016574,GO:0043066,GO:0042787,GO:0005524,GO:0051299,GO:0006281,GO:0051297,GO:0000790,GO:0004842,GO:0043518,GO:0016874,GO:0061631,GO:0031625,GO:0000422,GO:0007052,GO:0032456,GO:0002039,GO:0019904	CG2013-PC				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495	127~147				UPA00143				
aly577.59	Coiled-coil domain-containing protein 174		CG7183-PA						PF13300						16~36,252~292,317~355								
aly577.6	Uncharacterized oxidoreductase TM_0325	GO:0008152,GO:0016491	CG31549-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly577.60	Unknown		n/a																				
aly577.61	Unknown		n/a							PS50017			G3DSA:1.10.533.10	SSF47986									
aly577.7	Tubulin polyglutamylase TTLL4	GO:0005737,GO:0005856,GO:0015631,GO:0018095,GO:0042060,GO:0006464,GO:0005929,GO:0016874,GO:0004835	CG16833-PD						PF03133	PS51221			G3DSA:3.30.470.20	SSF56059,SSF56059									
aly577.8	Zinc finger MYM-type protein 3	GO:0043234,GO:0022604,GO:0007010,GO:0006697,GO:0016233,GO:0005634,GO:0005705,GO:0000792,GO:0006355,GO:0000791,GO:0006357,GO:0008270,GO:0005515,GO:0035012,GO:0022008,GO:0003682,GO:0003677	CG5965-PB				SM00746,SM00746,SM00746,SM00746,SM00746,SM00746,SM00746,SM00746		PF12012						269~296,135~155									
aly577.9	Putative DNA helicase Ino80	GO:0006310,GO:0006338,GO:0006281,GO:0005634,GO:0003677,GO:0031011,GO:0016817,GO:0005700,GO:0004386,GO:0000790,GO:0045892,GO:0006351,GO:0016887,GO:0000975,GO:0003678,GO:0032508,GO:0010468,GO:0005524,GO:0040034	CG31212-PA				SM00487,SM00490		PF13892,PF00271,PF00176	PS51192,PS51413,PS51194			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	260~280,285~305									
aly5770.1	Orexin receptor type 1	GO:0017046,GO:0008528,GO:0004930,GO:0042277,GO:0007631,GO:0007268,GO:0016021,GO:0016499,GO:0007218,GO:0004983,GO:0032870,GO:0045187,GO:1901652,GO:0005887,GO:0008188,GO:0008340,GO:0007186	CG10823-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR01064,PR01064,PR01064	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly57723.1	Semaphorin-1A	GO:0031987,GO:0045792,GO:0030215,GO:0048854,GO:0016021,GO:0005886,GO:0048813,GO:0008039,GO:0001964,GO:0016199,GO:0005515,GO:0008045,GO:0007411,GO:2000305,GO:0008201,GO:0007416,GO:0004872	CG18405-PG				SM00423		PF01403,PF01437	PS51004			G3DSA:3.30.1680.10,G3DSA:2.130.10.10	SSF101912,SSF103575									
aly5773.1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	GO:0007015,GO:0055059,GO:0045176,GO:0004871,GO:0005834,GO:0003924,GO:0061343,GO:0005515,GO:0005886,GO:0007186,GO:0005875	CG10545-PB			PIRSF002394	SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50082,PS50082,PS50082,PS50294	PR00319,PR00319,PR00319,PR00319,PR00319,PR00320,PR00320,PR00320	PS00678,PS00678,PS00678	G3DSA:2.130.10.10	SSF50978	4~24								
aly5773.2	Unknown		CG1674-PL																				
aly5773.3	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850	PR00171,PR00171,PR00171		G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						
aly5773.4	Heat shock protein 68	GO:0031427,GO:0006457,GO:0005215,GO:0016021,GO:0005811,GO:0051082,GO:0005875,GO:0005739,GO:0042594,GO:0009408,GO:0008340,GO:0022008,GO:0055085,GO:0005524	CG5436-PA						PF00083,PF00012	PS50850		PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:2.60.34.10,G3DSA:1.20.1270.10	SSF100934,SSF103473,SSF103473,SSF100920	106~126,171~191								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5773.5	Heat shock protein 83	GO:0009631,GO:0006457,GO:0006950,GO:0005737,GO:0042623,GO:0005813,GO:0005811,GO:0051082,GO:0010529,GO:0048471,GO:0048477,GO:0005524,GO:0008285,GO:0019094,GO:0008595,GO:0007283,GO:0045187,GO:0009408,GO:0007015,GO:0005705,GO:0007465,GO:0007052,GO:0008360,GO:0007098,GO:0008293	CG1242-PB	MF_00505		PIRSF002583	SM00387		PF02518,PF00183		PR00775,PR00775,PR00775,PR00775,PR00775,PR00775,PR00775	PS00298	G3DSA:3.30.565.10,G3DSA:3.30.565.10	SSF110942,SSF55874,SSF54211	216~240								
aly5773.6	Protein lethal(2)essential for life	GO:0006497,GO:0009790,GO:0010998,GO:0009408,GO:0010506,GO:0007275	CG4533-PA			PIRSF036514			PF00011	PS01031	PR00299,PR00299,PR00299,PR00299,PR00299,PR00299,PR00299		G3DSA:2.60.40.790	SSF49764									
aly5773.7	Phospholipid scramblase 2	GO:0017128,GO:0017121,GO:0016021,GO:0005886,GO:0048812,GO:0007268,GO:0046872	CG32056-PA						PF03803					SSF54518									
aly57735.1	Unknown	GO:0005319,GO:0005615,GO:0006869,GO:0015026,GO:0036122,GO:0043395,GO:0007474,GO:0030513	CG31150-PA										G3DSA:1.25.10.20	SSF48431			REACT_22258						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5787.1	Homeobox protein invected	GO:0035224,GO:0007485,GO:0001158,GO:0035288,GO:0035289,GO:0010629,GO:0048100,GO:0007386,GO:0003677,GO:0007411,GO:0001078,GO:0007275,GO:0007417,GO:0007388,GO:0043565,GO:0007367,GO:0000122,GO:0005634,GO:0008406,GO:0007474,GO:0035290,GO:0010468,GO:0000980,GO:0007487,GO:0007486,GO:0035215,GO:0048099,GO:0045892,GO:0035277,GO:0007400,GO:0007418,GO:0007447,GO:0003700,GO:0007448,GO:0021960,GO:0006355	CG9015-PB				SM00389		PF10525,PF00046	PS50071	PR00031,PR00031,PR00024,PR00024,PR00024,PR00026,PR00026	PS00033,PS00027	G3DSA:1.10.10.60	SSF46689	99~119								
aly5788.1	S-phase kinase associated protein 2	GO:0000086,GO:0000082,GO:0035220,GO:0016235,GO:0042981,GO:0000209,GO:0005737,GO:0045787,GO:0005730,GO:0005634,GO:0048661,GO:1902916,GO:0005654,GO:0042802,GO:0048749,GO:0000278,GO:0008283,GO:0033148,GO:0031145,GO:0061630,GO:0007113,GO:0051726,GO:0005829,GO:0031647,GO:0006511,GO:0071460,GO:0019005	CG9772-PA				SM00367,SM00367,SM00367,SM00367,SM00367		PF00646	PS50181			G3DSA:3.80.10.10	SSF52047,SSF81383									
aly5788.2	Unknown	GO:0003676	CG31301-PA						PF11952														
aly5788.3	Unknown		n/a												220~240								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly57941.1	Unknown		n/a																				
aly57941.2	Unknown		n/a											SSF53098	270~290								
aly57941.3	Unknown		n/a																				
aly57941.4	Zinc finger protein 846	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0022008,GO:0046872,GO:0006351	CG7386-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12171	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667	58~78								
aly5795.1	Unknown		n/a										G3DSA:3.60.10.10	SSF56219									
aly5795.2	ATP-dependent DNA helicase PIF1	GO:0000723,GO:0006310,GO:0000002,GO:0006281,GO:0005634,GO:0003677,GO:0005739,GO:0043141,GO:0003678,GO:0005524	CG3238-PA				SM00382		PF05970				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5795.3	Unknown		n/a																				
aly58.1	Vacuolar protein sorting associated protein 53 homolog	GO:0042147,GO:0000938,GO:0055037,GO:0032456,GO:0015031,GO:1990745,GO:0010008	CG3338-PA						PF04100						112~139								
aly58.10	Talin-2	GO:0005200,GO:0006909,GO:0015629,GO:0060439,GO:0035160,GO:0007043,GO:0045202,GO:0007298,GO:0005925,GO:0005737,GO:0001726,GO:0007430,GO:0007475,GO:0003779,GO:0016203,GO:0005178,GO:0005198,GO:0005158,GO:0005916,GO:0008360,GO:0045892,GO:0005911,GO:0005886,GO:0007155,GO:0007526,GO:0007016,GO:0005515	CG6831-PB				SM00295		PF09379,PF01608,PF09141,PF00373,PF02174,PF16511	PS50057			G3DSA:1.20.1420.10,G3DSA:2.30.29.30,G3DSA:1.20.1440.10,G3DSA:1.20.80.10	SSF109880,SSF50729,SSF47031,SSF109885	779~799,1019~1046								
aly58.11	Unknown		n/a																				
aly58.2	Polypeptide N acetylgalactosaminyltransferase 1	GO:0005795,GO:0046872,GO:0006486,GO:0016021,GO:0004653,GO:0030246,GO:0000139,GO:0009312	CG8182-PA				SM00458		PF00652,PF00535,PF00535	PS50231			G3DSA:3.90.550.10,G3DSA:3.90.550.10,G3DSA:3.90.550.10,G3DSA:2.80.10.50	SSF50370,SSF53448,SSF53448									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly58.3	Protein ERGIC-53	GO:0005794,GO:0007030,GO:0016021,GO:0006888,GO:0070062,GO:0005793,GO:0030017,GO:0007029,GO:0010638,GO:0044220,GO:0016020,GO:0033116,GO:0030246,GO:0000139,GO:0046872,GO:0015031,GO:0005789,GO:0030134,GO:0005537	CG6822-PA						PF03388	PS51328			G3DSA:2.60.120.200	SSF49899	211~238								
aly58.4	Protein ERGIC-53	GO:0005794,GO:0006888,GO:0005783,GO:0005793,GO:0016021,GO:0016020,GO:0033116,GO:0000139,GO:0042802,GO:0005509,GO:0015031,GO:0005789,GO:0005537,GO:0043231	CG6822-PA																				
aly58.5	Aldo-keto reductase AKR2E4	GO:0004032,GO:0008202,GO:0006081,GO:0055114,GO:0016491	CG10638-PA			PIRSF000097			PF00248		PR00069,PR00069,PR00069,PR00069,PR00069	PS00062,PS00798	G3DSA:3.20.20.100	SSF51430									
aly58.6	Aldo-keto reductase AKR2E4	GO:0004032,GO:0008202,GO:0055114,GO:0016491	CG12766-PA			PIRSF000097			PF00248		PR00069,PR00069,PR00069,PR00069,PR00069	PS00798,PS00062	G3DSA:3.20.20.100	SSF51430									
aly58.7	Aldo-keto reductase AKR2E4	GO:0004032,GO:0008202,GO:0006081,GO:0055114,GO:0016491	CG10638-PA			PIRSF000097			PF00248		PR00069,PR00069,PR00069,PR00069,PR00069	PS00798,PS00063,PS00062	G3DSA:3.20.20.100	SSF51430									
aly58.8	Unknown		n/a												230~257								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly58.9	Trypsin epsilon	GO:0004252,GO:0005615,GO:0006508	CG6457-PA				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly580.1	Pancreatic lipase-related protein 2	GO:0009395,GO:0047714,GO:0004806,GO:0005615,GO:0008970,GO:0016042,GO:0005575,GO:0005509,GO:0019376,GO:0022008,GO:0016298,GO:0004620,GO:0047372	CG6277-PA						PF00151		PR00821,PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly580.10	Unknown		n/a																				
aly580.11	PCNA-associated factor	GO:0051726,GO:0051297,GO:0019985,GO:0006974,GO:0009411,GO:0006260,GO:0048471,GO:0003682,GO:0005634	n/a						PF15715														
aly580.12	Catenin alpha	GO:0015629,GO:0034332,GO:0007293,GO:0060323,GO:0007163,GO:0030055,GO:0005737,GO:0030720,GO:0005198,GO:0003779,GO:0016342,GO:0060429,GO:0051015,GO:0005915,GO:0005914,GO:0005913,GO:0005912,GO:0005886,GO:0007155,GO:0007016,GO:0008092,GO:0045296,GO:0005515	CG17947-PA						PF01044		PR00805,PR00805,PR00805,PR00805		G3DSA:1.20.120.230,G3DSA:1.20.120.230	SSF47220,SSF47220									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly580.13	Bile salt-activated lipase	GO:0005737,GO:0005794,GO:0004771,GO:0005791,GO:0005615,GO:0043208,GO:0005829,GO:0045121,GO:0052689,GO:0016042,GO:0005575,GO:0032403,GO:0008150,GO:0008152,GO:0042588,GO:0004622,GO:0043234,GO:0042572,GO:0004806,GO:0050253,GO:0043231	CG10175-PD						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly580.14	Larval cuticle protein LCP-17	GO:0040003,GO:0005214,GO:0008011,GO:0008010,GO:0031012,GO:0042302	CG7673-PA						PF00379	PS51155													
aly580.15	Unknown		n/a																				
aly580.2	Zinc finger protein 236	GO:0005634,GO:0003677,GO:0006355,GO:0008270,GO:0003676,GO:0071333,GO:0046872,GO:0006351	CG8301-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60										
aly580.3	4-hydroxybenzoate polyprenyltransferase, mitochondrial	GO:0005736,GO:0004659,GO:0006360,GO:0016021,GO:0008412,GO:0002083,GO:0008299,GO:0050832,GO:0005743,GO:0050830,GO:0048009,GO:0047293,GO:0005666,GO:0050829,GO:0008340,GO:0006744,GO:0006743	CG9613-PA					TIGR01474	PF01040										UPA00232				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly580.4	Adult enhancer factor 1	GO:0031935,GO:0003700,GO:0005634,GO:0006355,GO:0048813,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG11352-PF				SM00355,SM00355			PS50157		PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667									
aly580.5	Unknown		n/a				SM00355,SM00355					PS00028,PS00028			518~538								
aly580.6	Ribonuclease H2 subunit C	GO:0005634,GO:0032299,GO:0005575,GO:0008150,GO:0006401,GO:0003674	CG30105-PA						PF08615														
aly580.7	Unknown		n/a																				
aly580.8	GTP-binding protein 2	GO:0003924,GO:0043231,GO:0005525	CG2017-PA						PF00009	PS51722			G3DSA:3.40.50.300,G3DSA:2.40.30.10	SSF50447,SSF52540,SSF52540	437~457								
aly580.9	Zinc finger protein 91	GO:0003700,GO:0005634,GO:0070895,GO:0045892,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG4707-PA				SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028		SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly581.1	Unknown		n/a																				
aly581.2	Viral cathepsin	GO:0003674,GO:0035071,GO:0035220,GO:0045169,GO:0005575,GO:0048102,GO:0004197,GO:0008150,GO:0004869,GO:0006508,GO:0008234,GO:0022416	CG12163-PA				SM00645		PF00112		PR00705,PR00705,PR00705	PS00639,PS00640	G3DSA:3.90.70.10	SSF54001									
aly581.3	Unknown		n/a																				
aly5811.1	Protein MON2 homolog	GO:0005794,GO:0016192,GO:0031532,GO:0005802,GO:0043547,GO:0005086,GO:0015031,GO:0005519,GO:0005768,GO:0007318	CG8683-PB						PF16206														
aly5811.2	Tubulin alpha chain	GO:0045298,GO:0051258,GO:0005200,GO:0019730,GO:0007017,GO:0005813,GO:0009987,GO:0003924,GO:0005737,GO:0007052,GO:0005819,GO:0000235,GO:0007094,GO:0006184,GO:0005874,GO:0005525	CG1913-PA				SM00864,SM00865		PF00091,PF03953		PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01162,PR01162,PR01162,PR011	PS00227	G3DSA:3.30.1330.20,G3DSA:1.10.287.600,G3DSA:3.40.50.1440	SSF55307,SSF52490	418~438									
aly5811.3	Unknown		CG8547-PE												136~156								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5811.4	Mediator of RNA polymerase II transcription subunit 26	GO:0006909,GO:0003700,GO:0005634,GO:0001104,GO:0006357,GO:0006351,GO:0006367,GO:0003677,GO:0016592	CG1793-PA				SM00509		PF08711	PS51319			G3DSA:1.20.930.10	SSF47676									
aly5829.1	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9512-PA						PF05199,PF05199,PF00732,PF00732			PS00624,PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF54373,SSF51905,SSF51905,SSF51905,SSF51905									
aly5831.1	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3	GO:0090141,GO:0005783,GO:0071260,GO:0090200,GO:0030425,GO:0097193,GO:1990144,GO:0048102,GO:0051020,GO:0010821,GO:0035694,GO:0008219,GO:0001666,GO:1903715,GO:1901998,GO:0043243,GO:0005737,GO:0005654,GO:0043653,GO:0016021,GO:0005635,GO:0005739,GO:0043065,GO:0043066,GO:0071456,GO:0043068,GO:0042802,GO:0042803,GO:0071279,GO:0008626,GO:2000378,GO:0006915,GO:0070301,GO:0050873,GO:0072593,GO:0031966,GO:0051402,GO:0046902,GO:0055093,GO:0097481,GO:0010637,GO:0051607,GO:0045837,GO:0031307,GO:0097345,GO:0005740,GO:0005741,GO:0046982,GO:0005634	n/a						PF06553														
aly58321.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5846.1	Unknown		n/a																				
aly5846.2	Unknown		n/a										G3DSA:3.60.10.10	SSF56219									
aly58463.1	Unknown	GO:0043234,GO:0003682,GO:0006357,GO:0005634,GO:0006355,GO:0000791,GO:0005515,GO:0003677,GO:0046872	CG8092-PC																				
aly5847.1	P protein	GO:0016020,GO:0005302,GO:0005215,GO:0016021,GO:0006810,GO:0033162,GO:0055085	CG12787-PC						PF03600						355~382								
aly5847.2	Sugar phosphate exchanger 2	GO:0005215,GO:0015169,GO:0008643,GO:0016021,GO:0055085	CG10069-PB			PIRSF002808			PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly5847.3	Putative tRNA pseudouridine synthase Pus10	GO:0008033,GO:0001522,GO:0003723,GO:0009982	CG3709-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5847.4	Sorting and assembly machinery component 50 homolog A	GO:0016021,GO:0019867,GO:0005741,GO:0008150,GO:0003674,GO:0001889	CG7639-PB																				
aly5864.1	Unknown		n/a																				
aly5864.2	Unknown	GO:0005575,GO:0008150,GO:0003674	CG32544-PA												186~216								
aly5864.3	Bleomycin hydrolase	GO:0005737,GO:0004177,GO:0070062,GO:0009636,GO:0042493,GO:0005654,GO:0004197,GO:0006508	CG1440-PD						PF03051			PS00139	G3DSA:3.90.70.10	SSF54001									
aly587.1	Unknown		n/a																				
aly587.10	Heterogeneous nuclear ribonucleoprotein A1	GO:0001745,GO:0043565,GO:0033119,GO:0000381,GO:0000166,GO:0005634,GO:0005703,GO:0030529,GO:0045727,GO:0003676,GO:0048027,GO:0048477,GO:0036099,GO:0003729	CG9983-PB				SM00360,SM00360		PF00076,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly587.11	Heterogeneous nuclear ribonucleoprotein A1, A2/B1 homolog	GO:0001745,GO:0043565,GO:0033119,GO:0000381,GO:0000166,GO:0005634,GO:0005703,GO:0030529,GO:0045727,GO:0003676,GO:0003723,GO:0048027,GO:0048477,GO:0036099,GO:0003729	CG9983-PB				SM00360,SM00360		PF00076,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									
aly587.12	Homeobox protein rough	GO:0048749,GO:0043565,GO:0050896,GO:0048054,GO:0003700,GO:0042067,GO:0005634,GO:0001012,GO:0007601,GO:0006355,GO:0045464,GO:0045944,GO:0007460,GO:0045680,GO:0007463	CG6348-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024,PR00031,PR00031	PS00027	G3DSA:1.10.10.60	SSF46689	95~115								
aly587.13	Unknown		n/a																				
aly587.14	Unknown		n/a																				
aly587.15	Mannose-6-phosphate isomerase	GO:0009298,GO:0005737,GO:0005975,GO:0004476,GO:0008270	CG8417-PA			PIRSF001480		TIGR00218	PF01238		PR00714,PR00714,PR00714,PR00714,PR00714,PR00714,PR00714,PR00714	PS00965,PS00966	G3DSA:2.60.120.10,G3DSA:1.10.441.10,G3DSA:1.10.441.10,G3DSA:2.60.120.10,G3DSA:2.60.120.10	SSF51182		00520+5.3.1.8,00051+5.3.1.8		PWY-882,PWY-7456,PWY-3881,PWY-5659,PWY-6992,PWY-3861,PWY-7586	UPA00126				
aly587.16	Chorion peroxidase	GO:0005615,GO:0020037,GO:0030707,GO:0006979,GO:0004666,GO:0001516,GO:0042744,GO:0007304,GO:0007306,GO:0042743,GO:0046872,GO:0004601,GO:0055114,GO:0005875	CG5873-PA						PF03098	PS50292	PR00457,PR00457,PR00457,PR00457,PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113	1450~1470,1228~1248								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly587.17	Prefoldin subunit 6	GO:0005737,GO:0051131,GO:0051087,GO:0016272,GO:0005634,GO:0006458,GO:0051082,GO:0006457,GO:0022008	CG7770-PA						PF01920				G3DSA:1.10.287.370	SSF46579	66~86,2~22,94~121,26~53								
aly587.18	Testin	GO:0005737,GO:0042127,GO:0015629,GO:0005938,GO:0001755,GO:0005925,GO:0008270	CG6522-PA				SM00132,SM00132,SM00132		PF06297,PF00412,PF00412,PF00412	PS50023,PS50023,PS51303,PS50023		PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716									
aly587.19	Ras-related C3 botulinum toxin substrate 1	GO:0016020,GO:0008152,GO:0008258,GO:0019901,GO:0030032,GO:0030036,GO:0051022,GO:0005622,GO:0005737,GO:0002009,GO:0007254,GO:0007435,GO:0016601,GO:0031410,GO:0002551,GO:0007390,GO:0045740,GO:0042067,GO:0042826,GO:0071260,GO:0005525,GO:0030334,GO:0006935,GO:0008283,GO:0051017,GO:0003924,GO:0017137,GO:0006974,GO:0042470,GO:0005886,GO:0007264,GO:0001737,GO:0045453,GO:0035099,GO:0007015,GO:0010592,GO:0048870,GO:0005829,GO:0007394,GO:0007391,GO:0000139,GO:0005575,GO:0071526,GO:0001934	CG5588-PB				SM00174,SM00173,SM00176,SM00175	TIGR00231	PF00071	PS51420	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly587.2	Tetraspanin-5	GO:0051604,GO:0008283,GO:0016021,GO:0045747,GO:0003674,GO:0005886,GO:0007155,GO:0007298,GO:0090002	CG9093-PB			PIRSF002419			PF00335		PR00259,PR00259,PR00259			SSF48652									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly587.20	Leucine-rich repeat protein soc-2 homolog	GO:0017016,GO:0000164,GO:0005515,GO:0046579	CG5407-PA				SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365		PF13855,PF13855,PF13855,PF13855,PF13306	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058										
aly587.21	Cleavage stimulation factor subunit 2	GO:0071920,GO:0005847,GO:0006397,GO:0005848,GO:0000166,GO:0003723,GO:0003676,GO:0022008,GO:0006379,GO:0003729	CG7697-PA				SM00360		PF00076,PF14304,PF14327	PS50102			G3DSA:3.30.70.330	SSF54928									
aly587.22	Protein CREG1	GO:0003714,GO:0040008,GO:0070062,GO:0000122,GO:0008134,GO:0008283,GO:1903507,GO:0006357,GO:0005667,GO:0010181,GO:0007275,GO:0055114,GO:0016491	CG5413-PA						PF13883				G3DSA:2.30.110.10	SSF50475									
aly587.23	Golgin-45	GO:0005794,GO:0007030,GO:0005796,GO:0005634,GO:0019899,GO:0000139,GO:0005654,GO:0043001,GO:0031625	CG9356-PA												190~210,150~184,253~273								
aly587.24	Glutaredoxin-3	GO:0046872,GO:0051536,GO:0005938,GO:0045454,GO:0009055,GO:0015035,GO:0015036	CG6523-PA					TIGR00365	PF00085,PF00462	PS51354			G3DSA:3.40.30.10,G3DSA:3.40.30.10	SSF52833,SSF52833									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly587.25	Probable prefoldin subunit 5	GO:0006457,GO:0016272,GO:0051082	CG7048-PB					TIGR00293	PF02996				G3DSA:1.10.287.370	SSF46579									
aly587.26	Homeotic protein proboscipedia	GO:0043565,GO:0003700,GO:0007381,GO:0005634,GO:0048728,GO:0006357,GO:0003677,GO:0007382	CG31481-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00032,PS00027	G3DSA:1.10.10.60	SSF46689									
aly587.27	Unknown		n/a											SSF50494									
aly587.28	Unknown		n/a																				
aly587.3	Transmembrane protease serine 11D	GO:0004252,GO:0070062,GO:0048812,GO:0005887,GO:0006508,GO:0008236	CG9372-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly587.4	Trypsin-7	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG4613-PB				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly587.5	Acyl-CoA desaturase 1	GO:0006633,GO:0006629,GO:0016717,GO:0016020,GO:0050872,GO:0050873,GO:0044130,GO:0032896,GO:0050830,GO:0030176,GO:0034435,GO:1903966,GO:0010873,GO:0004768,GO:0006723,GO:0055114,GO:0005783	CG5925-PA						PF00487		PR00075,PR00075,PR00075,PR00075,PR00075,PR00075													
aly587.6	Trypsin-7	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG4914-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly587.7	Proclotting enzyme	GO:0004252,GO:0005576,GO:0042381,GO:0006508	CG4914-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly587.8	Trypsin-7	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG4914-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly587.9	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005886,GO:0006508	CG11836-PI				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly5895.1	Kv channel-interacting protein 4	GO:0005737,GO:0005267,GO:0005244,GO:0005509,GO:0005886	CG44422-PA				SM00054,SM00054,SM00054		PF13499	PS50222,PS50222,PS50222	PR00450,PR00450,PR00450,PR00450,PR00450	PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5898.1	Unknown	GO:0006952,GO:0044564,GO:0003674,GO:0005615,GO:0032504	CG10433-PA							PS51345													
aly5898.2	Putative uncharacterized transposon-derived protein F52C9.6		n/a																				
aly59029.1	Protein bicaudal D	GO:0008103,GO:0030154,GO:0007293,GO:0007294,GO:0007309,GO:0051028,GO:0048488,GO:0005737,GO:0070727,GO:0045502,GO:0030727,GO:0030669,GO:0048477,GO:0005794,GO:0016325,GO:2000370,GO:0032050,GO:0017137,GO:0007314,GO:0007312,GO:0007310,GO:0030100,GO:0050658,GO:0005829,GO:0005856,GO:0008298,GO:0005515,GO:2000302,GO:0003729	CG6605-PD						PF09730				G3DSA:1.20.5.170		26~74								
aly5906.1	Unknown		n/a																				
aly5906.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly59093.1	Mini-chromosome maintenance complex-binding protein	GO:0005737,GO:0042555,GO:0005634,GO:0005654,GO:0008150,GO:0006261,GO:0005886,GO:0003674,GO:0007067,GO:0003682,GO:0051301,GO:0007062	CG3430-PA						PF09739														
aly5916.1	Unknown	GO:0048812,GO:0048190,GO:0005509	CG5890-PA																				
aly593.1	Pyrimidodiazepine synthase	GO:0005737,GO:0045174,GO:0004364,GO:0016782,GO:0006749,GO:0006728,GO:0004734,GO:0006726,GO:0005515,GO:0042803	CG6776-PA						PF13410,PF13417	PS50404,PS50405	PR01625,PR01625		G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF52833,SSF47616		00982+2.5.1.18,00053+1.8.5.1,00480+2.5.1.18+1.8.5.1,00980+2.5.1.18	REACT_11193,REACT_13433	PWY-6842,PWY-7112,PWY-6370,PWY-4061,PWY-7533,PWY-4202,PWY-2261					
aly593.2	Phosphatidate phosphatase PPAPDC1B	GO:0016311,GO:0016021,GO:0016020,GO:0046839,GO:0008195	CG12746-PB				SM00014		PF01569				G3DSA:1.20.144.10	SSF48317									
aly593.3	Putative Dol-P-Glc:Glc(2)Man(9)GlcNAc(2)-PP-Dol alpha-1,2-glucosyltransferase	GO:0005783,GO:0006486,GO:0006487,GO:0006488,GO:0016021,GO:0005789,GO:0046527,GO:0004576,GO:0004583	CG32076-PA			PIRSF028810			PF04922							00510+2.4.1.256	REACT_17015		UPA00378				
aly593.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly593.5	Unknown		n/a																				
aly59326.1	Lactosylceramide 1,3-N-acetyl-beta-D-glucosaminyltransferase	GO:0044267,GO:0008457,GO:0016266,GO:0047256,GO:0006486,GO:0016021,GO:0016020,GO:0009247,GO:0008039,GO:0000139,GO:0008378,GO:0008499,GO:0006493,GO:0005622,GO:0043687,GO:0007417	CG8668-PA						PF01762										UPA00378				
aly5933.1	2-(R)-hydroxypropyl-CoM dehydrogenase	GO:0050574,GO:0042208,GO:0008152,GO:0016491	CG31548-PA						PF00106		PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735	64~84,35~55								
aly5933.2	3-oxoacyl-[acyl-carrier-protein] reductase FabG	GO:0050661,GO:0051287,GO:0030497,GO:0004316,GO:0008152,GO:0016491	CG31548-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735	64~84,35~55								
aly5933.3	3-hydroxybutyrate dehydrogenase type 2	GO:0005737,GO:0042168,GO:0042541,GO:0016628,GO:0055072,GO:0003858,GO:0008152,GO:0019290,GO:0016491	CG31548-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									
aly594.1	DnaJ homolog subfamily B member 6	GO:0006457,GO:0005634,GO:0051082,GO:0005575,GO:0048471,GO:0030018	CG8448-PE				SM00271		PF00226	PS50076	PR00625,PR00625,PR00625,PR00625	PS00636	G3DSA:1.10.287.110	SSF46565	39~59								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly594.10	Nucleosome-remodeling factor subunit NURF301	GO:0035064,GO:0008270,GO:0003677,GO:0046426,GO:0042766,GO:0006325,GO:0045747,GO:0070577,GO:0045824,GO:0048515,GO:0010468,GO:0035076,GO:0035073,GO:0046331,GO:0007095,GO:0016922,GO:0006338,GO:0006334,GO:0016589,GO:0048813,GO:0006357,GO:0006351,GO:0005515,GO:0030097	CG32346-PH				SM00249,SM00249,SM00249,SM00297,SM00571		PF00439,PF00628,PF00628,PF00628,PF02791	PS50016,PS50014,PS50016,PS50827	PR00503,PR00503,PR00503,PR00503	PS01359,PS01359,PS00633,PS01359	G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:1.20.920.10,G3DSA:1.20.920.10	SSF47370,SSF57903,SSF57903,SSF57903	742~763,929~949,1501~1525									
aly594.11	Probable aminoacyl tRNA synthase complex-interacting multifunctional protein 2	GO:0005829,GO:0005634,GO:0006412	n/a										G3DSA:1.20.1050.10										
aly594.12	Protein sidekick	GO:0098595,GO:0005515,GO:0050931,GO:0042675,GO:0046533,GO:0005887,GO:0007155	CG5227-PG				SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060,SM00406,SM00406,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408,SM00408		PF07679,PF07679,PF07679,PF07679,PF07679,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041,PF13927	PS50853,PS50835,PS50853,PS50835,PS50853,PS50853,PS50853,PS50853,PS50853,PS50835,PS50853,PS50853,PS50835,PS50853,PS50853	PR00014,PR00014,PR00014,PR00014		G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF49265,SSF48726,SSF49265,SSF49265,SSF48726,SSF49265,SSF49265,SSF49265,SSF48726,SSF48726,SSF48726									
aly594.13	40S ribosomal protein S15a	GO:0022627,GO:0003735,GO:0007052,GO:0000022,GO:0006412,GO:0005840	CG2033-PF						PF00410			PS00053	G3DSA:3.30.1490.10,G3DSA:3.30.1370.30	SSF56047									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly594.14	CKLF-like MARVEL transmembrane domain-containing protein 4	GO:0016021,GO:0016020,GO:0006935,GO:0005615	CG15211-PA						PF01284	PS51225													
aly594.15	Unknown	GO:0035208,GO:0016020	CG1572-PA						PF01284	PS51225													
aly594.16	Unknown	GO:0007520,GO:0016020,GO:0003674	CG13011-PA						PF01284	PS51225													
aly594.17	Unknown		n/a																				
aly594.18	Unknown		n/a																				
aly594.19	SET and MYND domain-containing protein 4	GO:0005737,GO:0008168,GO:0010629,GO:0046872,GO:0042826	CG7759-PA						PF00856				G3DSA:2.170.270.10,G3DSA:2.170.270.10,G3DSA:1.25.40.10	SSF144232,SSF48452,SSF82199,SSF82199										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly594.2	Unknown		n/a																				
aly594.20	Outer dense fiber protein 2	GO:0006996,GO:0036064,GO:0072372,GO:0000278,GO:0000086,GO:0005813,GO:0005829,GO:0017137,GO:0005814,GO:0000922,GO:0005198,GO:0007286,GO:1902017,GO:0005634,GO:0005874,GO:0007275,GO:0001520	CG3213-PA												535~576,346~380,594~642,418~452,741~775,218~238,783~817,819~878,689~723									
aly594.21	Unknown		n/a																				
aly594.22	Acyl-coenzyme A:6-aminopenicillanic-acid-acyltransferase 40 kDa form	GO:0016787,GO:0050640,GO:0005829,GO:0007601,GO:0031964,GO:0007629,GO:0048067,GO:0042318,GO:0042416,GO:0003832,GO:0001694,GO:0017000,GO:0001692	CG12120-PA						PF03417														
aly594.23	Unknown		n/a						PF10961														
aly594.24	Rhythmically expressed gene 2 protein	GO:0016787,GO:0008152	CG15912-PA					TIGR01549,TIGR02252	PF13419				G3DSA:3.40.50.1000	SSF56784									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly594.25	Ephrin type-B receptor 2	GO:0016319,GO:0005887,GO:0018108,GO:0030424,GO:0007165,GO:0007411,GO:0007413,GO:0001525,GO:0004714,GO:0004713,GO:0060996,GO:0060997,GO:0005524,GO:0006468,GO:0035011,GO:0030425,GO:0007409,GO:0005886,GO:0048013,GO:0007422,GO:0005003,GO:0021963,GO:0005005,GO:0051965	CG1511-PC			PIRSF000666	SM00615,SM00060,SM00060,SM00219,SM00454		PF14575,PF01404,PF00536,PF00041,PF07714	PS50853,PS51550,PS50011,PS50853,PS50105	PR00109,PR00109,PR00109,PR00109,PR00109	PS00109,PS00107,PS00790	G3DSA:2.60.120.260,G3DSA:1.10.150.50,G3DSA:1.10.510.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.30.200.20,G3DSA:2.170.300.10	SSF56112,SSF49785,SSF47769,SSF49265										
aly594.26	UDP-sugar transporter UST74c	GO:0015297,GO:0072334,GO:0001745,GO:0007367,GO:0016021,GO:0007476,GO:0090481,GO:0005462,GO:0005461,GO:0005460,GO:0015790,GO:0015165,GO:0005464,GO:0005794,GO:0005797,GO:0009880,GO:1990569,GO:0007220,GO:0015788,GO:0007447,GO:0007423,GO:0015781,GO:0015787,GO:0015786,GO:0015785,GO:0000139,GO:0005458,GO:0005459,GO:0098656,GO:0005457	CG3874-PA						PF03151														
aly594.27	Longitudinals lacking protein like	GO:0006351,GO:0001700,GO:0007435,GO:0031519,GO:0007426,GO:0003700,GO:0006342,GO:0035167,GO:0000794,GO:0005700,GO:0016458,GO:0006357,GO:0031208,GO:0045893,GO:0005515,GO:0003677,GO:0045892,GO:0005634,GO:0016568,GO:0042803	CG13845-PA				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695									
aly594.28	Cytochrome b-c1 complex subunit 1, mitochondrial	GO:0031625,GO:0004222,GO:0003824,GO:0043209,GO:0014823,GO:0005811,GO:0008121,GO:0006122,GO:0005739,GO:0031122,GO:0005750,GO:0005743,GO:0005759,GO:0017087,GO:0043279,GO:0016485,GO:0006508,GO:0046872,GO:0005875	CG3731-PB						PF00675,PF05193				G3DSA:3.30.830.10,G3DSA:3.30.830.10	SSF63411,SSF63411									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly594.29	Cytochrome b-c1 complex subunit 1, mitochondrial	GO:1902600,GO:0008121,GO:0009060,GO:0044281,GO:0005875,GO:0043209,GO:0005811,GO:0005739,GO:0005750,GO:0022904,GO:0005759,GO:0006508,GO:0046872,GO:0006119,GO:0004222,GO:0014823,GO:0031122,GO:0003824,GO:0016485,GO:0043279,GO:0055114,GO:0031625,GO:0006122,GO:0044237,GO:0005743,GO:0005746,GO:0017087	CG3731-PB						PF00675,PF05193				G3DSA:3.30.830.10,G3DSA:3.30.830.10	SSF63411,SSF63411										
aly594.3	4-aminobutyrate aminotransferase, mitochondrial	GO:0051537,GO:0009448,GO:0009450,GO:0048148,GO:0047298,GO:0005829,GO:0006520,GO:0042135,GO:0005739,GO:0032145,GO:0003824,GO:0030170,GO:0005759,GO:0042803,GO:0032144,GO:0046872,GO:0003867,GO:0070062	CG7433-PB			PIRSF000521		TIGR00699	PF00202				G3DSA:3.90.1150.10,G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383		00250+2.6.1.19,00640+2.6.1.19,00650+2.6.1.19,00410+2.6.1.19		PWY-6537,PWY-4321,PWY-6535,PWY-5022,PWY-6536					
aly594.30	Unknown	GO:0046872,GO:0003676	CG32767-PC				SM00355,SM00355			PS50157		PS00028,PS00028		SSF57667									
aly594.4	Lys-63-specific deubiquitinase BRCC36	GO:0035204,GO:0032435,GO:0050821,GO:0031593,GO:0007275,GO:0008237,GO:0008180,GO:0005737,GO:0031572,GO:0045787,GO:0019781,GO:0005634,GO:0035207,GO:0070552,GO:0070531,GO:0046872,GO:0048477,GO:0070537,GO:0070536,GO:0034399,GO:0000338,GO:0007314,GO:0007409,GO:0007310,GO:0010212,GO:0001751,GO:0004843,GO:0008347,GO:0006302,GO:0005515,GO:0007095,GO:0045739	CG14884-PA				SM00232		PF01398				G3DSA:3.40.140.10	SSF102712	240~263,60~80									
aly594.5	Unknown		n/a						PF02453						339~346								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly594.6	Actin-binding protein IPP	GO:0005737,GO:0015629,GO:0051726,GO:0003779,GO:0005515,GO:0042994	CG9426-PA			PIRSF037037	SM00875,SM00225,SM00612,SM00612,SM00612,SM00612,SM00612		PF01344,PF01344,PF01344,PF01344,PF07707,PF00651	PS50097			G3DSA:3.30.710.10,G3DSA:2.130.10.80,G3DSA:2.130.10.80	SSF54695,SSF117281									
aly594.7	LanC-like protein 2	GO:0005737,GO:0004930,GO:0070273,GO:0010314,GO:0005829,GO:0032266,GO:0030864,GO:0005575,GO:0003824,GO:0045892,GO:0005886,GO:0009789,GO:0007186,GO:0005634	CG2061-PA						PF05147		PR01951,PR01951,PR01951,PR01951,PR01951,PR01951,PR01950,PR01950,PR01950,PR01950,PR01950			SSF158745									
aly594.8	Cyclic AMP-responsive element-binding protein 1	GO:0060430,GO:0007616,GO:0007613,GO:0007611,GO:0050821,GO:0003677,GO:0021983,GO:0040040,GO:0043565,GO:0001190,GO:0072375,GO:0071294,GO:0005634,GO:0005654,GO:0007595,GO:0045600,GO:0060509,GO:0010944,GO:0045893,GO:0045672,GO:0000980,GO:0006468,GO:0007623,GO:2000253,GO:0033762,GO:0007528,GO:0008361,GO:0045187,GO:1990589,GO:0007409,GO:0046887,GO:0005719,GO:0030431,GO:0000978,GO:0071363,GO:0003700,GO:0035497,GO:0042493,GO:0003705,GO:0006355,GO:0045944,GO:0033363,GO:0040018,GO:0046983,GO:0046889,GO:0045475	CG6103-PA				SM00338		PF00170,PF02173	PS50217,PS50953	PR00041,PR00041,PR00041,PR00041	PS00036	G3DSA:1.20.5.170	SSF57959	245~279								
aly594.9	UV excision repair protein RAD23 homolog A	GO:0005737,GO:0016032,GO:0032434,GO:0043161,GO:0005634,GO:1990381,GO:0045070,GO:0006289,GO:0005654,GO:0003697,GO:0005515,GO:0031593,GO:0000502,GO:0003684	CG1836-PA				SM00213,SM00727,SM00165,SM00165		PF09280,PF00627,PF00627,PF00240	PS50030,PS50030,PS50053	PR01839,PR01839,PR01839,PR01839		G3DSA:1.10.8.10,G3DSA:1.10.10.540,G3DSA:3.10.20.90,G3DSA:1.10.8.10	SSF54236,SSF46934,SSF46934,SSF101238									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly59452.1	Hemocytin	GO:0007155,GO:0030246,GO:0003676,GO:0008270	n/a																				
aly595.1	Unknown		n/a										G3DSA:3.30.530.20										
aly595.10	Mesoderm induction early response protein 1	GO:0031937,GO:0006351,GO:0017053,GO:0005634,GO:0005654,GO:0007165,GO:0004871,GO:0003677,GO:0003682,GO:0043123	CG1620-PA				SM00717		PF01448	PS51293,PS51156				SSF46689									
aly595.11	Protein KBP homolog	GO:0005856,GO:0006839,GO:0019894,GO:0007399,GO:0005739	CG14043-PA						PF12309				G3DSA:1.25.40.10,G3DSA:1.25.40.10		263~283								
aly595.12	UDP-glucuronosyltransferase 2B4	GO:0009813,GO:0052695,GO:0052696,GO:0016021,GO:0006711,GO:0005789,GO:0006805,GO:0032870,GO:0008152,GO:0016758,GO:0015020,GO:0008194,GO:0043231	CG17324-PB						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									
aly595.13	Protein cornichon	GO:0045451,GO:0009953,GO:0009952,GO:0009950,GO:0005789,GO:0016021,GO:0016020,GO:0030722,GO:0008069,GO:0008314,GO:0007314,GO:0008298,GO:0005887,GO:0007310,GO:0015031,GO:0006888,GO:0035556,GO:0007350,GO:0016192,GO:0045450,GO:0046843	CG5855-PA						PF03311			PS01340											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly595.14	Endoplasmic reticulum lectin 1	GO:0001948,GO:1904153,GO:0005788,GO:0030433	CG6766-PA						PF07915,PF07915					SSF50911,SSF50911	155~175								
aly595.15	CUGBP Elav-like family member 2	GO:0042078,GO:0031536,GO:2000738,GO:0002121,GO:0005737,GO:0043186,GO:0005634,GO:0030727,GO:0007476,GO:0000166,GO:0003730,GO:0048477,GO:0046011,GO:0007281,GO:0007286,GO:0000381,GO:0036099,GO:0007319,GO:0003723,GO:0005515,GO:0017148,GO:0006378,GO:0006397,GO:0003729	CG31762-PB				SM00360,SM00360,SM00360		PF00076,PF00076,PF00076	PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928									
aly595.2	Lysozyme	GO:0019835,GO:0003796,GO:0042742,GO:0019730,GO:0016998	CG9116-PA				SM00263		PF00062	PS51348	PR00137,PR00137,PR00137,PR00135,PR00135,PR00135,PR00135,PR00135,PR00135,PR00135		G3DSA:1.10.530.10	SSF53955									
aly595.3	Unknown		n/a												216~236,313~347,241~282,146~208								
aly595.4	N-acetylgalactosaminyltransferase 7	GO:0005795,GO:0046872,GO:0006486,GO:0016021,GO:0004653,GO:0030246,GO:0000139,GO:0012505,GO:0009312	CG6394-PA				SM00458		PF00652,PF00535	PS50231			G3DSA:2.80.10.50,G3DSA:3.90.550.10	SSF53448,SSF50370									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly595.5	Tubulin-specific chaperone C	GO:0007021,GO:0007023,GO:0000902,GO:0005829,GO:0003924,GO:0032391,GO:0022008	CG31961-PA				SM00673,SM00673		PF16752,PF07986	PS51329			G3DSA:2.160.20.70										
aly595.6	Protein CEBPZOS	GO:0016021,GO:0031966	CG42371-PA																				
aly595.7	Spondin-1	GO:0007155,GO:0005578,GO:0005576,GO:0005615,GO:0004867	CG17739-PA						PF06468,PF06468,PF02014,PF02014	PS51019,PS51020,PS51019,PS51020													
aly595.8	Engulfment and cell motility protein 1	GO:0006909,GO:0032045,GO:0017124,GO:0030036,GO:0006928,GO:0032863,GO:0005488,GO:0007298,GO:0005875,GO:0007417,GO:0005737,GO:0016601,GO:0005634,GO:0016020,GO:0016477,GO:0016203,GO:0016032,GO:0045087,GO:0006915,GO:0050690,GO:0006911,GO:0005886,GO:0007520,GO:0048010,GO:0038096,GO:0007015,GO:0005829,GO:0005515	CG5336-PA						PF16457,PF11841,PF04727	PS51335			G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:2.30.29.30	SSF48371,SSF48371,SSF50729	309~329								
aly595.9	Transmembrane protein 87A	GO:0016021	CG17660-PA						PF06814														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly59515.1	Unknown		n/a																				
aly59566.1	Unknown		n/a																				
aly59591.1	Unknown		n/a																				
aly596.1	Proton-coupled amino acid transporter 4	GO:0040007,GO:0015293,GO:0003333,GO:0006865,GO:0015171,GO:0016021	CG1139-PA						PF01490														
aly596.10	Unknown	GO:0005886	CG42258-PC																				
aly596.11	E3 ubiquitin-protein ligase RNF181	GO:0005575,GO:0016874,GO:0008150,GO:0008270,GO:0016567	CG7694-PA				SM00184		PF13639	PS50089			G3DSA:3.30.40.10	SSF57850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly596.12	6-phosphogluconate dehydrogenase, decarboxylating	GO:0000187,GO:0050661,GO:0031588,GO:0005975,GO:0070062,GO:0019521,GO:0005829,GO:0006098,GO:0004616,GO:0019322,GO:0009051,GO:0004679,GO:0005634,GO:0055114,GO:0044281	CG3724-PB			PIRSF000109		TIGR00873	PF03446,PF00393		PR00076,PR00076,PR00076,PR00076,PR00076,PR00076	PS00461	G3DSA:1.10.1040.10,G3DSA:1.20.5.320,G3DSA:3.40.50.720	SSF51735,SSF48179		00480+1.1.1.44,00030+1.1.1.44			UPA00115				
aly596.13	Unknown		n/a																				
aly596.14	Pleckstrin homology domain-containing family G member 5	GO:0005089,GO:0097190,GO:0030139,GO:0035025,GO:0004871,GO:0035023,GO:0005737,GO:0043065,GO:0048471,GO:0035767,GO:0043123,GO:0051056,GO:0007480,GO:0030027,GO:0008360,GO:0007155,GO:0005911,GO:0005886,GO:0048011,GO:0007264,GO:0005829,GO:0005575	CG42674-PC				SM00325		PF00621	PS50010			G3DSA:1.20.900.10	SSF48065									
aly596.15	Unknown		n/a																				
aly596.16	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly596.17	Unknown		n/a												5~25,80~83								
aly596.18	Unknown		n/a						PF14945														
aly596.2	Proton-coupled amino acid transporter 1	GO:0015804,GO:0016021,GO:0015992,GO:0035524,GO:1902600,GO:0003333,GO:0005280,GO:0015816,GO:0015193,GO:0005764,GO:0005765,GO:0015078,GO:0005886,GO:0015180,GO:0015175,GO:0015187,GO:0005774,GO:0015808,GO:0015171	CG7888-PB						PF01490														
aly596.3	Hepatic leukemia factor	GO:0048511,GO:0043565,GO:0007623,GO:0040007,GO:0019216,GO:0003700,GO:0005634,GO:0006366,GO:0007275,GO:0006355,GO:0042023,GO:0001077,GO:0006351,GO:0003690,GO:0003677,GO:0035914,GO:0007067,GO:0042803,GO:0007584,GO:0045893	CG17888-PD				SM00338		PF07716	PS50217			G3DSA:1.20.5.170	SSF57959	233~260								
aly596.4	Unknown		n/a												121~141								
aly596.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly596.6	Carnitine O-palmitoyltransferase 1, liver isoform	GO:0006635,GO:0031307,GO:0009437,GO:0044281,GO:0042594,GO:0007623,GO:0014070,GO:0016020,GO:0051260,GO:0005739,GO:0030855,GO:0071398,GO:0006853,GO:0006641,GO:0050796,GO:0042755,GO:0010038,GO:0001676,GO:0044255,GO:0006979,GO:0042493,GO:0005743,GO:0005741,GO:0004095,GO:0006006,GO:0032000	CG12891-PD						PF16484,PF00755			PS00439		SSF52777,SSF52777									
aly596.7	Alpha/beta hydrolase domain-containing protein 13	GO:0016787,GO:0016021,GO:0016020,GO:0005575,GO:0008150,GO:0003674	CG18642-PA						PF12695				G3DSA:3.40.50.1820	SSF53474									
aly596.8	Staphylococcal nuclease domain-containing protein 1	GO:0042470,GO:0044822,GO:0016020,GO:0070062,GO:0006355,GO:0004518,GO:0097433,GO:0005634,GO:0005811,GO:0003713,GO:0003712,GO:0016788,GO:0035194,GO:0005739,GO:0031047,GO:0003676,GO:0016442,GO:0005875,GO:0001649,GO:0006351	CG7008-PA			PIRSF017179	SM00333,SM00333,SM00318,SM00318,SM00318,SM00318		PF00565,PF00565,PF00565,PF00565,PF00567	PS50830,PS50830,PS50830,PS50304,PS50830			G3DSA:2.40.50.90,G3DSA:2.40.50.90,G3DSA:2.30.30.140,G3DSA:2.40.50.90,G3DSA:2.40.50.90,G3DSA:2.40.50.90	SSF50199,SSF50199,SSF50199,SSF50199,SSF50199,SSF63748									
aly596.9	Unknown	GO:0022008,GO:0005615,GO:0032504	CG9975-PA																				
aly5965.1	WD repeat-containing protein 7	GO:0008021,GO:0007035,GO:0005834,GO:0003924,GO:0002244,GO:0008593,GO:0007186	CG17766-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly5965.2	Putative ATP-dependent RNA helicase TDRD12	GO:0043186,GO:0070725,GO:0005829,GO:0030154,GO:0031965,GO:0004004,GO:0004386,GO:0007283,GO:0031047,GO:0003676,GO:0051321,GO:0010526,GO:0005694,GO:0007275,GO:0005524	CG31755-PB				SM00487,SM00333		PF00567,PF04969,PF00270	PS51203,PS50304			G3DSA:3.40.50.300,G3DSA:2.60.40.790,G3DSA:3.40.50.300,G3DSA:2.30.30.140,G3DSA:2.30.30.140	SSF63748,SSF49764,SSF63748,SSF52540									
aly5965.3	Dymeclin	GO:0005575,GO:0003674,GO:0008150	CG8230-PA						PF09742,PF09742														
aly5965.4	Pupal cuticle protein PCP52	GO:0042302	n/a							PS51257					76~96								
aly5965.5	Pupal cuticle protein PCP52	GO:0042302	n/a																				
aly5965.6	Pupal cuticle protein PCP52	GO:0042302	n/a																				
aly5975.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly598.1	Furin-like protease 1, isoforms 1/1-X/2	GO:0005795,GO:0004252,GO:0016021,GO:0008039,GO:0001139,GO:0030173,GO:0005886,GO:0016485,GO:0006508	CG10772-PJ						PF16470,PF00082,PF01483		PR00723,PR00723,PR00723	PS00136,PS00137,PS00138	G3DSA:3.30.70.850,G3DSA:3.40.50.200,G3DSA:2.60.120.260	SSF52743,SSF49785,SSF54897									
aly598.2	Unknown		n/a				SM00261						G3DSA:2.10.220.10,G3DSA:2.10.220.10	SSF57184,SSF57184									
aly598.3	Furin-like protease 1, isoforms 1/1-X/2	GO:0005795,GO:0004252,GO:0016021,GO:0008039,GO:0001139,GO:0030173,GO:0005886,GO:0016485,GO:0006508	CG10772-PJ						PF16470				G3DSA:3.30.70.850	SSF54897									
aly5992.1	Irregular chiasm C-roughest protein	GO:0061321,GO:0001745,GO:0046666,GO:0045177,GO:0007523,GO:1901739,GO:0097206,GO:0016021,GO:0050839,GO:0042802,GO:0048749,GO:0016202,GO:0046667,GO:0009986,GO:0005917,GO:0036059,GO:0030165,GO:0005913,GO:0005912,GO:0005886,GO:0007520,GO:0007157,GO:0007156,GO:0036058,GO:0046331,GO:0005515	CG3653-PB										G3DSA:2.60.40.10										
aly60.1	Carboxypeptidase B	GO:0006508,GO:0004181,GO:0004180,GO:0008270,GO:0005576	CG8560-PA				SM00631		PF00246		PR00765,PR00765,PR00765,PR00765	PS00132	G3DSA:3.40.630.10	SSF53187									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly60.10	Alpha-tocopherol transfer protein-like	GO:0005215,GO:0016020,GO:0005622	CG11550-PA						PF00650	PS50191			G3DSA:3.40.525.10	SSF52087									
aly60.11	Glucose 1-dehydrogenase 2	GO:0047936,GO:0008152,GO:0016491	CG31548-PA				SM00822		PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735									
aly60.12	Glucose 1-dehydrogenase 2	GO:0047936,GO:0008152,GO:0016491	CG31548-PA				SM00822		PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly60.13	Alpha-tocopherol transfer protein-like	GO:0005215,GO:0016020,GO:0005622	CG11550-PA						PF00650	PS50191			G3DSA:3.40.525.10	SSF52087									
aly60.14	Cuticle protein 16.8	GO:0040003,GO:0005214,GO:0008010,GO:0031012,GO:0008061,GO:0042302	CG18066-PA						PF00379	PS51155					156~186								
aly60.15	Clavesin-2	GO:0080025,GO:0005215,GO:0005802,GO:0007040,GO:0005768,GO:0031901,GO:0030136	CG11550-PA						PF00650	PS50191			G3DSA:3.40.525.10	SSF46938,SSF52087									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly60.16	Glucose dehydrogenase [FAD, qui]	GO:0042335,GO:0016614,GO:0008812,GO:0004344,GO:0006066,GO:0050660,GO:0046693,GO:0008364,GO:0006006,GO:0055114,GO:0005576	CG1152-PA						PF00732,PF05199			PS00623,PS00624	G3DSA:4.10.450.10,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.30.560.10,G3DSA:3.30.560.10	SSF51905,SSF51905,SSF54373		00030+1.1.3.4							
aly60.17	Unknown		n/a																				
aly60.18	Microprocessor complex subunit DGCR8	GO:0005737,GO:0070878,GO:0015630,GO:0007446,GO:0020037,GO:0005730,GO:0004525,GO:0035195,GO:0005634,GO:0030727,GO:0005654,GO:0031053,GO:0003725,GO:0007294,GO:0046872,GO:0072091,GO:0070877	CG1800-PA				SM00358		PF00035	PS50137			G3DSA:3.30.160.20	SSF54768									
aly60.19	BRCA1-associated protein	GO:0005737,GO:0009968,GO:0008139,GO:0031965,GO:0061630,GO:0000165,GO:0000151,GO:0000166,GO:0016567,GO:0004842,GO:0008270,GO:0007265,GO:0016874	CG5555-PB						PF02148,PF07576				G3DSA:3.30.40.10	SSF57850	385~389,261~316,236~256,328~348								
aly60.2	Carboxypeptidase A2	GO:0007039,GO:0005773,GO:0004181,GO:0004180,GO:0005576,GO:0008270,GO:0006508	CG8560-PA				SM00631		PF02244,PF00246		PR00765,PR00765,PR00765,PR00765	PS00132	G3DSA:3.40.630.10,G3DSA:3.30.70.340	SSF54897,SSF53187									
aly60.20	Ubiquitin carboxyl-terminal hydrolase 32	GO:0005737,GO:0005794,GO:0043161,GO:0016020,GO:0061136,GO:0004197,GO:0005509,GO:0006511,GO:0016579,GO:0004843	CG8334-PB				SM00054,SM00054,SM00695		PF06337,PF00443,PF13499	PS50222,PS50222,PS51283,PS50235	PR00450,PR00450,PR00450	PS00018,PS00018,PS00972	G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:3.30.2230.10,G3DSA:3.30.2230.10	SSF54001,SSF47473,SSF143791,SSF143791,SSF47473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly60.21	Ubiquitin carboxyl-terminal hydrolase 32	GO:0005737,GO:0005794,GO:0043161,GO:0016020,GO:0061136,GO:0004197,GO:0005509,GO:0006511,GO:0016579,GO:0004843	CG8334-PB						PF00443	PS50235		PS00973		SSF54001									
aly60.22	14-3-3 protein epsilon	GO:0008103,GO:0045927,GO:0009314,GO:0046579,GO:0009411,GO:0007294,GO:0007411,GO:0005875,GO:0005737,GO:0045172,GO:0005813,GO:0005634,GO:0005654,GO:0046958,GO:0007088,GO:0005694,GO:0048190,GO:0008426,GO:0007280,GO:0019904,GO:0005886,GO:0008340,GO:0007265,GO:0070374,GO:0000077,GO:0007444,GO:0005515,GO:0007095,GO:0046982,GO:0040008,GO:0007093	CG31196-PA			PIRSF000868	SM00101		PF00244		PR00305,PR00305,PR00305,PR00305,PR00305,PR00305	PS00796,PS00797	G3DSA:1.20.190.20	SSF48445	10~30								
aly60.23	PHD finger protein 12	GO:0070822,GO:0001222,GO:0016580,GO:0017053,GO:0000122,GO:0003700,GO:0005634,GO:0005654,GO:0035091,GO:0001106,GO:0045892,GO:0008270,GO:0006351	CG3815-PA				SM00249,SM00249		PF16737,PF00628,PF00628	PS50016		PS01359	G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57903,SSF57903	121~141,144~164,513~533								
aly60.24	GPN-loop GTPase 3	GO:0017076,GO:0022008,GO:0048812,GO:0016787,GO:0005525	CG2656-PA						PF03029				G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly60.25	Homeobox protein cut	GO:0008587,GO:0008585,GO:0003677,GO:0007417,GO:0060288,GO:0000122,GO:0005634,GO:0030707,GO:0045746,GO:0016360,GO:0048477,GO:0007443,GO:0061332,GO:0000278,GO:0007605,GO:0048098,GO:0008052,GO:0035277,GO:0007469,GO:0007424,GO:0045165,GO:0007422,GO:0003700,GO:0030713,GO:0070983,GO:0006355,GO:0048813,GO:0000976,GO:0006351	CG11387-PC				SM00389		PF02376,PF02376,PF02376,PF00046	PS51042,PS51042,PS50071,PS51042		PS00027	G3DSA:1.10.10.60,G3DSA:1.10.260.40,G3DSA:1.10.260.40,G3DSA:1.10.260.40	SSF47413,SSF46689,SSF47413,SSF47413	138~197,336~56								
aly60.26	Uncharacterized short-chain type dehydrogenase/reductase y4vI	GO:0008152,GO:0016491	CG31548-PA						PF00106,PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080	PS00061	G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735,SSF51735									
aly60.27	Nuclear pore complex protein Nup88	GO:0035147,GO:0007424,GO:0019730,GO:0005643,GO:0005635,GO:0006606,GO:0046826,GO:0005515,GO:0006955,GO:0015031,GO:0022008,GO:0005654,GO:0051028	CG6819-PA						PF10168				G3DSA:2.130.10.10	SSF50978	534~561,647~667								
aly60.28	Unknown		n/a																				
aly60.3	Carboxypeptidase B	GO:0006508,GO:0004181,GO:0004180,GO:0008270,GO:0005576	CG8560-PA				SM00631		PF00246		PR00765,PR00765,PR00765	PS00132	G3DSA:3.40.630.10	SSF53187									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly60.4	Unknown		n/a																				
aly60.5	Potassium channel subfamily K member 18	GO:0005267,GO:0071805,GO:0006813,GO:0016021,GO:0022841,GO:0071435,GO:0071467,GO:0005887,GO:0005886,GO:0005250,GO:0015271,GO:0015269,GO:0030322	CG8713-PA						PF07885,PF07885		PR01333,PR01333		G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324,SSF81324									
aly60.6	Attacin-A	GO:0019731,GO:0045087,GO:0050830,GO:0005576,GO:0042742,GO:0031201	CG7629-PA						PF03768,PF03769														
aly60.7	60S acidic ribosomal protein P2	GO:0022626,GO:0005840,GO:0022625,GO:0003735,GO:0006414,GO:0006412	CG4918-PA	MF_01478					PF00428														
aly60.8	17-beta-hydroxysteroid dehydrogenase 14	GO:0006706,GO:0005829,GO:0008152,GO:0004303,GO:0047045,GO:0016491	CG31548-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									
aly60.9	Uncharacterized oxidoreductase TM_0325	GO:0008152,GO:0016491	CG31548-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly600.1	U11/U12 small nuclear ribonucleoprotein 48 kDa protein	GO:0005737,GO:0005654,GO:0005689,GO:0046872,GO:0008380,GO:0006397	n/a						PF05253						203~227								
aly600.10	Vacuolar protein sorting associated protein 13D	GO:0070062,GO:0006623,GO:0045053,GO:0005623,GO:0019898,GO:0005622,GO:0005875,GO:0016192	CG32113-PB						PF16908,PF16908,PF06650,PF16910,PF12624,PF16909														
aly600.11	Unknown		n/a																				
aly600.12	Unknown	GO:0016192,GO:0005875	CG32113-PB																				
aly600.13	Ester hydrolase C11orf54	GO:0070062,GO:0005634,GO:0016788,GO:0005575,GO:0008150,GO:0008270,GO:0008152	CG9119-PA						PF08925					SSF117856									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly600.14	E3 ubiquitin-protein ligase rififylin	GO:1902042,GO:0055038,GO:0010804,GO:0002947,GO:0008270,GO:0070936,GO:0010008,GO:0005737,GO:0016023,GO:0043161,GO:0006886,GO:0043066,GO:0042787,GO:0010762,GO:1901797,GO:0005886,GO:0061630,GO:0005829,GO:2001271,GO:0006511,GO:0005515,GO:0016874	CG17019-PA				SM00184,SM00184		PF13920	PS50089			G3DSA:3.30.40.10	SSF68906,SSF68906,SSF57903,SSF57903										
aly600.15	Kielin/chordin like protein	GO:0002244,GO:0030513,GO:0005615	CG31869-PA				SM00214,SM00214			PS50184,PS50184			G3DSA:2.10.70.10	SSF57603,SSF57603										
aly600.16	Unknown		CG17127-PA																				
aly600.17	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment)	GO:0003964,GO:0004519,GO:0046872	n/a						PF00078	PS50878				SSF56672										
aly600.18	Extracellular matrix protein FRAS1	GO:0002009,GO:0030326,GO:0003338,GO:0016021,GO:0060021,GO:0061618,GO:0005886,GO:0015031,GO:0007154,GO:0046872,GO:0043588	CG17211-PA				SM00214,SM00214,SM00214,SM00214			PS50184,PS50184				SSF57603,SSF57603,SSF57603										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly600.19	Unknown	GO:0004252,GO:0016021	n/a						PF01694				G3DSA:1.20.1540.10	SSF144091									
aly600.2	Translational activator GCN1	GO:0005737,GO:0008135,GO:0005840,GO:0044822,GO:0016020,GO:0005488,GO:0006417,GO:0006412,GO:0008494	CG17514-PA						PF13646,PF13646	PS50077,PS50077,PS50077			G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371	770~790,734~754								
aly600.20	Unknown		n/a																				
aly600.21	Vacuolar protein sorting associated protein 13D	GO:0019898,GO:0070062,GO:0045053,GO:0005623,GO:0005622,GO:0006623	n/a																				
aly600.22	Unknown		n/a																				
aly600.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly600.4	Selenoprotein M	GO:0005737,GO:0005794,GO:0048471,GO:0005654,GO:0005783	n/a						PF08806					SSF52833									
aly600.5	Caspase Dronc	GO:0004175,GO:0097199,GO:0008258,GO:0097194,GO:0097190,GO:0048102,GO:0007291,GO:0035006,GO:0010623,GO:0010941,GO:0007417,GO:0005737,GO:0001700,GO:0007516,GO:0097200,GO:0007552,GO:0050700,GO:0031638,GO:0005739,GO:0006508,GO:0010506,GO:2001269,GO:0042803,GO:0048749,GO:0008285,GO:0035071,GO:0006919,GO:0035234,GO:0006915,GO:0051291,GO:0016322,GO:0012501,GO:0046668,GO:0045476,GO:0008340,GO:0035070,GO:0007423,GO:0046672,GO:0016540,GO:0048813,GO:0004197,GO:0043293	CG8091-PA			PIRSF038001	SM00115,SM00114		PF00656,PF00619	PS50208,PS50209,PS50207	PR00376,PR00376,PR00376,PR00376,PR00376		G3DSA:3.40.50.1460,G3DSA:1.10.533.10	SSF52129,SSF52129,SSF47986									
aly600.6	Unknown		n/a																				
aly600.7	Protein CNPPD1	GO:0019901,GO:0000079,GO:0016021	CG40191-PB						PF08613														
aly600.8	Unknown		CG14764-PA												35~62								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly600.9	Transmembrane protein 65	GO:0016021,GO:0005739	CG17715-PD						PF10507														
aly6002.1	Unknown		n/a																				
aly6002.2	Leucine-rich repeat protein soc-2 homolog	GO:0017016,GO:0000164,GO:0005515,GO:0046579	CG5407-PA				SM00369,SM00369,SM00369		PF13855	PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									
aly6002.3	PAB-dependent poly(A)-specific ribonuclease subunit PAN2	GO:0090503,GO:0000289,GO:0010606,GO:0005634,GO:0004535,GO:0000932,GO:0031251,GO:0000175,GO:0005515,GO:0003676,GO:0006397	CG8232-PA						PF13423	PS50235			G3DSA:2.130.10.10	SSF54001,SSF54001,SSF50978,SSF50978									
aly6002.4	Dynactin subunit 5	GO:0019886,GO:0005813,GO:0005829,GO:0007018,GO:0007283,GO:2001019,GO:0005869,GO:0000777	CG10846-PA						PF00132				G3DSA:2.160.10.10	SSF51161									
aly6002.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6002.6	Cyclic nucleotide-gated cation channel subunit A	GO:0030553,GO:0042391,GO:0005249,GO:0071805,GO:0005221,GO:0006812,GO:0005223,GO:0005222,GO:0005622,GO:0019934,GO:0005887,GO:0001666,GO:0055085,GO:0017071	CG42701-PB							PS50042			G3DSA:2.60.120.10	SSF51206									
aly6010.1	Unknown		n/a																				
aly6012.1	Prohormone-3	GO:0005575,GO:0003674,GO:0016021,GO:0008150	CG8216-PA																				
aly6012.2	Unknown		n/a																				
aly6012.3	Unknown		n/a																				
aly6012.4	Unknown		n/a												435~455,136~156,302~322								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6018.1	Histone-lysine N-methyltransferase eggless	GO:0018024,GO:0035220,GO:0002165,GO:0046974,GO:0008270,GO:0051567,GO:0005737,GO:0005634,GO:0040029,GO:0016571,GO:0045814,GO:0048477,GO:0010385,GO:0045892,GO:0044026,GO:0048132,GO:0051038,GO:0060968,GO:0005700,GO:0010369,GO:0006351,GO:0005515	CG30426-PA												319~339								
aly6018.2	Unknown		n/a												46~66								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6018.3	Neurofibromin	GO:0043547,GO:0048715,GO:0030325,GO:0045685,GO:0007616,GO:0007614,GO:0046578,GO:0021510,GO:0030036,GO:0030424,GO:0022011,GO:0008340,GO:0045886,GO:0001889,GO:0043525,GO:0019933,GO:0045124,GO:0030425,GO:0005634,GO:0043087,GO:0021987,GO:0043409,GO:0008355,GO:0005737,GO:0001666,GO:0008429,GO:0005730,GO:0042992,GO:0045762,GO:0016020,GO:0000165,GO:0030199,GO:0006469,GO:0008542,GO:0043065,GO:0048147,GO:0048485,GO:0001649,GO:0043005,GO:0045765,GO:0043407,GO:0007154,GO:0005099,GO:0043473,GO:0042066,GO:0048745,GO:0008017,GO:0048593,GO:0005096,GO:0042060,GO:0014044,GO:0014069,GO:0045475,GO:0001656,GO:0045545,GO:0014065,GO:0009408,GO:0007265,GO:0021897,GO:0031235,GO:0006979,GO:0007420,GO:0043234,GO:0007507,GO:0045664,GO:0040014,GO:0007422,GO:0040018,GO:0001952,GO:0048853,GO:0032320,GO:0030198,GO:0031210,GO:0048844,GO:0007406,GO:0046580	CG8318-PB				SM00516,SM00323		PF13716,PF00616	PS50191,PS50018			G3DSA:1.10.494.10,G3DSA:1.10.506.10	SSF48350,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371										
aly6018.4	Unknown		n/a												4~31								
aly6018.5	Sorting nexin-6	GO:0034452,GO:0030904,GO:0016023,GO:0035091,GO:0097422,GO:0006886,GO:0061357,GO:0060070,GO:0042147,GO:0005634,GO:0031901	CG8282-PB			PIRSF036924			PF09325,PF00787	PS50195			G3DSA:3.30.1520.10	SSF64268,SSF64268	333~356								
aly6018.6	Transmembrane protein 145	GO:0016021,GO:0007186,GO:0019236	CG9304-PA						PF10192														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6018.7	Protein SGT1 homolog	GO:0005737,GO:0030674,GO:0005813,GO:0051297,GO:0051087,GO:0032154,GO:0050821,GO:0045201,GO:0007405,GO:0005634,GO:0000776	CG9617-PA						PF04969,PF05002	PS51203,PS51048			G3DSA:2.60.40.790	SSF49764									
aly6018.8	Nitrilase and fragile histidine triad fusion protein NitFhit	GO:0000257,GO:0006139,GO:0047710,GO:0016810,GO:0000166,GO:0005575,GO:0003824	CG7067-PA						PF01230,PF00795	PS50263,PS51084			G3DSA:3.30.428.10,G3DSA:3.60.110.10	SSF54197,SSF56317									
aly60219.1	Unknown		n/a																				
aly603.1	Unknown		n/a																				
aly6034.1	Unknown		n/a												596~616								
aly6034.2	LETM1 and EF-hand domain-containing protein 1, mitochondrial	GO:0070584,GO:0006851,GO:0005432,GO:0005739,GO:0031966,GO:0005743,GO:0005509,GO:0007269,GO:0071456,GO:0015386,GO:0016021	CG4589-PA						PF07766						502~546,426~466,564~598								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6034.3	Oligoribonuclease, mitochondrial	GO:0090503,GO:0008946,GO:0005634,GO:0005739,GO:0000175,GO:0090305,GO:0003676,GO:0005759,GO:0005758,GO:0004527	CG10214-PA	MF_00045			SM00479		PF00929				G3DSA:3.30.420.10	SSF53098									
aly6034.4	BTB/POZ domain-containing protein KCTD16	GO:0043235,GO:0042734,GO:0051260,GO:0045211,GO:0008277,GO:0005886,GO:0030054	CG10830-PA						PF02214				G3DSA:3.30.710.10	SSF54695									
aly6034.5	Acylphosphatase-2	GO:0005739,GO:0003998,GO:0008152	CG18505-PA						PF00708	PS51160	PR00112,PR00112,PR00112	PS00151,PS00150	G3DSA:3.30.70.100	SSF54975		00620+3.6.1.7,00627+3.6.1.7							
aly6034.6	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	GO:0005749,GO:0020037,GO:0005743,GO:0016021,GO:0006121,GO:0006105,GO:0046872,GO:0006099,GO:0008177,GO:0008340,GO:0000104,GO:0006979,GO:0009055	CG6666-PA					TIGR02970	PF01127			PS01001,PS01000	G3DSA:1.20.1300.10,G3DSA:1.20.5.540	SSF81343					UPA00223				
aly6034.7	Transferrin	GO:0006879,GO:0005615,GO:0042048,GO:0006811,GO:0006952,GO:0008199,GO:0005381,GO:0006826,GO:0046872,GO:0055072,GO:0005576	CG6186-PA			PIRSF002549	SM00094,SM00094		PF00405,PF00405	PS51408,PS51408	PR00422,PR00422,PR00422,PR00422	PS00207,PS00206,PS00207,PS00205,PS00205	G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.190.10	SSF53850,SSF53850									
aly6034.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6034.9	Unknown		n/a						PF16009						198~218								
aly6052.1	Unknown		n/a																				
aly6069.1	Unknown		n/a																				
aly607.1	Unknown	GO:0003677	CG8359-PA				SM00595		PF10545	PS51029													
aly6070.1	Unknown		n/a												19~39,81~115,123~143,150~207								
aly60723.1	Unknown	GO:0007156,GO:0097206,GO:0005886,GO:0030036,GO:0005917,GO:0036059,GO:0007523,GO:0061321,GO:0007155,GO:0005515,GO:0007286,GO:0007520,GO:0007157,GO:0001745	CG33141-PB						PF08205	PS50835			G3DSA:2.60.40.10	SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6076.1	Unknown		n/a												39~59								
aly6079.1	Antichymotrypsin-2	GO:0005615,GO:0032504,GO:0050829,GO:0030162,GO:0004867,GO:0010951,GO:0045861	CG9334-PA						PF00079				G3DSA:3.30.497.10	SSF56574									
aly6079.2	Unknown		n/a						PF00079				G3DSA:2.30.39.10	SSF56574									
aly6079.3	Unknown		n/a																				
aly6095.1	Protein hu-li tai shao	GO:0061572,GO:0008302,GO:0007294,GO:0007411,GO:0005737,GO:0045170,GO:0045172,GO:0030724,GO:0005811,GO:0030721,GO:0030723,GO:0003779,GO:0072499,GO:0007527,GO:0048477,GO:0035183,GO:0016328,GO:0000212,GO:0051297,GO:0031987,GO:0007282,GO:0045214,GO:0005884,GO:0005886,GO:0045478,GO:0048134,GO:0048135,GO:0005856,GO:0070050,GO:0045169	CG43443-PP				SM01007		PF00596				G3DSA:3.40.225.10	SSF53639									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6103.1	Membrane-bound alkaline phosphatase	GO:0016791,GO:0004035,GO:0008152,GO:0005886,GO:0046872,GO:0031225	CG5150-PA				SM00098		PF00245		PR00113,PR00113,PR00113,PR00113,PR00113	PS00123	G3DSA:3.40.720.10	SSF53649		00627+3.1.3.1,00790+3.1.3.1		PWY-5491					
aly6103.2	Unknown	GO:0004383,GO:0004872,GO:0035556,GO:0006182	CG14501-PA						PF08376														
aly611.1	Mitogen-activated protein kinase ERK-A	GO:0007552,GO:0048149,GO:0050803,GO:0007476,GO:0008586,GO:0050804,GO:0045467,GO:0007258,GO:0090303,GO:0007169,GO:0007067,GO:0030054,GO:0005737,GO:0034334,GO:0045500,GO:0005634,GO:0007369,GO:0000165,GO:0007474,GO:0004674,GO:0043066,GO:0031594,GO:0004672,GO:0046579,GO:0016242,GO:0005524,GO:0008284,GO:0006468,GO:0007507,GO:0008134,GO:0034614,GO:0071276,GO:0006974,GO:0008595,GO:0007173,GO:0009267,GO:2001023,GO:0071243,GO:0019901,GO:0004705,GO:0006355,GO:0004707,GO:0046534,GO:0008293,GO:0070374	CG12559-PE				SM00220		PF00069	PS50011	PR01770,PR01770,PR01770,PR01770,PR01770	PS01351,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112			REACT_16888,REACT_11061,REACT_18266,REACT_9417,REACT_6900,REACT_498							
aly61150.1	Pro-resilin	GO:0040003,GO:0032992,GO:0005214,GO:0030023,GO:0008010,GO:0031012,GO:0005576,GO:0008061,GO:0042302	CG6305-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly61160.1	Unknown		n/a																				
aly6119.1	Zinc transporter ZIP9	GO:0016021,GO:0016020,GO:0030001,GO:0046873,GO:0006829,GO:0055085	CG2177-PE						PF02535,PF02535														
aly6119.2	Acetylcholine receptor subunit beta-like 2	GO:0006812,GO:0006811,GO:0005892,GO:0045211,GO:0004889,GO:0005887,GO:0017085,GO:0007271,GO:0098655,GO:0030054	CG6798-PA						PF02931				G3DSA:1.20.120.370,G3DSA:2.70.170.10	SSF63712									
aly6119.3	Fatty acyl-CoA reductase 1	GO:0005737,GO:0045177,GO:0005778,GO:0080019,GO:0016021,GO:0035149,GO:0035002,GO:0050062,GO:0010025,GO:0046474,GO:0035336,GO:0008611	CG1443-PA						PF03015,PF07993,PF07993				G3DSA:3.40.50.720	SSF51735	42~69		REACT_22258						
aly6119.4	Unknown		n/a												293~313								
aly61233.1	Bardet-Biedl syndrome 1 protein	GO:0006996,GO:0036064,GO:0050896,GO:0042384,GO:0035058,GO:0060170,GO:0005813,GO:0005829,GO:0001103,GO:0007601,GO:0043001,GO:0061512,GO:0003674,GO:0005119,GO:0005929,GO:0001895,GO:0005113,GO:0005930,GO:0045494,GO:0034464	CG14825-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6128.1	Calumenin-B	GO:0005737,GO:0042470,GO:0006325,GO:0005634,GO:0005703,GO:0005700,GO:0006265,GO:0003916,GO:0005509,GO:0005576,GO:0033018,GO:0009047,GO:0045893	CG9148-PA						PF13202	PS50222,PS50222,PS50222,PS50222,PS50222,PS50222		PS00018,PS00018,PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473,SSF47473									
aly6128.2	Ubiquitin carboxyl-terminal hydrolase 46	GO:0007610,GO:0032228,GO:0045746,GO:0006511,GO:0016579,GO:0004843	CG7023-PB						PF00443	PS50235			G3DSA:2.20.210.10	SSF54001,SSF54001									
aly6128.3	60S ribosomal protein L21	GO:0000184,GO:0022625,GO:0019083,GO:0006614,GO:0000022,GO:0005737,GO:0044267,GO:0005730,GO:0016020,GO:0003735,GO:0010467,GO:0019058,GO:0051298,GO:0044822,GO:0007052,GO:0005840,GO:0005829,GO:0003723,GO:0016032,GO:0006415,GO:0006414,GO:0006413,GO:0006412	CG12775-PA						PF01157			PS01171	G3DSA:2.30.30.70	SSF50104									
aly6128.4	Unknown	GO:0046872	n/a							PS50157		PS00028			237~257								
aly6128.5	Nitric oxide synthase-interacting protein homolog	GO:0005737,GO:0071013,GO:0000398,GO:0003674,GO:0051001,GO:0005634,GO:0043086	CG6179-PA			PIRSF023577			PF04641,PF15906				G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57850,SSF57850	71~108								
aly6128.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly613.1	Unknown		n/a						PF15359														
aly613.2	Unknown	GO:0004129,GO:0005751,GO:0006123	CG2249-PA						PF02935				G3DSA:4.10.49.10	SSF81427									
aly613.3	Actin-related protein 6	GO:0004129,GO:0005737,GO:0006338,GO:0005634,GO:0070828,GO:0005856,GO:0000785,GO:0003682	CG11678-PA				SM00268		PF02935,PF00022				G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.90.640.10,G3DSA:4.10.49.10	SSF81427,SSF53067,SSF53067									
aly613.4	T-complex protein 1 subunit epsilon	GO:0031681,GO:0006457,GO:0042623,GO:0051082,GO:0005815,GO:0007052,GO:0005832,GO:0022008,GO:0005875,GO:0005524	CG8439-PA						PF00118				G3DSA:1.10.560.10	SSF48592									
aly6139.1	Unknown		n/a																				
aly614.1	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005886,GO:0006508	CG8172-PF				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly614.10	Unknown		n/a																				
aly614.11	Ephrin-B2a	GO:0016319,GO:0005886,GO:0008039,GO:0035475,GO:0007422,GO:0016021,GO:0016020,GO:0050920,GO:0035011,GO:0048514,GO:0021654,GO:0005887,GO:0003404,GO:0007155,GO:0007411,GO:0007412,GO:0001756,GO:0046875,GO:0048013,GO:0002042,GO:0009952	CG1862-PA						PF00812	PS51551	PR01347,PR01347,PR01347,PR01347		G3DSA:2.60.40.420	SSF49503									
aly614.12	Unknown		CG5903-PA						PF09769														
aly614.13	Unknown		n/a																				
aly614.14	Unknown		n/a																				
aly614.15	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly614.16	Unknown		n/a																				
aly614.17	Unknown		n/a																				
aly614.2	Luciferin 4-monooxygenase	GO:0046872,GO:0006637,GO:0045289,GO:0004321,GO:0005777,GO:0003824,GO:0004467,GO:0046949,GO:0008152,GO:0001676,GO:0008218,GO:0047077,GO:0005524	CG6178-PA						PF00501,PF13193			PS00455	G3DSA:3.40.50.980,G3DSA:2.30.38.10,G3DSA:3.30.300.30,G3DSA:3.40.50.980	SSF56801										
aly614.3	Unknown		n/a				SM00355,SM00355																
aly614.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly614.5	Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha	GO:0016310,GO:0072661,GO:0048041,GO:0060326,GO:0005925,GO:0005737,GO:0031532,GO:0005634,GO:0005654,GO:0008582,GO:0010761,GO:0005524,GO:0016607,GO:0016308,GO:0030027,GO:0046854,GO:0016307,GO:0019900,GO:0046488,GO:0005886,GO:0032587,GO:0005847,GO:0097178,GO:0008654,GO:0090630,GO:0005575	CG3682-PI				SM00330		PF01504	PS51455			G3DSA:3.30.800.10,G3DSA:3.30.810.10,G3DSA:3.30.810.10	SSF56104	333~353									
aly614.6	Unknown		n/a																				
aly614.7	Halomucin	GO:0016020,GO:0005576,GO:0005509,GO:0007156,GO:0030246	CG7946-PA						PF11467					SSF140576	294~314,262~283								
aly614.8	Probable V-type proton ATPase subunit D 2	GO:0042626,GO:0015992,GO:0015991,GO:0016020,GO:0000221,GO:0046961,GO:0033176	CG8310-PB						PF01813,PF01813						683~713,724~748,124~147,403~423,632~652								
aly614.9	V-type proton ATPase subunit D	GO:0042626,GO:0015992	n/a						PF01813														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly615.1	Unknown	GO:0007157,GO:0005576,GO:0003674,GO:0031225	CG14064-PA						PF08205	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly616.1	Unknown		n/a																				
aly61640.1	Unknown	GO:0046872	n/a							PS50157		PS00028	G3DSA:3.30.160.60	SSF57667									
aly6168.1	Protein disconnected	GO:0007469,GO:0007479,GO:0007623,GO:0007420,GO:0003700,GO:0050896,GO:0005634,GO:0007601,GO:0001158,GO:0006355,GO:0045944,GO:0045475,GO:0008062,GO:0003677,GO:0046872,GO:0010468,GO:0045494,GO:0045893	CG32577-PA				SM00355,SM00355,SM00355,SM00355		PF12874,PF12874	PS50157,PS50157		PS00028,PS00028		SSF57667										
aly61803.1	Unknown		n/a						PF03372				G3DSA:3.60.10.10	SSF56219									
aly61829.1	Unknown	GO:0003676	n/a										G3DSA:3.30.420.10	SSF53098									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly619.1	Elongation of very long chain fatty acids protein AAEL008004	GO:0006633,GO:0005575,GO:0016021,GO:0030497,GO:0009922,GO:0016740,GO:0030176,GO:0000038	CG31522-PI						PF01151							00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					
aly619.10	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	GO:0006654,GO:0006644,GO:0005635,GO:0005783,GO:0008654,GO:0016021,GO:0016020,GO:0016024,GO:0003841,GO:0019432,GO:0016746,GO:0044281,GO:0008152,GO:0005886,GO:0046474,GO:0044255,GO:0005789	CG4729-PE				SM00563		PF01553,PF16076					SSF69593									
aly619.11	Peroxisome biogenesis factor 2	GO:0006635,GO:0048147,GO:0000038,GO:0050680,GO:0001764,GO:0008270,GO:0016593,GO:0000209,GO:0005779,GO:0005778,GO:0000122,GO:0016020,GO:0005777,GO:0045540,GO:0007112,GO:0007285,GO:0007286,GO:0042632,GO:0004842,GO:0048137,GO:0007031,GO:0031648,GO:0016558,GO:0006699	CG7081-PA						PF04757	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850									
aly619.12	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG9299-PC						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly619.14	Unknown		n/a																				
aly619.15	Cuticle protein 8	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.16	Cuticle protein 19	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG1919-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.17	Cuticle protein 7	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG1919-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.18	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.19	Cuticle protein 19	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly619.2	Sulfatase-modifying factor 1	GO:0044267,GO:0043687,GO:0005788,GO:0005575,GO:0008150,GO:0006687,GO:0003674,GO:0046872,GO:0044281,GO:0006665,GO:0016491	CG7049-PA						PF03781				G3DSA:3.90.1580.10	SSF56436									
aly619.20	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.21	Pupal cuticle protein Edg-84A	GO:0040003,GO:0005214,GO:0008011,GO:0007601,GO:0008010,GO:0005212,GO:0031012,GO:0005576,GO:0005509,GO:0048058,GO:0042302	CG16963-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.22	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG1919-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.23	Unknown		n/a																				
aly619.24	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG1919-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly619.25	Cuticle protein	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155													
aly619.26	Cuticle protein	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG1919-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.27	Cuticle protein 8	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.28	Cuticle protein 8	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG1919-PA						PF00379	PS51155		PS00233											
aly619.29	Cuticle protein 8	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.3	TraB domain-containing protein		CG12360-PA						PF01963														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly619.30	Cuticle protein 8	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG1919-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.31	Cuticle protein 8	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG34461-PA						PF00379,PF00379	PS51155,PS51155	PR00947,PR00947,PR00947	PS00233,PS00233											
aly619.32	Cuticle protein 18.6, isoform B	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.33	Cuticle protein 18.6, isoform B	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.34	Pupal cuticle protein Edg-84A	GO:0040003,GO:0005214,GO:0008011,GO:0008010,GO:0031012,GO:0042302	CG2345-PA						PF00379,PF00379	PS51155,PS51155	PR00947,PR00947,PR00947	PS00233,PS00233											
aly619.35	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947				151~152								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly619.36	Cuticle protein 7	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly619.37	Cuticle protein 18.6, isoform B	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG34461-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly619.38	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG1919-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly619.4	TraB domain-containing protein		CG12360-PA						PF01963														
aly619.5	ATP synthase subunit epsilon, mitochondrial	GO:0015986,GO:0015992,GO:0046933,GO:0000275,GO:0005739,GO:0005753,GO:0046331,GO:0046961,GO:0008340,GO:0008553,GO:0006979	CG9032-PA						PF04627				G3DSA:1.10.1620.20	SSF48690									
aly619.6	Probable tRNA N6-adenosine threonylcarbamoyltransferase, mitochondrial	GO:0004222,GO:0000408,GO:0005739,GO:0005575,GO:0008150,GO:0016747,GO:0003674,GO:0046872,GO:0070526	CG14231-PB	MF_01445				TIGR00329	PF00814		PR00789,PR00789,PR00789,PR00789,PR00789,PR00789		G3DSA:3.30.420.40	SSF53067									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly619.7	Osteopetrosis-associated transmembrane protein 1	GO:0005737,GO:0016021,GO:0043231,GO:0005829,GO:0030316,GO:0005765,GO:0005634	CG14969-PA						PF09777														
aly619.8	Chromatin modification-related protein MEAF6	GO:0044154,GO:0005730,GO:0043968,GO:0043983,GO:0043981,GO:0070776,GO:0006355,GO:0043982,GO:0003674,GO:0035267,GO:0008150,GO:0006351	CG12756-PA						PF09340						268~274,36~56								
aly619.9	Gonadal protein gdl	GO:0007283,GO:0048477	CG33756-PA						PF07324														
aly6190.1	Gametocyte-specific factor 1	GO:0046872	CG34283-PA						PF05253,PF05253					SSF57667									
aly62019.1	Unknown		n/a																				
aly6208.1	Protein FAM188B2		CG14142-PB						PF13898														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6209.1	Two pore calcium channel protein 1	GO:0072345,GO:0034220,GO:0016021,GO:0006816,GO:0005765,GO:0005886,GO:0005245,GO:0086010,GO:0010008	n/a																				
aly6209.10	Arginine kinase	GO:0004054,GO:0016772,GO:0016301,GO:0005576,GO:0016310,GO:0005524	CG32031-PA						PF02807,PF00217	PS51509,PS51510		PS00112	G3DSA:1.10.135.10,G3DSA:3.30.590.10	SSF55931,SSF48034			REACT_13						
aly6209.11	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	GO:0005737,GO:0019509,GO:0010309,GO:0005634,GO:0005506,GO:0055114	CG32068-PB	MF_03154					PF03079				G3DSA:2.60.120.10	SSF51182		00270+1.13.11.54		PWY-4361	UPA00904				
aly6209.12	Unknown		CG12991-PE																				
aly6209.2	Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase	GO:0040003,GO:0005783,GO:0006487,GO:0016021,GO:0016020,GO:0042281,GO:0046527,GO:0006490,GO:0005789	CG5091-PB						PF03155,PF00288		PR00959,PR00959,PR00959		G3DSA:3.30.70.890,G3DSA:3.30.230.10	SSF55060,SSF54211		00520+2.7.1.6,00052+2.7.1.6	REACT_17015	PWY-6317,PWY-6527,PWY-3821	UPA00214,UPA00378				
aly6209.3	DNA repair and recombination protein RAD54-like	GO:0030261,GO:0003677,GO:0007067,GO:0051301,GO:0010212,GO:0006302,GO:0000724,GO:0005634,GO:0048477,GO:0005524,GO:0006281,GO:0004003,GO:0004386,GO:0007131,GO:0006310,GO:0045003,GO:0006338,GO:0000711,GO:0008298,GO:0043150,GO:0006417,GO:0046843	CG3736-PA				SM00487,SM00490		PF00176,PF08658,PF00271	PS51192,PS51194			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	724~744								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6209.4	GPI mannosyltransferase 4	GO:0005783,GO:0016021,GO:0097502,GO:0005789,GO:0016757,GO:0006506,GO:0000026,GO:0000030	CG45068-PA						PF03901														
aly6209.5	Protein RRNAD1	GO:0016021	CG2906-PD						PF13679				G3DSA:3.40.50.150										
aly6209.6	Peptidyl-alpha-hydroxyglycine alpha-amidating lyase 1	GO:0004504,GO:0016021,GO:0016020,GO:0004598,GO:0005886,GO:0006518,GO:0005507,GO:0043025,GO:0055114	CG12130-PD						PF01436,PF01436	PS51125,PS51125,PS51125,PS51125,PS51125	PR00790,PR00790,PR00790,PR00790		G3DSA:2.120.10.30,G3DSA:2.120.10.30	SSF101898	40~60								
aly6209.7	Zinc finger CCHC domain containing protein 7	GO:0008270,GO:0003676,GO:0005730	CG9715-PA				SM00343,SM00343,SM00343,SM00343,SM00343			PS50158,PS50158			G3DSA:4.10.60.10	SSF57756										
aly6209.8	Unknown		n/a																				
aly6209.9	Chromatin accessibility complex protein 1	GO:0043565,GO:0003887,GO:0008622,GO:0008623,GO:0006338,GO:0006974,GO:0003677,GO:0046982,GO:0071897	CG15736-PA						PF00808				G3DSA:1.10.20.10	SSF47113									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6213.1	IQ motif and SEC7 domain-containing protein 1	GO:0005737,GO:0016020,GO:0016192,GO:0007476,GO:0005634,GO:0005802,GO:0005085,GO:0008289,GO:0030036,GO:0005086,GO:0045296,GO:0007520,GO:0032012,GO:0002121,GO:0030054,GO:0007417	CG32434-PB				SM00222		PF16453,PF01369	PS50190			G3DSA:1.10.1000.11,G3DSA:2.30.29.30,G3DSA:1.10.220.20	SSF48425,SSF50729	3~37								
aly6228.1	Unknown		n/a																				
aly6228.2	Ras-like protein family member 10B	GO:0003050,GO:0016020,GO:0005622,GO:0005575,GO:0090277,GO:0003674,GO:0008150,GO:0005886,GO:0006184,GO:0007264,GO:0005525	CG14669-PA				SM00175,SM00173,SM00174	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly625.1	Protein Dok-7	GO:0008289,GO:0019901,GO:0045202,GO:0005886,GO:0061098,GO:0030054	n/a						PF02174	PS51064			G3DSA:2.30.29.30,G3DSA:2.30.29.30	SSF50729,SSF50729									
aly625.2	Membrane-bound alkaline phosphatase	GO:0016791,GO:0004035,GO:0008152,GO:0005886,GO:0046872,GO:0031225	CG1809-PA				SM00098		PF00245		PR00113,PR00113,PR00113,PR00113,PR00113,PR00113	PS00123	G3DSA:3.40.720.10	SSF53649		00627+3.1.3.1,00790+3.1.3.1		PWY-5491					
aly625.3	Membrane-bound alkaline phosphatase	GO:0004035,GO:0003824,GO:0008152,GO:0005886,GO:0046872,GO:0031225	CG1809-PA				SM00098		PF00245		PR00113,PR00113,PR00113,PR00113,PR00113,PR00113		G3DSA:3.40.720.10	SSF53649		00627+3.1.3.1,00790+3.1.3.1		PWY-5491					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly62506.1	Unknown	GO:0035253	CG6129-PD												89~109,124~183,30~74								
aly6261.1	Unknown		n/a																				
aly6266.1	G-protein coupled receptor Mth2	GO:0006950,GO:0004930,GO:0007186,GO:0016021,GO:0005886	CG31720-PC						PF00002	PS50261													
aly6266.2	G-protein coupled receptor Mth2	GO:0004930,GO:0016021,GO:0006950,GO:0005886,GO:0008340,GO:0007186	CG17061-PB											SSF63877										
aly6271.1	Cleavage and polyadenylation specificity factor subunit CG7185	GO:0000381,GO:0006397,GO:0005634,GO:0005849,GO:0000166,GO:0003676,GO:0006379,GO:0003729	CG7185-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly6271.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6271.3	Synaptotagmin 9	GO:0008021,GO:0006887,GO:0050803,GO:0060024,GO:0031045,GO:0031594,GO:0031340,GO:0030285,GO:0048488,GO:0048489,GO:0030667,GO:0016021,GO:0016020,GO:0005544,GO:0017158,GO:0045956,GO:0005509,GO:0005886,GO:0001786,GO:0042803,GO:0005215,GO:0050796,GO:0007317,GO:0030276,GO:0007269,GO:0007268,GO:0030672,GO:0008345,GO:0043195,GO:0016192,GO:0016079,GO:0030054,GO:0048791,GO:1900073,GO:0005515,GO:0019905,GO:0000149	CG3139-PA				SM00239,SM00239		PF00168,PF00168	PS50004,PS50004	PR00360,PR00360,PR00360,PR00399,PR00399,PR00399,PR00399		G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562									
aly62754.1	Putative glucosylceramidase 3	GO:0006665,GO:0005975,GO:0034620,GO:0004348	CG31148-PA						PF02055				G3DSA:2.60.40.1180,G3DSA:3.20.20.80	SSF51445									
aly62816.1	Protocadherin-like protein	GO:0016324,GO:0046843,GO:0016339,GO:0016020,GO:0005902,GO:0005509,GO:0005887,GO:0005886,GO:0044331,GO:0007156,GO:0016021,GO:0042803	CG6445-PB				SM00112		PF00028	PS50268			G3DSA:2.60.40.60	SSF49313									
aly6282.1	Unknown		n/a																				
aly6286.1	Sodium-dependent nutrient amino acid transporter 1	GO:0017032,GO:0005328,GO:0003333,GO:0016021,GO:0006814,GO:0015804,GO:0005283,GO:1903825,GO:0015807,GO:0015179,GO:0005887,GO:0006836,GO:0042940,GO:0042943,GO:0015175,GO:0005326	CG3252-PA						PF00209	PS50267	PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176	PS00610		SSF161070									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6286.10	Unknown	GO:0016324,GO:0007370	CG5507-PA																				
aly6286.11	Dynein intermediate chain 3, ciliary	GO:0005737,GO:0042623,GO:0007605,GO:0005929,GO:0007018,GO:0005875,GO:0005515,GO:0005868,GO:0030286,GO:0005874,GO:0003774	CG6053-PC				SM00320,SM00320,SM00320,SM00320,SM00320		PF00400				G3DSA:2.130.10.10	SSF50978											
aly6286.12	Unknown		n/a																				
aly6286.2	Carboxypeptidase B	GO:0006508,GO:0004181,GO:0005576,GO:0008270	CG3097-PA				SM00631		PF00246				G3DSA:3.40.630.10	SSF53187									
aly6286.3	Carboxypeptidase B	GO:0006508,GO:0004181,GO:0005576,GO:0008270	CG8539-PA				SM00631		PF00246				G3DSA:3.40.630.10	SSF53187									
aly6286.4	Unknown		CG13671-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6286.5	Thioredoxin domain-containing protein 11	GO:0045454,GO:0016021,GO:0005789	CG13671-PA										G3DSA:3.40.30.10	SSF52833									
aly6286.6	Nuclear distribution protein nudE-like 1-B	GO:0005874,GO:0031616,GO:0005871,GO:0007298,GO:0051303,GO:0051225,GO:0005737,GO:0007020,GO:0007100,GO:0005819,GO:0005813,GO:0047496,GO:0005635,GO:0007060,GO:0007080,GO:0016477,GO:0051298,GO:0008017,GO:0007052,GO:0010975,GO:0007059,GO:0051642,GO:0000776,GO:0000132,GO:0070732	CG8104-PC						PF04880						135~179,12~99		REACT_152,REACT_383							
aly6286.7	Phosphatidylinositol N-acetylglucosaminyltransferase subunit Q	GO:0017176,GO:0016021,GO:0005789,GO:0000506,GO:0006506	CG32578-PB						PF05024										UPA00196				
aly6286.8	Putative RNA-binding protein Luc7-like 1	GO:0045843,GO:0071011,GO:0000398,GO:0006376,GO:0005685,GO:0042802,GO:0003729	CG7564-PA						PF03194						271~291,229~249,156~176,98~118								
aly6286.9	Putative homeodomain transcription factor	GO:0003700,GO:0005634,GO:0006357,GO:0006351,GO:0003677,GO:0046983	CG3268-PA						PF12129						810~818								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6295.1	Unknown	GO:0016747	CG42329-PA																				
aly62965.1	Unknown		n/a																				
aly62979.1	Unknown		n/a																				
aly6301.1	Fatty acid synthase	GO:0006633,GO:0047451,GO:0008144,GO:0008270,GO:0001649,GO:0016491,GO:0070062,GO:0016295,GO:0005835,GO:0004320,GO:0071353,GO:0005739,GO:0030879,GO:0042802,GO:0042803,GO:0005794,GO:0044822,GO:0004315,GO:0016788,GO:0047117,GO:0042587,GO:0005886,GO:0055114,GO:0008610,GO:0006084,GO:0042470,GO:0005829,GO:0004312,GO:0004313,GO:0016296,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319	CG17374-PC				SM00825,SM00827		PF00109,PF16197,PF00698				G3DSA:3.40.47.10,G3DSA:3.40.366.10,G3DSA:3.40.47.10	SSF52151,SSF53901,SSF53901	325~345								
aly6301.2	Unknown		n/a										G3DSA:3.90.180.10	SSF50129									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6301.3	Unknown		n/a							PS51257			G3DSA:3.90.180.10	SSF50129									
aly63070.1	Unknown		n/a																				
aly631.1	Unknown		n/a																				
aly631.2	Unknown		n/a																				
aly631.3	Unknown		n/a																				
aly631.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6311.1	Nuclear factor NF-kappa-B p110 subunit	GO:0006963,GO:0034198,GO:0006967,GO:0006964,GO:0045429,GO:0001077,GO:0010628,GO:0007165,GO:0008063,GO:0050829,GO:0005737,GO:0043565,GO:0005719,GO:0005634,GO:0009617,GO:0006366,GO:2000647,GO:0000981,GO:0045089,GO:0045088,GO:0045087,GO:0006974,GO:0006955,GO:0061057,GO:0003677,GO:0051607,GO:0003700,GO:0006355,GO:0048813,GO:0002230,GO:0045944,GO:0005515,GO:0048935	CG11992-PC						PF00554	PS50254			G3DSA:2.60.40.340	SSF49417										
aly6311.10	Venom allergen 3	GO:0008150,GO:0005576,GO:0003674	CG8483-PA				SM00198		PF00188		PR00837,PR00837,PR00837,PR00838,PR00838,PR00838		G3DSA:3.40.33.10	SSF55797									
aly6311.11	Neuropeptide Y receptor	GO:0004930,GO:0005887,GO:0016021,GO:0005886,GO:0007218,GO:0004983,GO:0001653,GO:0007166,GO:0008188,GO:0007186	CG5811-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR01012,PR01012,PR01012,PR01012,PR01012,PR01012	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly6311.12	Unknown		n/a																				
aly6311.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6311.14	Neuropeptide Y receptor	GO:0004930,GO:0007166,GO:0016021,GO:0005886,GO:0007218,GO:0004983,GO:0001653,GO:0005887,GO:0008188,GO:0007186	CG5811-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR01012,PR01012,PR01012,PR01012,PR01012	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly6311.15	Retinol dehydrogenase 12	GO:0016614,GO:0050896,GO:0007601,GO:0005622,GO:0008152,GO:0042572,GO:0004745	CG7675-PB						PF00106		PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									
aly6311.16	Aldehyde dehydrogenase	GO:0004029,GO:0005739,GO:0006068,GO:0008152,GO:0005759,GO:0006090,GO:0055114,GO:0016491	CG31075-PB						PF00171			PS00070,PS00687	G3DSA:3.40.605.10,G3DSA:3.40.309.10	SSF53720									
aly6311.2	Bifunctional purine biosynthesis protein PURH	GO:0003937,GO:0005829,GO:0004643,GO:0042060,GO:0006189,GO:0044281,GO:0006164,GO:0006144,GO:0055086,GO:0042803	CG11089-PB	MF_00139		PIRSF000414	SM00851,SM00798	TIGR00355	PF01808,PF02142				G3DSA:3.40.140.20,G3DSA:3.40.140.20,G3DSA:3.40.140.20,G3DSA:1.10.287.440,G3DSA:3.40.50.1380	SSF52335,SSF53927		00230+3.5.4.10+2.1.2.3,00670+2.1.2.3		PWY-6123,PWY-6124,PWY-7234	UPA00074				
aly6311.3	Putative methyltransferase C9orf114	GO:0044822,GO:0005575,GO:0003674,GO:0007049,GO:0008168,GO:0008150,GO:0051301,GO:0000777	CG12128-PA						PF02598				G3DSA:3.40.1280.10,G3DSA:3.40.1280.10	SSF75217,SSF75217,SSF50249	37~61								
aly6311.4	Ribulose-phosphate 3-epimerase	GO:0016857,GO:0019323,GO:0005975,GO:0070062,GO:0005829,GO:0006098,GO:0044281,GO:0009052,GO:0044262,GO:0004750,GO:0046872,GO:0042802,GO:0042803	CG30499-PA			PIRSF001461		TIGR01163	PF00834			PS01085,PS01086	G3DSA:3.20.20.70	SSF51366		00040+5.1.3.1,00030+5.1.3.1,00710+5.1.3.1		PWY-5723,PWY-1861					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6311.5	Complex III assembly factor LYRM7	GO:0005759	CG34150-PB												30~50								
aly6311.6	NADH dehydrogenase [ubiqui] 1 beta subcomplex subunit 2, mitochondrial	GO:0005747,GO:0055114	CG40472-PC						PF14813						9~29								
aly6311.7	SH3 domain-containing kinase-binding protein 1	GO:0017124,GO:0045202,GO:0007298,GO:0001745,GO:0042981,GO:0048260,GO:0005070,GO:0005925,GO:0045171,GO:0043063,GO:0016477,GO:0048749,GO:0005856,GO:0043005,GO:0006915,GO:0032154,GO:0030659,GO:0046331,GO:0005911,GO:0007010,GO:0050839,GO:0000910,GO:0007015,GO:0006897,GO:0030496,GO:0008360,GO:0005515	CG31012-PJ				SM00326,SM00326,SM00326		PF14604,PF14604,PF14604	PS50002,PS50002,PS50002	PR00452,PR00452,PR00452,PR00499,PR00499,PR00499		G3DSA:2.30.30.40,G3DSA:2.30.30.40,G3DSA:2.30.30.40,G3DSA:2.30.30.40	SSF50044,SSF50044,SSF50044										
aly6311.8	Unknown	GO:0005070,GO:0007015,GO:0001745,GO:0048749,GO:0045171,GO:0030496,GO:0017124,GO:0032154,GO:0046331,GO:0043063,GO:0000910,GO:0007298,GO:0050839,GO:0048260	CG31012-PJ												360~394								
aly6311.9	Leucine-rich repeat-containing protein C10orf11 homolog	GO:0005575,GO:0003674,GO:0046579,GO:0030318	CG31447-PA						PF14580	PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6315.1	Forkhead box protein O	GO:0035206,GO:0003677,GO:0010259,GO:0009790,GO:0001077,GO:0034198,GO:0001745,GO:0007049,GO:0005737,GO:0043565,GO:0040027,GO:0030308,GO:0000122,GO:0005634,GO:0009617,GO:0007476,GO:0006979,GO:0003690,GO:0010506,GO:0006171,GO:0016241,GO:0008285,GO:0008286,GO:0030154,GO:0007623,GO:0007389,GO:2000253,GO:0008134,GO:0009888,GO:0046626,GO:0046627,GO:0006974,GO:0001558,GO:0008301,GO:0045893,GO:0009267,GO:0019216,GO:0008340,GO:0034599,GO:0036099,GO:0019901,GO:0045792,GO:0040015,GO:0005977,GO:0042593,GO:0003700,GO:0001578,GO:0005829,GO:0003705,GO:0006355,GO:0048813,GO:0051090,GO:0045944,GO:0006351,GO:0005667,GO:1900078,GO:0040008,GO:0010888	CG3143-PF				SM00339		PF00250,PF16676	PS50039	PR00053,PR00053,PR00053	PS00658	G3DSA:1.10.10.10	SSF46785										
aly6315.2	Unknown		n/a						PF16020														
aly6315.3	DnaJ homolog subfamily C member 8		CG10375-PA				SM00271		PF00226	PS50076	PR00625,PR00625,PR00625		G3DSA:1.10.287.110	SSF46565	176~196,113~136								
aly6315.4	Tropi reductase 2	GO:0009710,GO:0050358,GO:0008152,GO:0016491	CG31548-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735									
aly6315.5	Peptidoglycan recognition protein	GO:0032500,GO:0005887,GO:0005515,GO:0008329,GO:0008745,GO:0045087,GO:0006955,GO:0006965,GO:0008063,GO:0006952,GO:0016045,GO:0050830,GO:0005576,GO:0008270,GO:0008592,GO:0009253,GO:0032494,GO:0016019,GO:0042834	CG11709-PA				SM00701,SM00644		PF01510				G3DSA:3.40.80.10	SSF55846										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6315.6	Peptidoglycan recognition protein	GO:0032500,GO:0005887,GO:0005515,GO:0008329,GO:0008745,GO:0045087,GO:0006955,GO:0006965,GO:0008063,GO:0006952,GO:0016045,GO:0050830,GO:0005576,GO:0008270,GO:0008592,GO:0009253,GO:0032494,GO:0016019,GO:0042834	CG11709-PA				SM00701,SM00644		PF01510				G3DSA:3.40.80.10	SSF55846	209~229								
aly6315.7	Peptidoglycan recognition protein	GO:0032500,GO:0005887,GO:0005515,GO:0008329,GO:0008745,GO:0045087,GO:0006955,GO:0006965,GO:0008063,GO:0006952,GO:0016045,GO:0050830,GO:0005576,GO:0008270,GO:0008592,GO:0009253,GO:0032494,GO:0016019,GO:0042834	CG11709-PA				SM00701		PF01510				G3DSA:3.40.80.10	SSF55846									
aly632.1	Unknown		n/a																				
aly632.10	Chaoptin	GO:0004930,GO:0016028,GO:0042052,GO:0050896,GO:0007601,GO:0035996,GO:0046658,GO:0005515,GO:0005886,GO:0007156	CG4168-PC				SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00369,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364		PF13855,PF13855,PF13855,PF13855,PF13855	PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52058,SSF52058,SSF52058									
aly632.11	60S ribosomal protein L38	GO:0003735,GO:0005622,GO:0022625,GO:0006412,GO:0005840	CG18001-PA						PF01781														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly632.12	NAD-dependent protein deacetylase Sirt7	GO:0016787,GO:0046872,GO:0070403	CG11305-PA						PF02146	PS50305			G3DSA:3.40.50.1220,G3DSA:3.40.50.1220	SSF52467									
aly632.13	Unknown		n/a																				
aly632.14	Unknown		n/a												51~71,82~102								
aly632.2	Unknown		n/a																				
aly632.3	28S ribosomal protein S33, mitochondrial	GO:0003735,GO:0005743,GO:0005840,GO:0006412,GO:0005763	CG10406-PA						PF08293														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly632.4	Tuberin	GO:0033596,GO:0008104,GO:0006909,GO:0030308,GO:0005794,GO:0014065,GO:0046323,GO:0048009,GO:0007165,GO:0050918,GO:0001666,GO:0008543,GO:0038202,GO:0005737,GO:0016032,GO:0043547,GO:0030100,GO:0005634,GO:0016020,GO:0006469,GO:0030178,GO:0051898,GO:0010467,GO:0006367,GO:0071456,GO:0001843,GO:0048477,GO:0045087,GO:0044861,GO:0042803,GO:0008285,GO:0008286,GO:0005099,GO:0006629,GO:0007507,GO:0046621,GO:0007584,GO:0005096,GO:0046626,GO:0046627,GO:0006974,GO:0019900,GO:0046331,GO:0007173,GO:0038095,GO:0048011,GO:0008340,GO:0014067,GO:0048015,GO:0048471,GO:0042325,GO:0007050,GO:0019902,GO:0045792,GO:0006897,GO:0016192,GO:0051726,GO:0043491,GO:0005829,GO:0006606,GO:0032320,GO:0045886,GO:0045944,GO:0005515,GO:0032007,GO:0001934	CG6975-PA						PF03542,PF02145	PS50085	PR01431,PR01431			SSF111347									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly632.5	Tuberin	GO:0033596,GO:0008104,GO:0006909,GO:0030308,GO:0005794,GO:0014065,GO:0046323,GO:0048009,GO:0005488,GO:0050918,GO:0001666,GO:0008543,GO:0038202,GO:0005737,GO:0016032,GO:0043547,GO:0030100,GO:0005634,GO:0016020,GO:0006469,GO:0030178,GO:0051898,GO:0010467,GO:0006367,GO:0071456,GO:0001843,GO:0048477,GO:0045087,GO:0044861,GO:0042803,GO:0008285,GO:0008286,GO:0005099,GO:0006629,GO:0007507,GO:0046621,GO:0007584,GO:0005096,GO:0046626,GO:0046627,GO:0006974,GO:0019900,GO:0046331,GO:0007173,GO:0038095,GO:0048011,GO:0008340,GO:0014067,GO:0048015,GO:0048471,GO:0042325,GO:0007050,GO:0019902,GO:0045792,GO:0006897,GO:0016192,GO:0051726,GO:0043491,GO:0005829,GO:0006606,GO:0032320,GO:0045886,GO:0045944,GO:0005515,GO:0032007,GO:0001934,GO:0007165	CG6975-PA						PF11864				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371										
aly632.6	Alpha-1,6-mannosyl-glycoprotein 2 beta-N-acetylglucosaminyltransferase	GO:0005795,GO:0008455,GO:0005797,GO:0006487,GO:0018279,GO:0016021,GO:0016020,GO:0009311,GO:0030246,GO:0009312,GO:0005794,GO:0008375,GO:0000139,GO:0044267,GO:0043687	CG7921-PA						PF05060				G3DSA:3.90.550.10			00513+2.4.1.143,00510+2.4.1.143		PWY-7426	UPA00378				
aly632.7	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9512-PA			PIRSF000137			PF05199,PF00732			PS00623,PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly632.8	Unknown		n/a																				
aly632.9	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9512-PA			PIRSF000137			PF05199,PF00732			PS00623,PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly63340.1	Aconitate hydratase, mitochondrial	GO:0051538,GO:0051539,GO:0043209,GO:0005634,GO:0005811,GO:0005739,GO:0006099,GO:0006101,GO:0044237,GO:0006102,GO:0005759,GO:0003994,GO:0006091,GO:0005506,GO:0044281	CG9244-PB						PF00330		PR00415,PR00415	PS00450	G3DSA:3.40.1060.10,G3DSA:3.30.499.10	SSF53732		00290+4.2.1.33			UPA00048				
aly6339.1	Glucose 1,6-bisphosphate synthase	GO:0004614,GO:0005829,GO:0000287,GO:0016052,GO:0071704,GO:0047933,GO:0004615,GO:0016868,GO:0006006,GO:0046872	CG8073-PA						PF00408				G3DSA:3.30.310.50	SSF55957		00520+5.4.2.10		PWY-6749					
aly6339.2	cGMP-dependent 3',5' cyclic phosphodiesterase	GO:0004118,GO:0005783,GO:0047555,GO:0004115,GO:0071260,GO:0004112,GO:0008144,GO:0019934,GO:0035690,GO:0007165,GO:0006198,GO:0019933,GO:0046068,GO:0046069,GO:0061028,GO:0005737,GO:0097011,GO:0050729,GO:0036006,GO:0030818,GO:0000122,GO:0005634,GO:0005759,GO:0048471,GO:0046872,GO:0005794,GO:0046058,GO:0046038,GO:0030814,GO:0006626,GO:0046331,GO:0008152,GO:0005886,GO:0033159,GO:0030553,GO:0042734,GO:0071321,GO:0005575,GO:0005829,GO:0043117,GO:0043116	CG34341-PF				SM00065		PF01590,PF00233		PR00387,PR00387,PR00387	PS00126	G3DSA:1.10.1300.10,G3DSA:3.30.450.40	SSF109604,SSF55781	688~704								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6339.3	UBX domain-containing protein 1	GO:0005737,GO:0046872	CG8209-PA				SM00166,SM00165		PF00627,PF00789	PS50157,PS50030,PS50033		PS00028	G3DSA:1.10.8.10,G3DSA:3.10.20.90	SSF54236,SSF54236,SSF46934	119~146								
aly6339.4	Ribonuclease Oy	GO:0033897,GO:0005615,GO:0032504,GO:0004540,GO:0004521,GO:0005576,GO:0003723,GO:0006401	CG8194-PA						PF00445			PS00531	G3DSA:3.90.730.10	SSF55895									
aly6339.5	Unknown		n/a																				
aly6345.1	Unknown		n/a																				
aly636.1	Unknown		n/a												56~83								
aly636.10	Mitochondrial import inner membrane translocase subunit Tim23	GO:0044267,GO:0015450,GO:0006626,GO:0005739,GO:0031305,GO:0005743,GO:0005744,GO:0005758	CG40042-PA						PF02466						187~193								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly636.11	Sister chromatid cohesion protein DCC1	GO:0034088,GO:0006275,GO:0005654,GO:0000785,GO:0003677,GO:0006260,GO:0000775,GO:0031390	CG11788-PA						PF09724														
aly636.12	Unknown		n/a																				
aly636.13	Unknown		n/a																				
aly636.2	Dysbindin	GO:0008021,GO:0007616,GO:0007614,GO:0007596,GO:0030426,GO:0005789,GO:0048047,GO:0048167,GO:0060155,GO:0010628,GO:0031175,GO:0043506,GO:0014059,GO:0030054,GO:0010008,GO:0031532,GO:0005634,GO:0008089,GO:0043005,GO:0060159,GO:0033162,GO:0042383,GO:0045211,GO:0014069,GO:0048490,G	CG6856-PA												171~200,123~150									
aly636.3	Unknown		n/a																				
aly636.4	Unknown		CG14982-PB						PF14160						61~81								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly636.5	CCAAT/enhancer-binding protein gamma	GO:0001077,GO:0001889,GO:0003677,GO:0043388,GO:0000978,GO:0043565,GO:0045078,GO:0005634,GO:0005654,GO:0006366,GO:0003690,GO:0030183,GO:0008134,GO:0006955,GO:0022008,GO:0043433,GO:0016071,GO:0051091,GO:0003700,GO:0042267,GO:0043353,GO:0006355,GO:0006357,GO:0045944,GO:0045739,GO:0046982	CG6272-PA				SM00338		PF07716	PS50217			G3DSA:1.20.5.170	SSF57959	51~85								
aly636.6	Phosphoinositide 3-kinase regulatory subunit 4	GO:0002784,GO:0005770,GO:0032801,GO:0006963,GO:0030242,GO:0016236,GO:0008286,GO:0034271,GO:0034272,GO:0045324,GO:0044281,GO:0034198,GO:0031410,GO:0016020,GO:0005776,GO:0004674,GO:0004672,GO:0032465,GO:0006661,GO:0005524,GO:0006468,GO:0035032,GO:0045087,GO:0006623,GO:0034162,GO:0002224,GO:0042149,GO:0005930,GO:0043552,GO:0005643,GO:0005829,GO:0006644,GO:0071561	CG9746-PA				SM00320,SM00320		PF00400	PS50294,PS50082,PS50082			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50998									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly636.7	Phosphoinositide 3-kinase regulatory subunit 4	GO:0002784,GO:0005770,GO:0032801,GO:0006963,GO:0030242,GO:0016236,GO:0008286,GO:0034271,GO:0034272,GO:0045324,GO:0044281,GO:0034198,GO:0031410,GO:0016020,GO:0005776,GO:0004674,GO:0004672,GO:0032465,GO:0006661,GO:0005524,GO:0006468,GO:0035032,GO:0045087,GO:0006623,GO:0034162,GO:0002224,GO:0042149,GO:0005930,GO:0043552,GO:0005643,GO:0005829,GO:0006644,GO:0071561	CG9746-PA				SM00320,SM00320,SM00320,SM00220		PF00069	PS50011,PS50294,PS50082		PS00108	G3DSA:2.130.10.10,G3DSA:1.10.510.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:3.30.200.20	SSF50978,SSF56112,SSF48371,SSF48371										
aly636.8	Stromal membrane-associated protein 2	GO:0005737,GO:0005654,GO:0032312,GO:0005096,GO:0005575,GO:0008060,GO:0008270,GO:0046872	CG8243-PA				SM00105		PF01412	PS50115	PR00405,PR00405			SSF57863									
aly636.9	Protein DENND6B	GO:0055037,GO:0043547,GO:0017112	CG3309-PA						PF08616,PF09794														
aly63633.1	SAM50-like protein CG7639	GO:0008150,GO:0016021,GO:0005741,GO:0003674,GO:0019867	CG7639-PB						PF01103														
aly63667.1	Actin-related protein 2	GO:0005737,GO:0003779,GO:0005200,GO:0007010,GO:0015629,GO:0007015,GO:0072553,GO:0008064,GO:0045887,GO:0051489,GO:0005885,GO:0005884,GO:0034314,GO:0005524,GO:0000902	CG9901-PC						PF00022		PR00190,PR00190	PS01132	G3DSA:3.30.420.40	SSF53067									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly637.1	Zinc finger protein 835	GO:0006351,GO:0003700,GO:0005634,GO:0006355,GO:0000790,GO:0008270,GO:0005515,GO:0003677,GO:0046872,GO:0043035	CG2711-PA				SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667									
aly637.2	Hypermethylated in cancer 1 protein	GO:0005737,GO:0043565,GO:0008630,GO:0000122,GO:0003700,GO:0016055,GO:0030178,GO:0005654,GO:0000785,GO:0006351,GO:0003676,GO:0043517,GO:0046872,GO:0042826,GO:0007275	CG3407-PA				SM00355,SM00355,SM00355,SM00355		PF13912	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly637.3	Zinc finger protein 624	GO:0051726,GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG11247-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667									
aly637.4	Unknown	GO:0046872,GO:0003676	CG12299-PA				SM00355,SM00355,SM00355			PS50157,PS50157		PS00028,PS00028,PS00028											
aly6370.1	Dihydroxyacetone phosphate acyltransferase	GO:0004366,GO:0005778,GO:0006650,GO:0021587,GO:0030913,GO:0005777,GO:0070542,GO:0016287,GO:0005739,GO:0061024,GO:0016290,GO:0007416,GO:0042594,GO:0042493,GO:0007584,GO:0008611	CG4625-PC																				
aly6370.10	Ubiquitin-associated and SH3 domain-containing protein B	GO:0005737,GO:0051279,GO:0006469,GO:0009968,GO:0045779,GO:0005634,GO:0090331,GO:0003824,GO:0045670,GO:0045671,GO:0035335,GO:0004725	CG13604-PE				SM00165		PF00300,PF00627,PF14604	PS50002,PS50030			G3DSA:1.10.8.10,G3DSA:3.90.1140.10,G3DSA:3.40.50.1240,G3DSA:3.40.50.1240,G3DSA:3.40.50.1240,G3DSA:2.30.30.40	SSF50044,SSF53254,SSF53254,SSF46934									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6370.11	H/ACA ribonucleoprotein complex subunit 3	GO:0072588,GO:0005730,GO:0042254,GO:0060215,GO:0006364,GO:0030515,GO:0001522	CG7637-PA						PF04135				G3DSA:2.20.28.40	SSF144210									
aly6370.12	Anaphase-promoting complex subunit 2	GO:0050804,GO:0090129,GO:0045886,GO:0051439,GO:0090302,GO:0051437,GO:0051436,GO:0007067,GO:0051301,GO:0070979,GO:0005654,GO:0042787,GO:0000278,GO:0000090,GO:0031145,GO:0050775,GO:0031625,GO:0051726,GO:0005829,GO:0045773,GO:0000151,GO:0007094,GO:0031915,GO:0005680	CG3060-PA				SM01013,SM00182		PF08672,PF00888	PS50069			G3DSA:4.10.1030.10,G3DSA:1.10.10.10	SSF75632,SSF46785					UPA00143				
aly6370.13	Ral GTPase-activating protein subunit alpha-1	GO:0005737,GO:0043547,GO:0090630,GO:0005634,GO:0005096,GO:0032861,GO:0006355,GO:0046582,GO:0005829	CG5521-PB						PF02145	PS50085				SSF111347	1455~1475								
aly6370.14	Larval cuticle protein LCP-17	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG32405-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly6370.2	Putative helicase mov-10-B.1	GO:0000932,GO:0004386,GO:0048813,GO:0003723,GO:0035279,GO:0016246,GO:0046872,GO:0005524	CG6701-PE						PF13086,PF13086,PF13087				G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6370.3	Putative helicase mov-10-B.1	GO:0000184,GO:0007616,GO:0030425,GO:0030424,GO:0045202,GO:0000578,GO:0003678,GO:0005737,GO:0070725,GO:0016246,GO:0043025,GO:0005524,GO:0031023,GO:0016325,GO:0004386,GO:0007317,GO:0035279,GO:0007319,GO:0007318,GO:0000932,GO:0003723,GO:0005515,GO:0046843	CG11513-PB						PF13086,PF13087				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540										
aly6370.4	RING finger protein 145	GO:0045926,GO:0005783,GO:0016021,GO:0007418,GO:0008270,GO:0005515	CG2304-PD				SM00184		PF13639	PS50089			G3DSA:3.30.40.10	SSF57850										
aly6370.5	Unknown		n/a																				
aly6370.6	Putative transferase CAF17 homolog, mitochondrial	GO:0005737,GO:0004047,GO:0006783,GO:0006546,GO:0005739,GO:0016740	CG8043-PA					TIGR03317	PF01571,PF10170		PR01995,PR01995,PR01995,PR01995		G3DSA:3.30.70.1400	SSF103025										
aly6370.7	Ubiquitin carboxyl-terminal hydrolase 34	GO:0005737,GO:0016055,GO:0005829,GO:0090263,GO:0030307,GO:0043687,GO:0031647,GO:0035220,GO:0004843,GO:0061136,GO:0006511,GO:0071108,GO:0043161,GO:0004197,GO:0005634,GO:0016579,GO:0036459,GO:0060968	CG5794-PH						PF00443	PS50235		PS00973,PS00972	G3DSA:2.20.210.10	SSF54001,SSF54001	356~376									
aly6370.8	Ubiquitin carboxyl-terminal hydrolase 34	GO:0005737,GO:0016055,GO:0005829,GO:0090263,GO:0030307,GO:0043687,GO:0031647,GO:0035220,GO:0004843,GO:0061136,GO:0006511,GO:0071108,GO:0043161,GO:0004197,GO:0016579,GO:0005634,GO:0060968	CG5794-PH																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6370.9	Probable Dol-P-Man:Man(7)GlcNAc(2)-PP-Dol alpha-1,6-mannosyltransferase	GO:0005783,GO:0006486,GO:0006487,GO:0006488,GO:0016021,GO:0097502,GO:0005789,GO:0052917,GO:0000009,GO:0000030	CG8412-PA						PF03901						615~639								
aly63730.1	Unknown		n/a																				
aly6377.1	HEAT repeat-containing protein 1 (Fragment)	GO:0005730,GO:0030529,GO:0005575,GO:0003674,GO:0006364,GO:0022008,GO:0005488	CG10805-PA				SM01036		PF08146,PF12397	PS50181			G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371									
aly6377.2	Lysosomal thioesterase PPT2 homolog	GO:0016790,GO:0098599,GO:0005764,GO:0098734,GO:0002084,GO:0008474	CG4851-PA						PF02089		PR00414,PR00414		G3DSA:3.40.50.1820	SSF53474									
aly6377.3	Unknown	GO:0050777,GO:0009609,GO:0045824,GO:0005515,GO:0061060,GO:0005102	CG15678-PA																				
aly638.1	GTP-binding protein RAD	GO:0016020,GO:0003924,GO:0005622,GO:0005575,GO:0008150,GO:0005886,GO:0006184,GO:0007264,GO:0005525	CG44011-PB				SM00173,SM00175		PF00071	PS51421	PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540	90~110								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly638.10	Syntaxin-16	GO:0016021,GO:0005783,GO:0006906,GO:0005484,GO:0005925,GO:0031201,GO:0005737,GO:0031985,GO:0005730,GO:0000149,GO:0016020,GO:0090161,GO:0048471,GO:0005794,GO:0048193,GO:0016081,GO:0042147,GO:0048278,GO:0019905,GO:0012505,GO:0007269,GO:0005886,GO:0043231,GO:0006891,GO:0016192,GO:0005829,GO:0005802,GO:0000139,GO:0005764,GO:0005515,GO:0006886	CG1467-PA				SM00397		PF05739	PS50192		PS00914	G3DSA:1.20.58.70,G3DSA:1.20.58.70	SSF47661,SSF47661			REACT_11184						
aly638.11	Actin-related protein 8	GO:0006310,GO:0006338,GO:0006281,GO:0005634,GO:0031011,GO:0006355,GO:0006351,GO:0043140,GO:0005524	CG7846-PA				SM00268		PF00022				G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.30.420.40	SSF53067,SSF53067,SSF53067,SSF53067									
aly638.12	XK-related protein 6	GO:0016021	CG32579-PB						PF09815														
aly638.13	Unknown		n/a																				
aly638.14	Vacuolar protein sorting associated protein 28 homolog	GO:0048749,GO:0060429,GO:0007293,GO:0043328,GO:0006914,GO:0032509,GO:0000046,GO:0030713,GO:0000813,GO:0032403,GO:0010796,GO:0007291,GO:0030036,GO:0005515,GO:0008593,GO:0009792,GO:0042059,GO:0043162,GO:0044130	CG12770-PB			PIRSF017535			PF03997	PS51313,PS51310				SSF140427,SSF140111									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly638.15	Protein 4.1 homolog	GO:0006612,GO:0009790,GO:0007163,GO:0003015,GO:0005920,GO:0005856,GO:0007435,GO:0045170,GO:0019991,GO:0005198,GO:0003779,GO:0060857,GO:0007527,GO:0048598,GO:0035151,GO:0016327,GO:0008362,GO:0035321,GO:0045216,GO:0005886,GO:0005918,GO:0007010,GO:0008092,GO:0007391,GO:0045169,GO:0061343	CG11949-PA				SM00295		PF09379,PF09380,PF05902,PF00373,PF08736	PS50057	PR00935,PR00935,PR00935,PR00935	PS00661	G3DSA:1.20.80.10,G3DSA:3.10.20.90,G3DSA:2.30.29.30	SSF50729,SSF47031,SSF50998,SSF54236									
aly638.16	Pancreatic lipase-related protein 2	GO:0009395,GO:0047714,GO:0004806,GO:0005615,GO:0016042,GO:0005575,GO:0005509,GO:0019376,GO:0004620,GO:0016298,GO:0047372	CG6472-PB						PF00151		PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly638.17	Band 4.1-like protein 2	GO:0006612,GO:0019898,GO:0009790,GO:0007163,GO:0003015,GO:0005925,GO:0005920,GO:0005856,GO:0005654,GO:0007435,GO:0045170,GO:0005634,GO:0019991,GO:0005198,GO:0003779,GO:0060857,GO:0030054,GO:0007527,GO:0048598,GO:0035151,GO:0016327,GO:0008362,GO:0035321,GO:0045216,GO:0005886,G	CG11949-PA				SM00295		PF09380,PF09379	PS50057			G3DSA:2.30.29.30,G3DSA:1.20.80.10,G3DSA:3.10.20.90	SSF54236,SSF50729									
aly638.18	Nucleolar protein 9	GO:0044822,GO:0003723	CG11123-PA				SM00025,SM00025,SM00025,SM00025			PS50302,PS50302,PS50302,PS50302			G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371									
aly638.19	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly638.2	Phospholipase A2	GO:0004623,GO:0006644,GO:0005576,GO:0005509,GO:0016042	CG30503-PA						PF05826			PS00118	G3DSA:1.20.90.10	SSF48619	392~412	00564+3.1.1.4,00590+3.1.1.4,00592+3.1.1.4,00591+3.1.1.4,00565+3.1.1.4		PWY-7409,PWY-7417,PWY-6803,PWY-7416					
aly638.20	Protein CBFA2T1	GO:0005737,GO:0007517,GO:0016363,GO:0017053,GO:0003700,GO:0005634,GO:0003714,GO:0051101,GO:0008407,GO:0005739,GO:0005654,GO:0006355,GO:0048813,GO:0010977,GO:0006351,GO:0045444,GO:0045892,GO:0007411,GO:0046872,GO:0042802,GO:0042803	CG3385-PD						PF01753	PS50865				SSF144232	5~25								
aly638.21	Protein CBFA2T2	GO:0007517,GO:0003700,GO:0005634,GO:0003714,GO:0008407,GO:0006355,GO:0048813,GO:0045944,GO:0010977,GO:0010976,GO:0030855,GO:0045892,GO:0007411,GO:0046872	CG3385-PD						PF07531	PS51119				SSF158553									
aly638.22	Unknown		n/a												84~108,28~48								
aly638.23	KxDL motif-containing protein CG10681	GO:0005575,GO:0003674,GO:0008150	CG10681-PA						PF10241														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly638.24	Ubiquitin-conjugating enzyme E2 T	GO:0007067,GO:0001745,GO:0005875,GO:0007140,GO:0006513,GO:0001751,GO:0005634,GO:0051865,GO:0048477,GO:0005524,GO:0006281,GO:0016322,GO:0006974,GO:0008054,GO:0007286,GO:0048132,GO:0022008,GO:0004842,GO:0030718,GO:0051276,GO:0031647,GO:0045676,GO:0016567,GO:0006511,GO:0005515,GO:0003682,GO:0016874	CG7425-PA				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				
aly638.25	Ubiquitin-conjugating enzyme E2 T	GO:0005737,GO:0005654,GO:0044314,GO:0070936,GO:0006281,GO:0070979,GO:0016874,GO:0005634,GO:0035519,GO:0051865,GO:0006974,GO:0006513,GO:0085020,GO:0061630,GO:0061631,GO:0003682,GO:0004842,GO:0070534,GO:0005524,GO:0031625	CG3473-PA				SM00212		PF00179	PS50127			G3DSA:3.10.110.10	SSF54495									
aly638.26	Unknown		n/a										G3DSA:3.50.50.60										
aly638.27	Oxidative stress-induced growth inhibitor 1	GO:0043065,GO:0030154,GO:0008083,GO:0030308,GO:0007275	n/a										G3DSA:3.50.50.60										
aly638.28	Protein Vhl	GO:0007424,GO:0007427,GO:0030154,GO:0007010,GO:0030891,GO:0006611,GO:0060438,GO:0005634,GO:0007026,GO:1900037,GO:0035149,GO:0016567,GO:0090307,GO:0016334,GO:0005515,GO:0061630,GO:0001525,GO:0004842,GO:0051297	CG13221-PA						PF01847				G3DSA:2.60.40.780	SSF49468					UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly638.29	Trafficking protein particle complex subunit 2-like protein	GO:0005794,GO:0048471,GO:0006888,GO:0005783,GO:0005622	CG9067-PA						PF04628				G3DSA:3.30.450.70	SSF64356									
aly638.3	Unknown		n/a												294~321,332~359,646~666								
aly638.30	40S ribosomal protein S20	GO:0015935,GO:0003735,GO:0005840,GO:0003723,GO:0006412,GO:0022627	CG15693-PA	MF_00508				TIGR01046	PF00338		PR00971,PR00971,PR00971		G3DSA:3.30.70.600	SSF54999									
aly638.31	Tubulin beta-1 chain	GO:0045298,GO:0051258,GO:0007017,GO:0003924,GO:0005737,GO:0007435,GO:0005200,GO:0006184,GO:0005874,GO:0005525	CG9359-PA				SM00865,SM00864		PF03953,PF00091		PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163	PS00227,PS00228	G3DSA:3.40.50.1440,G3DSA:1.10.287.600,G3DSA:3.30.1330.20	SSF55307,SSF52490	408~442		REACT_152						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly638.32	Tubulin beta-1 chain	GO:0045298,GO:0051258,GO:0007017,GO:0003924,GO:0005737,GO:0007435,GO:0005200,GO:0006184,GO:0005874,GO:0005525	CG9359-PA				SM00864,SM00865		PF00091,PF03953		PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161	PS00227,PS00228	G3DSA:3.30.1330.20,G3DSA:3.40.50.1440,G3DSA:1.10.287.600	SSF55307,SSF52490	402~436		REACT_152						
aly638.33	Uridine 5'-monophosphate synthase	GO:0044205,GO:0006207,GO:0009116,GO:0004588,GO:0004590,GO:0005875	CG3593-PA	MF_01208				TIGR00336	PF00156				G3DSA:3.40.50.2020	SSF53271		00983+2.4.2.10,00240+2.4.2.10		PWY-5686	UPA00070				
aly638.34	Tubulin beta-3 chain	GO:0045298,GO:0007507,GO:0030537,GO:0007017,GO:0051258,GO:0003924,GO:0005737,GO:0005200,GO:0009416,GO:0007409,GO:0007411,GO:0006184,GO:0022008,GO:0005874,GO:0005525	CG3401-PA				SM00864,SM00865		PF03953,PF00091		PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01161,PR011	PS00227,PS00228	G3DSA:3.40.50.1440,G3DSA:3.30.1330.20,G3DSA:1.10.287.600	SSF52490,SSF55307	411~431		REACT_152						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly638.35	Activin receptor type-1	GO:0018107,GO:0010694,GO:0007507,GO:0032924,GO:0042078,GO:0008101,GO:2000017,GO:0035222,GO:0061445,GO:0007300,GO:0030509,GO:0008358,GO:2001237,GO:0007304,GO:0030501,GO:0050829,GO:0003289,GO:0035556,GO:0001745,GO:0050431,GO:0001702,GO:0045177,GO:0010862,GO:0042118,GO:0005057,GO:0007368,GO:0016020,GO:0007476,GO:0030707,GO:0003143,GO:0004674,GO:0001755,GO:0004672,GO:0016361,GO:0016477,GO:0048477,GO:0005524,GO:0048762,GO:0006468,GO:0001707,GO:0007015,GO:0000082,GO:0060037,GO:0007281,GO:0060317,GO:0045893,GO:0005887,GO:0005886,GO:0060923,GO:0002526,GO:0032926,GO:0030514,GO:0030513,GO:0030512,GO:0007179,GO:0048179,GO:0030718,GO:0046872,GO:0009953,GO:0001569,GO:0010718,GO:0045669,GO:0007448,GO:0045887,GO:0005025,GO:0005622,GO:0045824,GO:0045944,GO:0003183,GO:0005515,GO:0004702,GO:0051145,GO:0060389,GO:0048185	CG1891-PC				SM00220,SM00467		PF07714,PF08515	PS51256,PS50011		PS00108,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:2.10.60.10	SSF56112									
aly638.36	Unknown		n/a																				
aly638.37	Unknown	GO:0008104,GO:0051233,GO:0016572,GO:0000281,GO:0007052,GO:0000785,GO:0045448,GO:0005515,GO:0003677,GO:0007067,GO:0032133,GO:0005938	CG4454-PB						PF10512														
aly638.38	Cilia- and flagella-associated protein 45	GO:0005654,GO:0005634,GO:0005929	CG11449-PA						PF13868						187~236,326~346,352~395,429~475,268~295								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly638.39	S-adenosylmethionine mitochondrial carrier protein	GO:1901962,GO:0005743,GO:0000095,GO:0016021,GO:0022857,GO:0015805,GO:0005740,GO:0055085	CG4743-PA						PF00153,PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506	232~232								
aly638.4	Unknown		n/a												554~574,713~733								
aly638.40	Rhophilin-2	GO:0005737,GO:0043231,GO:0017049,GO:0005654,GO:0007165,GO:0048471	CG8497-PB				SM00742,SM00228,SM01041		PF02185,PF00595,PF03097	PS50106,PS51180			G3DSA:2.30.42.10,G3DSA:1.25.40.280,G3DSA:1.10.287.160	SSF46585,SSF50156	85~112,578~580								
aly638.5	Unknown		n/a																				
aly638.6	Beta-1,3-galactosyltransferase 1	GO:0016333,GO:0042248,GO:0006486,GO:0006688,GO:0016021,GO:0016020,GO:0030707,GO:0000139,GO:0007293,GO:0005576,GO:0008378,GO:0046981,GO:0008375,GO:0001744,GO:0007299,GO:0048477,GO:0007298	CG4934-PA						PF01762					SSF53448					UPA00378				
aly638.7	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly638.8	Protein SDE2 homolog		CG5986-PA						PF13019						115~138								
aly638.9	Ubiquitin-conjugating enzyme E2 C	GO:0005737,GO:0010458,GO:2000600,GO:0045842,GO:0051726,GO:0016874,GO:0005634,GO:0000151,GO:0031145,GO:0005815,GO:0004842,GO:0061631,GO:0005524	CG10682-PA				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				
aly63818.1	Sodium/potassium-transporting ATPase subunit alpha	GO:0007630,GO:0051124,GO:0060439,GO:0007268,GO:0005890,GO:0050905,GO:0005737,GO:0001700,GO:0005634,GO:0019991,GO:0009612,GO:0005391,GO:0035158,GO:0035725,GO:0005886,GO:0006812,GO:0046872,GO:0015672,GO:0005524,GO:0007626,GO:0035152,GO:0007605,GO:0035159,GO:0008324,GO:0016323,GO:0008360,GO:0009266,GO:0008340,GO:0001894,GO:0008344,GO:0005918,GO:0098655,GO:0006754	CG5670-PA										G3DSA:3.40.50.1000	SSF56784									
aly6387.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly63911.1	F-box/WD repeat-containing protein 11	GO:0008589,GO:0008588,GO:0046599,GO:0045849,GO:0006470,GO:0007611,GO:0007293,GO:0030111,GO:0007304,GO:0007298,GO:0030178,GO:0007049,GO:0008355,GO:0005737,GO:0030708,GO:0005813,GO:0005634,GO:0030727,GO:0030720,GO:0030707,GO:0000209,GO:0048511,GO:0045893,GO:0006508,GO:0007088,GO:0007623,GO:0031146,GO:0060623,GO:0045879,GO:0060253,GO:0046627,GO:0042752,GO:0042753,GO:0030162,GO:0045475,GO:0045862,GO:0031648,GO:0004842,GO:0030512,GO:0042347,GO:0030713,GO:0016055,GO:0051219,GO:0000151,GO:0016567,GO:0016322,GO:0019005,GO:0005515,GO:0043161,GO:0032007,GO:0045892,GO:0046983,GO:0005829,GO:0046843	CG3412-PB							PS50294,PS50082			G3DSA:1.20.1280.50	SSF50978									
aly6398.1	Integrin-linked protein kinase	GO:0008284,GO:0010667,GO:0018105,GO:0034446,GO:0090263,GO:0014912,GO:0045197,GO:0032288,GO:0031012,GO:0007160,GO:0007155,GO:0043234,GO:0043025,GO:0043524,GO:0004871,GO:0005925,GO:0051897,GO:0030054,GO:0045669,GO:0005737,GO:0001725,GO:0043206,GO:0009966,GO:0016020,GO:0030017,GO:0007475,GO:0005654,GO:0004674,GO:0045663,GO:0004672,GO:0010761,GO:2000178,GO:0005524,GO:0016203,GO:0003151,GO:0006468,GO:0006469,GO:0048662,GO:0032956,GO:0008283,GO:0030027,GO:0030335,GO:0051291,GO:0042327,GO:0007050,GO:0045893,GO:0005911,GO:0005886,GO:0001658,GO:0021675,GO:0030513,GO:0034329,GO:0050775,GO:0022011,GO:0007016,GO:0043195,GO:0007569,GO:0043406,GO:0043198,GO:0007229,GO:0001954,GO:0045773,GO:0070527,GO:0019901,GO:0048812,GO:0005515,GO:0043491,GO:0005829,GO:0043034	CG10504-PA			PIRSF000654	SM00248,SM00248,SM00248		PF12796,PF12796,PF07714	PS50088,PS50088,PS50011,PS50297,PS50088			G3DSA:3.30.200.20,G3DSA:1.25.40.20,G3DSA:1.10.510.10,G3DSA:1.25.40.20	SSF56112,SSF48403									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6398.10	Peptide transporter family 1	GO:0006857,GO:0005427,GO:0016020,GO:0005887,GO:0015031,GO:0035672	CG2930-PE						PF00854,PF00854				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473			REACT_19419,REACT_15518						
aly6398.11	Neuropeptide Y receptor type 2	GO:0004930,GO:0036400,GO:0040018,GO:0016021,GO:0005886,GO:0007218,GO:0004983,GO:0005887,GO:0008188,GO:0070374,GO:0007186,GO:2000253	CG7395-PA						PF00001	PS50262	PR01012,PR01012,PR01012,PR01012,PR01012,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321	233~253		REACT_14797						
aly6398.12	Unknown		n/a																				
aly6398.2	U2 small nuclear ribonucleoprotein B"	GO:0007539,GO:0030529,GO:0000381,GO:0005730,GO:0030620,GO:0005634,GO:0000166,GO:0005654,GO:0005692,GO:0048477,GO:0008380,GO:0042802,GO:0019099,GO:0071011,GO:0071013,GO:0008266,GO:0043234,GO:0030619,GO:0030532,GO:0097158,GO:0000398,GO:0017069,GO:0002230,GO:0005515,GO:0005686,G	CG4528-PA				SM00360,SM00360		PF00076,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									
aly6398.3	Mini-chromosome maintenance complex-binding protein	GO:0042555,GO:0005634,GO:0008150,GO:0006261,GO:0003674,GO:0007067,GO:0003682,GO:0051301,GO:0007062	CG3430-PA						PF09739,PF07019						93~113								
aly6398.4	Probable tRNA N6-adenosine threonylcarbamoyltransferase	GO:0005737,GO:0004222,GO:0005634,GO:0005575,GO:0016746,GO:0008033,GO:0022008,GO:0046872	CG4933-PA	MF_01446				TIGR00329	PF00814		PR00789,PR00789,PR00789,PR00789,PR00789,PR00789,PR00789	PS01016	G3DSA:3.30.420.40	SSF53067									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6398.5	Proline-, glutamic acid- and leucine-rich protein 1	GO:0005737,GO:0071391,GO:0045944,GO:0005488,GO:0035327,GO:0003682,GO:0071339,GO:0006351	n/a										G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371									
aly6398.6	RAB6-interacting golgin	GO:0005654,GO:0005794,GO:0005730	CG33052-PA						PF04949						105~154								
aly6398.7	Protein FAM166B		n/a						PF10629,PF10629														
aly6398.8	Drebrin-like protein	GO:0030665,GO:0002376,GO:0071800,GO:0002102,GO:0070062,GO:0016601,GO:0030027,GO:0005829,GO:0006898,GO:0001726,GO:0051015,GO:0000139,GO:0003779,GO:0048812,GO:0005938,GO:0007416,GO:0005886,GO:0005622,GO:0097178,GO:0030054,GO:0045202	n/a				SM00102		PF00241	PS51263			G3DSA:3.40.20.10	SSF55753									
aly6398.9	Replicase polyprotein 1a	GO:0039520,GO:0008270,GO:0019079,GO:0044220,GO:0039648,GO:0033644,GO:0004197,GO:0003968,GO:0003723,GO:0019082,GO:0039579,GO:0039502,GO:0039595,GO:0008242,GO:0016021,GO:0039548	n/a												873~893,831~858,734~786,1153~1177								
aly640.1	Iodotyrosine dehalogenase 1	GO:0016021,GO:0016491	CG6279-PA						PF00881				G3DSA:3.40.109.10	SSF55469									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly640.10	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0030672,GO:0016021,GO:0016020,GO:0022857,GO:0001669,GO:0005886,GO:0006836,GO:0055085,GO:0030054	CG3168-PC						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473									
aly640.11	Unknown		n/a																				
aly640.12	Unknown		n/a																				
aly640.13	Unknown		n/a										G3DSA:1.20.1250.20										
aly640.14	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0030672,GO:0016021,GO:0016020,GO:0008513,GO:0022857,GO:0001669,GO:0005886,GO:0006836,GO:0055085,GO:0030054	CG15221-PB						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly640.15	Scavenger receptor class B member 1	GO:0034375,GO:0015914,GO:0043691,GO:0005901,GO:0051000,GO:0070328,GO:0032497,GO:0010867,GO:0070062,GO:0010886,GO:0016020,GO:0043654,GO:0035461,GO:0010899,GO:0008035,GO:0006707,GO:0015920,GO:0006952,GO:0043534,GO:0005887,GO:0007155,GO:0042632,GO:0001530,GO:0030169,GO:0005044,GO:0044406,GO:0034384,GO:0005765,GO:0033344,GO:0034383,GO:0001875,GO:0070506,GO:0001935	CG10345-PA						PF01130		PR01609,PR01609,PR01609,PR01609												
aly640.16	Unknown		n/a																				
aly640.17	Mitogen-activated protein kinase kinase kinase 4	GO:0000187,GO:0000186,GO:0034605,GO:0071243,GO:0043507,GO:0035556,GO:0005622,GO:0002385,GO:0005737,GO:0031434,GO:0043652,GO:0000165,GO:0071475,GO:0004672,GO:0048471,GO:0046872,GO:0010468,GO:0005524,GO:0006468,GO:0019100,GO:0071276,GO:0046330,GO:0010225,GO:0006979,GO:0001890,GO:0045793,GO:0060718,GO:0070059,GO:0031452,GO:0004708,GO:1900745,GO:0004702,GO:0004709,GO:0001934	CG7717-PB				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112	798~818									
aly640.18	Choline O-acetyltransferase	GO:0015893,GO:0005277,GO:0005829,GO:0007399,GO:0004102,GO:0016021,GO:0007268,GO:0005278,GO:0015238,GO:0006836,GO:0008292,GO:0005634,GO:0007274,GO:0055085	CG12345-PA						PF00755			PS00439,PS00440		SSF52777,SSF52777									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly640.19	Pro-resilin	GO:0040003,GO:0005201,GO:0032992,GO:0030023,GO:0008010,GO:0031012,GO:0005576,GO:0008061,GO:0022008,GO:0042302	CG7709-PA						PF16058,PF16058														
aly640.2	Alpha-1,6-mannosyl-glycoprotein 2 beta-N-acetylglucosaminyltransferase	GO:0008455,GO:0005795,GO:0005797,GO:0006487,GO:0016021,GO:0030246,GO:0009312,GO:0008375,GO:0000139,GO:0018279	CG7921-PA						PF05060				G3DSA:3.90.550.10			00513+2.4.1.143,00510+2.4.1.143		PWY-7426	UPA00378				
aly640.20	High-affinity choline transporter 1	GO:0015220,GO:0006810,GO:0016021,GO:0015293,GO:0005215,GO:0003333,GO:0016020,GO:0015871,GO:0015171,GO:0008292,GO:0006814,GO:0005298,GO:0055085	CG7708-PA						PF00474	PS50283													
aly640.21	Unknown	GO:0005509	CG10841-PA										G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473,SSF47473,SSF47473,SSF47473									
aly640.22	Endochitinase	GO:0000272,GO:0005576,GO:0008061,GO:0004568,GO:0006030,GO:0006032,GO:0016490	CG7248-PA				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly640.23	RNA-binding protein squid	GO:0035062,GO:0033119,GO:0007293,GO:0000184,GO:0000785,GO:0007297,GO:0003676,GO:0030529,GO:0008069,GO:0005737,GO:0000381,GO:0005730,GO:0005634,GO:0030720,GO:0000166,GO:0003730,GO:0048477,GO:0006405,GO:0006406,GO:0071011,GO:0016325,GO:0071013,GO:0019094,GO:0007314,GO:0045451,GO:0009953,GO:0005703,GO:0000398,GO:0008298,GO:0017148,GO:0003729	CG16901-PB				SM00360,SM00360		PF00076,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									
aly640.24	Ras GTPase-activating protein-binding protein 2	GO:0005737,GO:0016318,GO:0005811,GO:0051028,GO:0071011,GO:0005829,GO:0006810,GO:0044822,GO:0017124,GO:0000398,GO:0005622,GO:0007264,GO:0003729,GO:0003676,GO:0007265,GO:0000166,GO:0071013,GO:0001752	CG9412-PB						PF02136	PS50177			G3DSA:3.10.450.50	SSF54427									
aly640.25	SPARC	GO:0007443,GO:0005604,GO:0061327,GO:0007498,GO:0060438,GO:0007165,GO:0070278,GO:0007275,GO:0007419,GO:0005509,GO:0005515,GO:0007155,GO:0005578,GO:0005615	CG6378-PA						PF09289,PF10591			PS00018,PS00613	G3DSA:1.10.238.10,G3DSA:3.30.60.30	SSF100895,SSF47473									
aly640.26	Histone H2A.V (Fragment)	GO:0005694,GO:0005634,GO:0005811,GO:0006333,GO:0005700,GO:0005701,GO:0006974,GO:0071168,GO:0000786,GO:0046982,GO:0003677,GO:0006334	CG5499-PA				SM00414		PF16211,PF00125		PR00620,PR00620,PR00620,PR00620,PR00620	PS00046	G3DSA:1.10.20.10	SSF47113									
aly640.27	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly640.28	Splicing factor 1	GO:0000245,GO:0033327,GO:0007476,GO:0008270,GO:0003676,GO:0002121,GO:0005634,GO:0003714,GO:0000389,GO:0005654,GO:0006351,GO:0048662,GO:0030238,GO:0071011,GO:0044822,GO:1903507,GO:0050810,GO:0022008,GO:0005840,GO:0000398,GO:0006355,GO:0003723,GO:0005681	CG5836-PA				SM00343,SM00343		PF00098	PS50158			G3DSA:4.10.60.10,G3DSA:3.30.1370.10	SSF57756,SSF54791										
aly640.29	MOB kinase activator-like 1	GO:0071174,GO:0005829,GO:0008283,GO:0005813,GO:0005634,GO:0006915,GO:0019901,GO:0007165,GO:0005515,GO:0005886,GO:0007059,GO:0046872,GO:0007275	CG13852-PA						PF03637				G3DSA:1.20.140.30	SSF101152									
aly640.3	Unknown		n/a												156~190								
aly640.30	Cytochrome c oxidase subunit NDUFA4	GO:0004129,GO:0070062,GO:1902600,GO:0005739,GO:0006120,GO:0005751,GO:0005743,GO:0005747,GO:0032403,GO:0003954	CG32230-PA						PF06522														
aly640.31	Programmed cell death 6-interacting protein	GO:0031871,GO:0039702,GO:0048306,GO:1903553,GO:0010824,GO:1903551,GO:0004871,GO:0005925,GO:0007049,GO:0005737,GO:0070062,GO:0043209,GO:0043162,GO:0016020,GO:0000920,GO:0005815,GO:0042803,GO:0070971,GO:0006915,GO:0046330,GO:0001772,GO:0030041,GO:1903561,GO:0004843,GO:1903543,GO:0042470,GO:0005829,GO:0090611,GO:0005515,GO:0015031,GO:0046983,GO:0005768	CG12876-PA						PF13949				G3DSA:1.20.140.50		136~174								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly640.32	Apoptosis-linked gene 2-interacting protein X 1	GO:0007032,GO:0008022,GO:0032456,GO:0031410,GO:0043162,GO:0006915,GO:0042176,GO:0005112,GO:0043226,GO:0033365,GO:0046330,GO:0005771,GO:0004871,GO:0055037,GO:0030041,GO:0016323,GO:0005768,GO:0004843	CG12876-PA				SM01041		PF03097	PS51180			G3DSA:1.25.40.280											
aly640.33	Glutamate-rich protein 2		CG14853-PB											SSF48452									
aly640.34	Unknown	GO:0016459,GO:0008150,GO:0003774,GO:0005524,GO:0042623	CG5501-PE																				
aly640.35	Unconventional myosin-Ib	GO:0030175,GO:0071944,GO:0010008,GO:0005737,GO:0070062,GO:0042623,GO:0005546,GO:0005547,GO:0016459,GO:0048471,GO:0003774,GO:0005524,GO:0006892,GO:0051017,GO:0030898,GO:0030048,GO:0008150,GO:0051015,GO:0008152,GO:0005886,GO:0000146,GO:0007015,GO:0005903,GO:0005769,GO:0005884	CG5501-PE						PF00063	PS51456				SSF52540,SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly640.36	Unconventional myosin-Ib	GO:0030175,GO:0071944,GO:0010008,GO:0005737,GO:0070062,GO:0042623,GO:0005546,GO:0005547,GO:0016459,GO:0048471,GO:0003774,GO:0005524,GO:0006892,GO:0051017,GO:0030898,GO:0030048,GO:0008150,GO:0051015,GO:0008152,GO:0005886,GO:0000146,GO:0007015,GO:0005903,GO:0005769,GO:0005884	CG5501-PE						PF00063	PS51456				SSF52540										
aly640.37	ATP synthase mitochondrial F1 complex assembly factor 1	GO:0006461,GO:0005739	CG10340-PA						PF06644,PF06644														
aly640.38	WD40 repeat-containing protein SMU1	GO:0005737,GO:0071011,GO:0071013,GO:0000398,GO:0007528,GO:0003674,GO:0005634,GO:0007274,GO:0072553	CG5451-PA				SM00668,SM00667,SM00220,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00069,PF00069	PS50294,PS50082,PS50082,PS50082,PS50082,PS50897,PS50082,PS50011,PS50896	PR00320,PR00320,PR00320	PS00108,PS00107,PS00678	G3DSA:3.30.200.20,G3DSA:2.130.10.10,G3DSA:1.10.510.10	SSF50978,SSF56112										
aly640.39	Unknown		n/a																				
aly640.4	Unknown	GO:0005575,GO:0008150,GO:0003674	CG9626-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly640.40	Unknown		n/a																				
aly640.41	Unknown		n/a																				
aly640.42	Vesicular acetylcholine transporter	GO:0015893,GO:0005277,GO:0016021,GO:0005278,GO:0015238,GO:0006836,GO:0055085	CG32848-PA					TIGR00880	PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly640.5	Protogenin A	GO:0016021,GO:0030425,GO:0030424,GO:0045886,GO:0016322,GO:0005515,GO:0007275	CG6490-PE				SM00408,SM00408,SM00408,SM00409,SM00409,SM00409,SM00060,SM00060,SM00060		PF00041,PF07679,PF07679,PF13895	PS50853,PS50835,PS50853,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF49265,SSF49265									
aly640.6	41 kDa peptidyl-prolyl cis-trans isomerase	GO:0006457,GO:0005829,GO:0071011,GO:0005634,GO:0000398,GO:0042026,GO:0003755,GO:0042277,GO:0007088,GO:0071013	CG1866-PA						PF00160	PS50072	PR00153,PR00153,PR00153		G3DSA:2.40.100.10	SSF50891	739~771								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly640.7	Heterogeneous nuclear ribonucleoprotein F	GO:0017025,GO:0003676,GO:0000166,GO:0005634,GO:0043484,GO:0060810,GO:0005654,GO:0048477,GO:0008380,GO:0046427,GO:0008134,GO:0042060,GO:0007311,GO:0045451,GO:0043234,GO:0051276,GO:0003727,GO:0005515,GO:0006417,GO:0006397,GO:0005681,GO:0003729	CG6946-PB				SM00360,SM00360		PF14259,PF14259,PF14259	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928	278~298								
aly640.8	Mothers against decapentaplegic homolog 6	GO:0007448,GO:0034713,GO:0016335,GO:0008285,GO:0001657,GO:0048635,GO:0030509,GO:0045886,GO:0007352,GO:0045444,GO:0035556,GO:0005737,GO:0005634,GO:0007476,GO:0043066,GO:0061353,GO:0070410,GO:0070411,GO:0070412,GO:0031290,GO:0010991,GO:0042802,GO:0007443,GO:0031589,GO:0035214,GO:0005515,GO:0044212,GO:0017015,GO:0034616,GO:0007488,GO:0031625,GO:0090254,GO:0006955,GO:0043627,GO:0043234,GO:0030514,GO:0030512,GO:0007179,GO:0042325,GO:0030718,GO:0016477,GO:0046872,GO:0003700,GO:0005829,GO:0030617,GO:0060394,GO:0005622,GO:0070698,GO:0006355,GO:0006351,GO:0005667,GO:0000978,GO:0003682	CG5201-PA				SM00524		PF03166	PS51076			G3DSA:2.60.200.10	SSF49879									
aly640.9	Synaptic vesicle glycoprotein 2C	GO:0008021,GO:0030672,GO:0006629,GO:0005215,GO:0016021,GO:0006810,GO:0022857,GO:0007268,GO:0006836,GO:0016298,GO:0055085,GO:0030054	CG31272-PA						PF07690,PF07690	PS50850,PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473,SSF103473									
aly64124.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly64171.1	NADH dehydrogenase [ubiqui] complex I, assembly factor 7 homolog	GO:0005575,GO:0008150,GO:0003674,GO:0005739,GO:0032981	CG17726-PA						PF02636					SSF53335									
aly6423.1	Acyl-CoA desaturase	GO:0006633,GO:0006629,GO:0016717,GO:0005789,GO:0004768,GO:0016021,GO:0055114	CG9743-PA						PF00487		PR00075,PR00075,PR00075,PR00075,PR00075,PR00075				30~50								
aly6423.2	Unknown		n/a												64~84								
aly64244.1	Serine/threonine-protein kinase ULK3	GO:0005737,GO:0006468,GO:0006914,GO:0045879,GO:0004674,GO:0045880,GO:0004672,GO:0046777,GO:0005524	CG8866-PA						PF00069	PS50011			G3DSA:1.10.510.10	SSF56112									
aly6435.1	Periodic tryptophan protein 2 homolog	GO:0022008,GO:0005515,GO:0005730	CG12325-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF04003	PS50082,PS50082,PS50294,PS50294,PS50082,PS50082		PS00678,PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50998,SSF50978,SSF50978									
aly6435.2	V-type proton ATPase 16 kDa proteolipid subunit	GO:0033227,GO:0015992,GO:0015991,GO:0016021,GO:0007476,GO:0045169,GO:0033181,GO:0033179,GO:0000220,GO:0046961,GO:0005774,GO:0015078	CG3161-PC	MF_01396				TIGR01100	PF00137,PF00137		PR00122,PR00122,PR00122,PR00122		G3DSA:1.20.120.610	SSF81333,SSF81333									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6435.3	Magnesium transporter protein 1	GO:0016021,GO:0006810,GO:0005789,GO:0035010,GO:0005886,GO:0045454	CG7830-PA						PF04756				G3DSA:3.40.30.10	SSF52833									
aly6435.4	Polyprenol reductase	GO:0005737,GO:0006629,GO:0006486,GO:0006488,GO:0016021,GO:0005789,GO:0016095,GO:0003865,GO:0016627,GO:0019348	CG7840-PA						PF02544	PS50244							REACT_22258						
aly6435.5	Bombyxin A-1 homolog	GO:0005179,GO:0060180,GO:0008286,GO:0005615,GO:0005158,GO:0005576	CG33273-PA				SM00078		PF00049		PR00276,PR00276	PS00262	G3DSA:1.10.100.10	SSF56994,SSF56994									
aly6435.6	Unknown		n/a																				
aly64732.1	Protein scarlet	GO:0006856,GO:0042626,GO:0031409,GO:0016887,GO:0043190,GO:0016021,GO:0006810,GO:0006727,GO:0006726,GO:0005395,GO:0005887,GO:0005524	CG4314-PA										G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly649.1	Microtubule-associated protein futsch	GO:0008582,GO:0030425,GO:0030424,GO:0000226,GO:0005874,GO:0005875,GO:0008355,GO:0005737,GO:0008088,GO:0043025,GO:0048749,GO:0016787,GO:0015630,GO:0060052,GO:0008017,GO:0007528,GO:0019900,GO:0007409,GO:1901215,GO:0007017,GO:0007399,GO:0048813,GO:0005515,GO:0043524	CG34387-PC											G3DSA:3.60.15.10,G3DSA:3.60.15.10,G3DSA:3.60.15.10		1172~1192,4233~4253,3644~3671,1054~1081,1691~1711,1596~1616								
aly64950.1	Dual oxidase	GO:0012505,GO:0042335,GO:0072593,GO:0005509,GO:0020037,GO:0048085,GO:0016021,GO:0016175,GO:0016174,GO:0035220,GO:0006979,GO:0042742,GO:0051591,GO:0043066,GO:0042744,GO:0055114,GO:0008365,GO:0019221,GO:0004601,GO:0002385,GO:0016491	CG3131-PC						PF08030				G3DSA:3.40.50.80	SSF52343									
aly6498.1	Homeobox protein PKNOX2	GO:0034504,GO:0015629,GO:0003677,GO:0035282,GO:0005737,GO:0043565,GO:0007479,GO:0007432,GO:0007380,GO:0005634,GO:0007383,GO:0007476,GO:0045664,GO:0000981,GO:0048749,GO:0015630,GO:0005515,GO:0007480,GO:0008134,GO:0051015,GO:0001654,GO:0003785,GO:0007525,GO:0001752,GO:0009954,GO:0007420,GO:0007422,GO:0003700,GO:0010092,GO:0003705,GO:0006357,GO:0045944,GO:0000977,GO:0005667,GO:0042659,GO:0048735	CG17117-PC				SM00389		PF16493,PF05920	PS50071			G3DSA:1.10.10.60	SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6498.2	Scavenger receptor class B member 1	GO:0034375,GO:0006869,GO:0015914,GO:0043691,GO:0005901,GO:0051000,GO:0070328,GO:0032497,GO:0010867,GO:0005737,GO:0050764,GO:0070062,GO:0010886,GO:0016020,GO:0043654,GO:0035461,GO:0010899,GO:0001786,GO:0042803,GO:0005319,GO:0006702,GO:0008035,GO:0006707,GO:0015920,GO:0009986,GO:0006910,GO:0006952,GO:0043534,GO:0005887,GO:0005886,GO:0007155,GO:0042632,GO:0001530,GO:0030169,GO:0031528,GO:0005044,GO:0006898,GO:0044406,GO:0034384,GO:0005765,GO:0033344,GO:0006694,GO:0034383,GO:0001875,GO:0070506,GO:0001935	CG1887-PD						PF01130		PR01609,PR01609,PR01609,PR01609,PR01609,PR01609													
aly65.1	Unknown		CG15601-PA				SM00595,SM00595		PF10545,PF10545	PS51029,PS51029													
aly65.2	Macoilin	GO:0044306,GO:0007420,GO:0016021,GO:0031965,GO:0030424,GO:0045202,GO:0043005,GO:0005634	CG30389-PE						PF09726,PF09726						401~449,357~384,505~525								
aly65.3	RecQ-mediated genome instability protein 1	GO:0005737,GO:0005634,GO:0046331,GO:0006260,GO:0003723,GO:0006397	CG13472-PA						PF08585,PF16099														
aly65.4	Ubiquitin carboxyl-terminal hydrolase 16	GO:0006351,GO:0042393,GO:0045901,GO:0051289,GO:0005634,GO:0004197,GO:0003713,GO:0016578,GO:0006974,GO:0004843,GO:0006511,GO:0051726,GO:0008270,GO:0043130,GO:0007067,GO:0070537,GO:0016579,GO:0036459,GO:0051301,GO:0045893	CG4165-PA						PF00443,PF02148	PS50271,PS50235		PS00972,PS00973	G3DSA:3.30.40.10	SSF54001,SSF54001,SSF54001,SSF54001,SSF57850	729~749								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly65.5	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GO:0016020,GO:0006909,GO:0005085,GO:0035149,GO:0005086,GO:0032940,GO:0006888,GO:0000902,GO:0007431,GO:0032312,GO:0005811,GO:0035158,GO:0032012,GO:0002064,GO:0005794,GO:0005793,GO:0009306,GO:0005798,GO:0008289,GO:0007030,GO:0000137,GO:0006891,GO:0005801,GO:0005802,GO:0015031	CG8487-PB				SM00222		PF12783,PF01369	PS50190			G3DSA:1.10.1000.11,G3DSA:1.10.220.20	SSF48425										
aly65.6	Frizzled-10	GO:0048675,GO:0016318,GO:0008105,GO:0008104,GO:0035206,GO:0001944,GO:0032956,GO:0009790,GO:0007163,GO:0007164,GO:0007165,GO:0030010,GO:0043507,GO:0007298,GO:0001745,GO:0008356,GO:0035317,GO:0005737,GO:0032231,GO:0004930,GO:0007435,GO:0043547,GO:0016021,GO:0007476,GO:0007275,GO:0045746,GO:0042067,GO:0016360,GO:0007186,GO:0038031,GO:0035159,GO:0009986,GO:0034260,GO:0060070,GO:0030165,GO:0045198,GO:0005938,GO:0005887,GO:0005886,GO:0007156,GO:0001737,GO:0001736,GO:0001738,GO:0007507,GO:0008406,GO:0032589,GO:0007420,GO:0035320,GO:0016055,GO:0007464,GO:0042813,GO:0004888,GO:0006357,GO:0005515,GO:0017147,GO:0005768	CG17697-PC				SM00063		PF01392,PF01534	PS50038,PS50261	PR00489,PR00489,PR00489,PR00489,PR00489		G3DSA:1.10.2000.10	SSF63501			REACT_14797						
aly65.7	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly65.8	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GO:0043547,GO:0005811,GO:0006909,GO:1903409,GO:0034067,GO:0030155,GO:0005085,GO:0048205,GO:0035149,GO:0005086,GO:0061024,GO:0032940,GO:0061162,GO:0016020,GO:0070973,GO:0006888,GO:0000902,GO:0007431,GO:0032312,GO:0090166,GO:0002263,GO:0005777,GO:0005739,GO:0005547,GO:0035158,GO:0007346,GO:0032012,GO:1903420,GO:0002064,GO:0005795,GO:0005794,GO:0030593,GO:0005793,GO:0006892,GO:0009306,GO:0005798,GO:0031252,GO:0005788,GO:0042147,GO:0005886,GO:0007030,GO:0080025,GO:0006996,GO:0000137,GO:0006891,GO:0006890,GO:0006895,GO:0005801,GO:0005802,GO:0000139,GO:0097111,GO:0016032,GO:0015031,GO:2000008	CG8487-PB																				
aly6505.1	Transmembrane and TPR repeat-containing protein 1	GO:0016021,GO:0017122,GO:0008150,GO:0005739,GO:0016262	CG4050-PA				SM00028,SM00028,SM00028		PF08409,PF00515,PF00515	PS50005,PS50293,PS50005			G3DSA:1.25.40.10	SSF48452									
aly6505.2	Unknown		n/a																				
aly6506.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly651.1	Unknown		n/a																				
aly651.2	ABC transporter G family member 23	GO:0043190,GO:0042626,GO:0005215,GO:0016021,GO:0006810,GO:0016887,GO:0022008,GO:0005524	CG11147-PA				SM00382		PF12698,PF00005	PS50893		PS00211	G3DSA:3.40.50.300	SSF52540									
aly651.3	Protein phosphatase PP2A 55 kDa regulatory subunit	GO:0006470,GO:0050821,GO:0034047,GO:0045201,GO:0008601,GO:0030071,GO:0005737,GO:0001700,GO:0005634,GO:0005875,GO:0007088,GO:0000278,GO:0051297,GO:0000090,GO:0007406,GO:0007447,GO:0000159,GO:0007423,GO:0005829,GO:0016055,GO:0004722,GO:0007099,GO:0007091	CG6235-PA																				
aly651.4	Protein phosphatase PP2A 55 kDa regulatory subunit	GO:0006470,GO:0050821,GO:0034047,GO:0045201,GO:0008601,GO:0005875,GO:0005737,GO:0001700,GO:0005634,GO:0030071,GO:0007088,GO:0000278,GO:0051297,GO:0000090,GO:0007406,GO:0007447,GO:0000159,GO:0007423,GO:0005829,GO:0016055,GO:0004722,GO:0007099,GO:0005515,GO:0007091	CG6235-PA				SM00320,SM00320,SM00320,SM00320,SM00320				PR00600,PR00600,PR00600,PR00600,PR00600	PS01025,PS01024	G3DSA:2.130.10.10	SSF50978										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly651.5	Unknown	GO:0008270,GO:0003676	n/a				SM00451,SM00451								307~327,27~47								
aly651.6	Unknown	GO:0046872	n/a									PS00028,PS00028											
aly651.7	Probable small nuclear ribonucleoprotein Sm D2	GO:0030532,GO:0071011,GO:0071013,GO:0000398,GO:0008380,GO:0007052,GO:0007067,GO:0022008,GO:0005681,GO:0006397	CG1249-PA				SM00651		PF01423				G3DSA:2.30.30.100	SSF50182									
aly651.8	Disintegrin and metalloproteinase domain-containing protein 15	GO:0016337,GO:0030308,GO:0042246,GO:0001669,GO:0008270,GO:0001525,GO:0070062,GO:0016021,GO:1900121,GO:0006509,GO:0006508,GO:0009986,GO:0042802,GO:0030336,GO:0004222,GO:0045087,GO:0060317,GO:0005912,GO:0042995,GO:0051259,GO:0007229,GO:0001953,GO:0030574,GO:0070528	CG7649-PC				SM00608		PF01421,PF01562	PS50215,PS50026		PS01186	G3DSA:3.40.390.10	SSF55486	166~186								
aly651.9	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6516.1	UBX domain-containing protein 4	GO:0005635,GO:0006986,GO:0005789,GO:0005515,GO:0030433	CG8042-PA				SM00166		PF00789	PS50033			G3DSA:3.10.20.90	SSF54236	114~150,73~107								
aly6517.1	Unknown		n/a																				
aly6517.2	Unknown		n/a																				
aly6517.3	Poly(A) polymerase gamma	GO:0005737,GO:0005634,GO:0016020,GO:0004652,GO:0005654,GO:0003723,GO:0043631,GO:0006378,GO:0046872,GO:0005524	CG9854-PD			PIRSF018425			PF04926,PF01909,PF04928				G3DSA:1.10.1410.10,G3DSA:3.30.70.590	SSF81631,SSF81301,SSF55003									
aly6517.4	Myoneurin	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872,GO:0008270	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF12874,PF07776	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:4.10.1050.10,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667	151~171								
aly6517.5	Zinc finger protein 271	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667	327~347								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6517.6	Neutral alpha-glucosidase AB	GO:0017177,GO:0006457,GO:0042470,GO:0005975,GO:0070062,GO:0005794,GO:0043687,GO:0044822,GO:0016020,GO:0030246,GO:0005788,GO:0018279,GO:0005576,GO:0004553,GO:0044267,GO:0033919,GO:0004558,GO:0005875	CG14476-PB						PF01055					SSF51011										
aly653.1	Phosphatidylinositide phosphatase SAC1	GO:0052866,GO:0012505,GO:0016791,GO:0071683,GO:0016311,GO:0016021,GO:0016199,GO:0030424,GO:0046329,GO:0060074,GO:0046488,GO:0052744,GO:0046664,GO:0005789,GO:0046856,GO:0031122,GO:0043025,GO:0008088	CG9128-PB																					
aly653.2	Zinc transporter 2	GO:0005737,GO:0016023,GO:0006812,GO:0016021,GO:0005770,GO:0005622,GO:0061090,GO:0005765,GO:0005385,GO:0055085	CG11163-PA					TIGR01297	PF01545				G3DSA:1.20.1510.10,G3DSA:1.20.1510.10	SSF161111,SSF161111										
aly653.3	SH3 domain-binding protein 5-like	GO:0005737,GO:0007517,GO:0009952,GO:0007498,GO:0017124,GO:0012501,GO:0030292,GO:0048644,GO:0042694	CG7761-PB						PF05276						16~50,190~245									
aly653.4	Dynein light chain roadblock-type 2	GO:0016319,GO:0070062,GO:0042623,GO:0006810,GO:0007018,GO:0005858,GO:0003774,GO:0048813,GO:0005868,GO:0030286,GO:0005874,GO:0005875	CG10751-PA			PIRSF009998	SM00960		PF03259				G3DSA:3.30.450.30	SSF103196										
aly653.5	KH domain-containing, RNA-binding, signal transduction-associated protein 2	GO:0005737,GO:0006351,GO:0008143,GO:0005634,GO:0008266,GO:0006355,GO:0003723,GO:0003729	CG4816-PE				SM00322						G3DSA:3.30.1370.10	SSF54791										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly653.6	Transient receptor potential channel pyrexia	GO:0005261,GO:0005262,GO:0048060,GO:0006812,GO:0016021,GO:0070588,GO:0006816,GO:0051290,GO:0034703,GO:0005515,GO:0009408,GO:0098655,GO:0055085	CG17142-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF13637,PF13857,PF00520,PF12796,PF12796,PF12796,PF12796	PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50297,PS50088,PS50088,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403									
aly653.7	KH domain-containing, RNA-binding, signal transduction-associated protein 2	GO:0008143,GO:0005634,GO:0008266,GO:0006355,GO:0006351,GO:0003723	CG10384-PD				SM00322		PF00013	PS50084			G3DSA:3.30.1370.10	SSF54791									
aly653.8	Unknown		n/a																				
aly65305.1	Chloride channel protein 2	GO:0015629,GO:0030554,GO:0016020,GO:0034707,GO:0006821,GO:0005247,GO:0005254,GO:0055085	CG31116-PD							PS51371,PS51371			G3DSA:3.10.580.10,G3DSA:3.10.580.10,G3DSA:1.10.3080.10	SSF54631,SSF54631,SSF81340									
aly65331.1	Unknown		n/a						PF11935														
aly6551.1	GAS2-like protein 1	GO:0009267,GO:0045746,GO:0010629,GO:0015629,GO:0008093,GO:0097067,GO:0045647,GO:0001578,GO:0030713,GO:0005856,GO:0007050,GO:0030707,GO:0005737,GO:0005881,GO:0046966,GO:0030308,GO:0051726,GO:0007026,GO:0005515,GO:0008017	CG3973-PA				SM00033,SM00243		PF02187,PF00307	PS50021,PS51460			G3DSA:1.10.418.10,G3DSA:3.30.920.20	SSF47576,SSF47576,SSF143575	691~711								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6551.2	Protein takeout	GO:0007631,GO:0007623,GO:0005615,GO:0007617,GO:0005576,GO:0042594,GO:0042595,GO:0008343,GO:0008049,GO:0007622	CG13618-PA				SM00700		PF06585														
aly6551.3	Unknown		n/a																				
aly6568.1	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494	800~820								
aly657.1	Unknown		n/a																				
aly657.2	Unknown		n/a																				
aly65803.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6586.1	Unknown		n/a																				
aly659.1	Facilitated trehalose transporter Tret1	GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG15406-PA						PF00083			PS00217	G3DSA:1.20.1250.20	SSF103473	219~239								
aly6592.1	Esterase FE4	GO:0052689	CG6018-PA						PF00135			PS00941	G3DSA:3.40.50.1820	SSF53474									
aly6599.1	Unknown		n/a																				
aly6599.2	Unknown		n/a																				
aly65999.1	Dystrophin, isoform B	GO:0005200,GO:0008586,GO:0046716,GO:0045202,GO:0030010,GO:0007274,GO:0005856,GO:0007517,GO:0007474,GO:0005198,GO:0003779,GO:0005509,GO:0005737,GO:0042383,GO:0050699,GO:0008307,GO:0046928,GO:0048172,GO:0005938,GO:0008092,GO:0016010,GO:0008270	CG31175-PH										G3DSA:1.20.58.60	SSF46966									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly660.1	Protein phosphatase 1D	GO:0008285,GO:0035970,GO:0000086,GO:0006470,GO:0005634,GO:0009617,GO:0004722,GO:0003824,GO:0009267,GO:0009314,GO:0046872,GO:0055114,GO:0016491	CG2984-PA				SM00332		PF00481	PS51746		PS01032	G3DSA:3.60.40.10	SSF81606									
aly660.2	39S ribosomal protein L18, mitochondrial	GO:0008097,GO:0005615,GO:0035928,GO:0006412,GO:0003735,GO:0005743,GO:0005762,GO:0032543,GO:0005840	CG12373-PA						PF00861				G3DSA:3.30.420.100	SSF53137									
aly660.3	Eukaryotic translation initiation factor 4E transporter	GO:0005737,GO:0016607,GO:0016605,GO:0043231,GO:0019827,GO:0005829,GO:0016020,GO:0000932,GO:0045665,GO:0044822,GO:0017148,GO:0008565,GO:0005634,GO:0003729	CG32016-PB						PF10477,PF10477,PF10477						637~664,485~505								
aly660.4	Unknown		n/a																				
aly660.5	Unknown	GO:0046872	CG14438-PA				SM00355,SM00355			PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028		SSF57667	2013~2033,54~74,1806~1843,1624~1644,3968~3988							
aly660.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly660.7	Unknown		n/a										G3DSA:2.60.40.770										
aly66007.1	Unknown		n/a																				
aly66079.1	Transposon Tf2-8 polyprotein	GO:0006310,GO:0004519,GO:0003887,GO:0015074,GO:0004190,GO:0003723,GO:0003677,GO:0003964,GO:0046872	n/a							PS50994			G3DSA:3.30.420.10	SSF53098									
aly6625.1	Dystrophin, isoforms A/C/F/G/H	GO:0005200,GO:0008586,GO:0046716,GO:0045202,GO:0030010,GO:0007274,GO:0005856,GO:0007517,GO:0007474,GO:0005198,GO:0003779,GO:0005509,GO:0005737,GO:0042383,GO:0050699,GO:0008307,GO:0046928,GO:0048172,GO:0005938,GO:0008092,GO:0016010,GO:0008270	CG34157-PI										G3DSA:1.20.58.60	SSF46966									
aly663.1	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly663.10	Cuticle protein 7	GO:0040003,GO:0005214,GO:0008011,GO:0008010,GO:0031012,GO:0022008,GO:0042302	CG31876-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly663.11	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly663.12	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly663.13	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly663.14	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly663.15	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly663.16	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly663.17	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly663.18	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly663.19	Cuticle protein 19	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly663.2	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly663.20	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly663.21	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947												

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly663.3	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly663.4	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155		PS00233											
aly663.5	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly663.6	Cuticle protein 7	GO:0005214,GO:0040003,GO:0042302,GO:0008010,GO:0031012	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly663.7	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947												
aly663.8	Cuticle protein 7	GO:0040003,GO:0005214,GO:0008011,GO:0008010,GO:0031012,GO:0022008,GO:0042302	CG31876-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly663.9	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG7076-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly66410.1	Unknown		n/a												243~270								
aly6648.1	Proline synthase co-transcribed bacterial homolog protein	GO:0070062,GO:0005739,GO:0005622,GO:0005575,GO:0008150,GO:0030170	CG1983-PB			PIRSF004848		TIGR00044	PF01168			PS01211	G3DSA:3.20.20.10	SSF51419		00473+5.1.1.1		PWY-7383	UPA00042				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6648.2	Huntingtin	GO:0051881,GO:0048666,GO:0050809,GO:0005770,GO:0005783,GO:1901215,GO:0007626,GO:0007612,GO:0030425,GO:0030424,GO:0048487,GO:0021988,GO:0051938,GO:0043524,GO:0005739,GO:0021990,GO:0044325,GO:0009653,GO:0008542,GO:0007005,GO:0007417,GO:0005737,GO:0042445,GO:0007029,GO:0006888,GO:0045505,GO:0016023,GO:0005634,GO:0007369,GO:0030073,GO:0005776,GO:0008088,GO:0007283,GO:0005654,GO:0043234,GO:0043066,GO:0030072,GO:0021756,GO:0005522,GO:0048489,GO:0042802,GO:0034452,GO:0005794,GO:0007625,GO:0035176,GO:0006606,GO:0008134,GO:0006915,GO:0031587,GO:0051592,GO:0030659,GO:0051402,GO:0008306,GO:0016234,GO:0048167,GO:0007569,GO:0006839,GO:0008340,GO:0022008,GO:0007611,GO:0019805,GO:0009952,GO:0016197,GO:0007030,GO:0046902,GO:0000132,GO:0007420,GO:0048341,GO:0005829,GO:0000052,GO:0034047,GO:0055072,GO:0007212,GO:0048812,GO:2001237,GO:0006890,GO:0019244,GO:0002039,GO:0047496,GO:0000050	CG9995-PA							PS50077	PR00375,PR00375,PR00375,PR00375		G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371	2032~2054								
aly6648.3	Unknown		n/a																				
aly6654.1	Halomucin	GO:0040003,GO:0022600,GO:0007586,GO:0016021,GO:0016020,GO:0030246,GO:0005576,GO:0016747,GO:0009651,GO:0007156,GO:0048477,GO:0030421,GO:0005509	CG32589-PA				SM00703																

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6654.10	Unknown		n/a																				
aly6654.11	WD repeat-containing protein 19	GO:0030326,GO:0031076,GO:0055123,GO:0061512,GO:0003674,GO:0005929,GO:0005737,GO:0001701,GO:0000902,GO:0031514,GO:0008406,GO:0031513,GO:0005654,GO:0060831,GO:0060830,GO:0035721,GO:0005856,GO:0030991,GO:0042384,GO:0048701,GO:0035058,GO:0060271,GO:0050877,GO:0061055,GO:0042471,GO:0007224,GO:0032391,GO:0005515	CG11237-PA				SM00320,SM00320,SM00320,SM00320						G3DSA:2.130.10.10	SSF50978										
aly6654.12	Unknown		n/a																				
aly6654.13	WD repeat-containing protein 19	GO:0005737,GO:0005856,GO:0030991,GO:0042384,GO:0006996,GO:0031514,GO:0032391,GO:0031513,GO:0005654,GO:0097542,GO:0072372,GO:0035721,GO:0005929	n/a																				
aly6654.2	Nose resistant to fluoxetine protein 6	GO:0040003,GO:0022600,GO:0006869,GO:0007586,GO:0016021,GO:0008289,GO:0007275,GO:0016747,GO:0009651,GO:0048477,GO:0030421	CG32589-PA				SM00703		PF01757	PS51257													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6654.3	Unknown		CG16959-PA						PF16033														
aly6654.4	TNF receptor-associated factor 6	GO:0035631,GO:0071222,GO:0070498,GO:0007249,GO:0048468,GO:0009887,GO:0009898,GO:0051023,GO:0001503,GO:0007165,GO:0004871,GO:0008063,GO:0050829,GO:0043507,GO:0008219,GO:0002726,GO:0042981,GO:0000209,GO:0007250,GO:0000122,GO:0016874,GO:0005811,GO:0031098,GO:0005739,GO:0045944,GO:0001843,GO:0070534,GO:0043122,GO:0043123,GO:0050852,GO:0019886,GO:0048471,GO:0045084,GO:0045087,GO:0030316,GO:0042102,GO:0006952,GO:0032743,GO:0005938,GO:0042475,GO:0004842,GO:0045453,GO:0051092,GO:0045410,GO:0042088,GO:0005829,GO:0005730,GO:0031666,GO:0007391,GO:0005622,GO:0051865,GO:0045672,GO:0046849,GO:0005515,GO:0061630,GO:0043011,GO:2000679,GO:0008270	CG10961-PA				SM00184		PF00097	PS50144,PS50089		PS00518	G3DSA:3.90.890.10,G3DSA:2.60.210.10,G3DSA:3.30.40.10	SSF49599,SSF57850,SSF49599										
aly6654.5	Breast carcinoma-amplified sequence 3 homolog	GO:0005737,GO:0005829,GO:0044351,GO:0003674	CG43154-PC						PF12490				G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978									
aly6654.6	Iduronate 2-sulfatase	GO:0030207,GO:0043202,GO:0030204,GO:0005975,GO:0004423,GO:0044281,GO:0008152,GO:0030203,GO:0046872,GO:0006027	CG12014-PA						PF00884			PS00149,PS00523	G3DSA:3.30.1120.10,G3DSA:3.40.720.10	SSF53649									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6654.7	GDP-fucose transporter 1	GO:0036085,GO:0000139,GO:0036066,GO:0016021,GO:0008643,GO:0005463,GO:0005462,GO:0005461,GO:0005460,GO:0005794,GO:0007625,GO:0048193,GO:0005798,GO:0015789,GO:0015788,GO:0036071,GO:0015783,GO:0015782,GO:0015787,GO:0015786,GO:0015785,GO:0015784,GO:0005458,GO:0005459,GO:0005456,GO:0005457	CG9620-PA						PF03151					SSF103481									
aly6654.8	Membrane-associated progesterone receptor component 1	GO:0070062,GO:0020037,GO:0005730,GO:0016021,GO:0035100,GO:0005789,GO:0005886,GO:0005496	CG9066-PA						PF00173				G3DSA:3.10.120.10	SSF55856									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6654.9	CREB-binding protein	GO:0032922,GO:0043974,GO:0001102,GO:0043971,GO:0004402,GO:0034605,GO:0008140,GO:0007165,GO:0008589,GO:0001228,GO:0042592,GO:0045466,GO:0006473,GO:0045893,GO:0008270,GO:0004871,GO:0034644,GO:0044017,GO:0001745,GO:0001078,GO:0044255,GO:0040040,GO:0005737,GO:0001191,GO:0043426,GO:0000123,GO:0000122,GO:0006325,GO:0061418,GO:0005634,GO:0000940,GO:0003713,GO:1900034,GO:0005654,GO:0048511,GO:0010467,GO:0007416,GO:0016573,GO:0071456,GO:0000987,GO:0007088,GO:0044281,GO:0045087,GO:1900087,GO:0048749,GO:0001085,GO:0005667,GO:0008283,GO:0008134,GO:0006461,GO:0018076,GO:0001666,GO:0001105,GO:0000790,GO:0007219,GO:0045475,GO:0007269,GO:0003700,GO:0016032,GO:0022008,GO:0016604,GO:0008347,GO:0070555,GO:0043234,GO:0042733,GO:0002223,GO:0000076,GO:0007224,GO:0043982,GO:0043983,GO:0016055,GO:0006367,GO:0007464,GO:0003684,GO:0006355,GO:0016407,GO:0045944,GO:0000977,GO:0005515,GO:0032481,GO:0030097,GO:0003682,GO:0002039,GO:0043993,GO:0030718	CG15319-PC				SM00551,SM00551,SM00297,SM00291		PF00569,PF08214,PF02172,PF09030,PF02135,PF02135,PF06001,PF00439	PS50135,PS50952,PS50134,PS50134,PS50014,PS51727	PR00503,PR00503,PR00503,PR00503	PS01357,PS00633	G3DSA:1.10.1630.10,G3DSA:1.20.1020.10,G3DSA:1.20.1020.10,G3DSA:1.20.920.10,G3DSA:1.10.246.20	SSF47040,SSF47370,SSF57850,SSF57933,SSF69125,SSF57933	588~612,311~347,1400~1424,1103~1127		REACT_22258							
aly666.1	Ejaculatory bulb-specific protein 3	GO:0007362,GO:0006468,GO:0007552,GO:0019992,GO:0009615,GO:0009617,GO:0045297,GO:0004674,GO:0005576,GO:0004672	CG9358-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.10	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly666.11	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.12	Ejaculatory bulb-specific protein 3	GO:0007362,GO:0006468,GO:0007552,GO:0019992,GO:0009615,GO:0009617,GO:0045297,GO:0004674,GO:0005576,GO:0004672	CG9358-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.13	Ejaculatory bulb-specific protein 3	GO:0007362,GO:0006468,GO:0007552,GO:0019992,GO:0009615,GO:0009617,GO:0045297,GO:0004674,GO:0005576,GO:0004672	CG9358-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.14	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.15	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.16	Ejaculatory bulb-specific protein 3	GO:0007362,GO:0006468,GO:0007552,GO:0019992,GO:0009615,GO:0009617,GO:0045297,GO:0004674,GO:0005576,GO:0004672	CG9358-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly666.17	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.18	Unknown		n/a						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.19	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	GO:0030956,GO:0006425,GO:0005739,GO:0050567,GO:0005524,GO:0032543,GO:0070681,GO:0016884	CG5463-PA	MF_00121			SM00845	TIGR00133	PF02637,PF02934					SSF89095,SSF55931									
aly666.2	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.20	Unknown		n/a							PS51257					432~452								
aly666.21	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly666.22	Putative glycerol kinase 5	GO:0004370,GO:0019563,GO:0005975,GO:0005524	CG1271-PA			PIRSF000538			PF02782,PF00370			PS00445	G3DSA:3.30.420.40,G3DSA:3.30.420.40	SSF53067,SSF53067		00561+2.7.1.30		PWY-4261	UPA00618				
aly666.23	CREB-regulated transcription coactivator 1	GO:0005737,GO:0016032,GO:1900273,GO:0043153,GO:1900006,GO:0051289,GO:0005634,GO:0008140,GO:0032793,GO:0007613,GO:0030425,GO:0005654,GO:0048511,GO:0045944,GO:0045202,GO:0042594,GO:0005886,GO:0060081,GO:0043025,GO:0006979,GO:0006351	CG6064-PB						PF12884														
aly666.24	Unknown		n/a																				
aly666.25	RNA-binding protein 12B	GO:0044822,GO:0000166	CG30069-PA																				
aly666.26	Ubiquitin-conjugating enzyme E2 R2	GO:0004842,GO:0006513,GO:0022008,GO:0070936,GO:0016874,GO:0005524	CG7656-PD				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				
aly666.27	Maspardin	GO:0005654,GO:0030140,GO:0005829,GO:0042609	n/a						PF12697				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly666.28	Stomatin-like protein 2, mitochondrial	GO:0019897,GO:0032623,GO:0034982,GO:0007005,GO:0005856,GO:1900210,GO:0005739,GO:0005758,GO:0050852,GO:0006851,GO:0006874,GO:1990046,GO:0042776,GO:0010876,GO:0010918,GO:0051259,GO:0090297,GO:0045121,GO:0051020,GO:0005743,GO:1901612,GO:0005102,GO:0035710	CG2970-PA				SM00244		PF01145,PF16200		PR00721,PR00721,PR00721,PR00721,PR00721,PR00721			SSF117892	383~403								
aly666.29	Coiled-coil domain-containing protein 112		n/a																				
aly666.3	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.30	Tetratricopeptide repeat protein 19 homolog, mitochondrial	GO:0007630,GO:0005515,GO:0097033,GO:0005739,GO:0005743,GO:0034551,GO:0071632	CG15173-PA						PF13424	PS50005,PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452	77~97								
aly666.31	Peptidyl-prolyl cis-trans isomerase 6	GO:0006457,GO:0005615,GO:0032504,GO:0005811,GO:0005576,GO:0003755,GO:0005875	CG2852-PA						PF00160	PS50072	PR00153,PR00153,PR00153,PR00153,PR00153,PR00153	PS00170	G3DSA:2.40.100.10	SSF50891									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly666.32	Transmembrane protein adipocyte-associated 1 homolog	GO:0016021	n/a						PF10160														
aly666.33	Serine/threonine-protein kinase PRP4 homolog	GO:0006468,GO:0071011,GO:0071013,GO:0044822,GO:0000398,GO:0005654,GO:0004674,GO:0008360,GO:0004672,GO:0007155,GO:0022008,GO:0005694,GO:0008380,GO:0005524,GO:0006397	CG7028-PC				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112	57~77								
aly666.34	Pentatricopeptide repeat-containing protein 2, mitochondrial	GO:0007507,GO:0055010,GO:0050684,GO:0044822,GO:0001822,GO:0005739,GO:0001889,GO:0048747,GO:0010468,GO:0007005,GO:0006397	n/a																				
aly666.35	Unknown		n/a																				
aly666.36	Diuretic hormone receptor	GO:0009755,GO:0008036,GO:0004930,GO:0005184,GO:0016021,GO:0005886,GO:0005887,GO:0008188,GO:0009651,GO:0007186,GO:0004948	CG12370-PB				SM00008		PF00002,PF02793	PS50261,PS50227	PR00249,PR00249,PR00249,PR00249,PR00249,PR00249,PR00249,PR01127,PR01127,PR01127,PR01127,PR01127,PR01127,PR01127,PR01127,PR01127	PS00649,PS00650	G3DSA:1.20.1070.10	SSF81321,SSF111418										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly666.37	EF-hand domain-containing family member B	GO:0005575,GO:0003674,GO:0008150,GO:0005509	CG33490-PA																				
aly666.4	Putative odorant-binding protein A10	GO:0007362,GO:0006468,GO:0007552,GO:0019992,GO:0009617,GO:0004674,GO:0005576,GO:0004672	CG9358-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.5	Ejaculatory bulb-specific protein 3	GO:0007362,GO:0006468,GO:0007552,GO:0019992,GO:0009615,GO:0009617,GO:0045297,GO:0005576,GO:0004672	CG9358-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.6	Putative odorant-binding protein A10	GO:0005549,GO:0007606,GO:0005550,GO:0005576	CG6642-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly666.7	EF-hand domain-containing family member B	GO:0005575,GO:0003674,GO:0008150,GO:0005509	CG33489-PA										G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473,SSF47473									
aly666.8	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly666.9	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly66736.1	Unconventional myosin-Va	GO:0031036,GO:0032027,GO:0035277,GO:0007496,GO:0008258,GO:0007443,GO:0030424,GO:0008152,GO:0007297,GO:0045200,GO:0032869,GO:0007298,GO:0009653,GO:0042642,GO:0035317,GO:0030018,GO:0035072,GO:0005856,GO:0007435,GO:0000146,GO:0042623,GO:0000149,GO:0048306,GO:0045179,GO:0000281,GO:0032252,GO:0016459,GO:0043005,GO:0030141,GO:0017075,GO:0043008,GO:0043025,GO:0003774,GO:0005524,GO:0017157,GO:0016203,GO:0000910,GO:0032507,GO:0006936,GO:0030239,GO:0035159,GO:0031252,GO:0042060,GO:0032154,GO:0030048,GO:0045214,GO:0005938,GO:0035017,GO:0046664,GO:0022008,GO:0072659,GO:0030050,GO:0001736,GO:0046663,GO:0051259,GO:0043473,GO:0016192,GO:0051726,GO:0007391,GO:0007395,GO:0070986,GO:0016461,GO:0016460,GO:0008021,GO:0015031,GO:0046983,GO:0046982,GO:0032593	CG15792-PA						PF00063	PS51456				SSF52540									
aly66737.1	Protein lin-10	GO:0008105,GO:0030425,GO:0003674,GO:0045202,GO:0007270,GO:0030054,GO:0005737,GO:0040026,GO:0001540,GO:0005615,GO:0097120,GO:0043005,GO:0043025,GO:0005794,GO:0050975,GO:1903361,GO:0032504,GO:0030140,GO:0006810,GO:0005886,GO:0032580,GO:0007399,GO:0000138,GO:0005515	CG32677-PA				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly668.1	Unknown	GO:0007157,GO:0005576,GO:0003674,GO:0016201,GO:0008045	CG15138-PA						PF13927,PF08205	PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly668.10	TAF6-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 6L	GO:0051090,GO:0070062,GO:0006338,GO:0006325,GO:0003713,GO:0005634,GO:0043966,GO:0030914,GO:0000118,GO:0006357,GO:0006352,GO:0003677	n/a						PF02969				G3DSA:1.25.10.10,G3DSA:1.10.20.10										
aly668.11	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0022857,GO:0005886,GO:0055085	CG8249-PA						PF00083				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly668.12	Gremlin-1	GO:0014032,GO:0032525,GO:0005615,GO:0007399,GO:0014029,GO:0036122,GO:0035582,GO:0016015,GO:0048263,GO:0039022	n/a				SM00041		PF03045	PS51257													
aly668.13	Neuroendocrine protein 7B2	GO:0007218,GO:0016486,GO:0030141,GO:0006886,GO:0051082,GO:0005576,GO:0046883,GO:0016504,GO:0045862,GO:0004857,GO:0010952,GO:0005525	CG1168-PB						PF05281														
aly668.14	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly668.2	Unknown	GO:0007157,GO:0005576,GO:0003674,GO:0016201,GO:0008045	CG15138-PA						PF08205,PF07686	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly668.3	Pro-resilin	GO:0040003,GO:0032992,GO:0005214,GO:0030023,GO:0008010,GO:0031012,GO:0005576,GO:0008061,GO:0042302	CG15920-PA						PF00379	PS51155		PS00233											
aly668.4	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171,PR00171,PR00171	PS00217	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473			REACT_15518						
aly668.5	Retinoid-inducible serine carboxypeptidase	GO:0070062,GO:0045776,GO:0005829,GO:0045909,GO:0004185,GO:0006508,GO:0042573	CG32483-PA						PF00450		PR00724,PR00724,PR00724		G3DSA:3.40.50.1820	SSF53474									
aly668.6	Retinoid-inducible serine carboxypeptidase	GO:0070062,GO:0045776,GO:0005829,GO:0045909,GO:0004185,GO:0006508,GO:0042573	CG31821-PA						PF00450				G3DSA:3.40.50.1820	SSF53474									
aly668.7	Serine carboxypeptidase-like 51	GO:0006508,GO:0005576,GO:0004185	CG32483-PA						PF00450				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly668.8	DNA methyltransferase 1-associated protein 1	GO:0005737,GO:0006306,GO:0000122,GO:0003714,GO:0006909,GO:0045471,GO:0006338,GO:0006281,GO:0043968,GO:0005634,GO:0043967,GO:0040008,GO:0005654,GO:0006325,GO:0005657,GO:0045892,GO:0035267,GO:0001103,GO:0003682,GO:0042993,GO:0006351	CG11132-PA						PF16282,PF05499						68~122									
aly668.9	rRNA-processing protein FCF1 homolog	GO:0032040,GO:0005730,GO:0005634,GO:0048096,GO:0048812,GO:0006364,GO:0044822	CG4539-PA				SM00670		PF04900				G3DSA:3.40.50.1010	SSF88723										
aly66830.1	Unknown	GO:0003676	n/a										G3DSA:3.30.420.10	SSF53098										
aly6687.1	Mitochondrial 2-oxoglutarate/malate carrier protein	GO:0006810,GO:0005975,GO:0005887,GO:0005634,GO:0005811,GO:0044822,GO:0022857,GO:0005739,GO:0005743,GO:0005740,GO:0044281,GO:0015367,GO:0006839,GO:0006006,GO:0015743,GO:0015742,GO:0006094	CG1907-PA						PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506										
aly6687.10	Unknown	GO:0006508,GO:0032504,GO:0005615,GO:0005515,GO:0004867	CG31704-PA				SM00280		PF00050	PS51465			G3DSA:3.30.60.30	SSF100895										
aly6687.11	Zinc finger CCHC domain containing protein 24	GO:0044822,GO:0008270,GO:0003676	n/a						PF13696,PF13695				G3DSA:4.10.60.10	SSF57756										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6687.12	Cyclin-dependent kinase-like 2	GO:0005737,GO:0006468,GO:0005634,GO:0000281,GO:0004674,GO:0004672,GO:0004693,GO:0005524	CG7236-PC				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly6687.13	Unknown		n/a																				
aly6687.14	SH2 domain-containing protein 4A	GO:0007614,GO:0010923,GO:0007613,GO:0038202,GO:0008355,GO:0005070,GO:0001700,GO:0045500,GO:0007476,GO:0005118,GO:0005737,GO:0043410,GO:0008595,GO:0007175,GO:0008360,GO:0005886,GO:0007265,GO:0007015,GO:0019902,GO:0008306,GO:0005515,GO:0008293,GO:0045678	CG6033-PC				SM00252		PF00017	PS50001	PR00401,PR00401,PR00401,PR00401		G3DSA:3.30.505.10	SSF55550	99~119,263~290								
aly6687.2	SET and MYND domain-containing protein 4	GO:0005737,GO:0005634,GO:0010629,GO:0008168,GO:0046872,GO:0042826	CG8378-PA						PF00856	PS50280		PS01360	G3DSA:2.170.270.10,G3DSA:2.170.270.10	SSF82199,SSF82199,SSF144232									
aly6687.3	Unknown		n/a							PS50838													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6687.4	Glutathione S-transferase 2	GO:0005737,GO:0004364,GO:0006749,GO:0005515,GO:0006979,GO:0004602	CG8938-PD						PF02798,PF00043	PS50405,PS50404			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF47616,SSF52833									
aly6687.5	Glutathione S-transferase 2	GO:0005737,GO:0004364,GO:0006979,GO:0004602,GO:0006749	CG8938-PD						PF02798	PS50404,PS50405			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF52833,SSF47616									
aly6687.6	Glutathione S-transferase 2	GO:0005737,GO:0004364,GO:0006979,GO:0004602,GO:0006749	CG8938-PD						PF00043,PF02798	PS50405,PS50404			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF52833,SSF47616									
aly6687.7	Solute carrier family 22 member 3	GO:0015844,GO:0019534,GO:0051615,GO:0005329,GO:0015697,GO:0032098,GO:0005215,GO:0016021,GO:0015695,GO:0008513,GO:0098779,GO:0015101,GO:0005887,GO:0051608,GO:0015872,GO:0055085,GO:0015651	CG7458-PA						PF00083	PS50850		PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly6687.8	Solute carrier family 22 member 15	GO:0006811,GO:0016021,GO:0008513,GO:0022857,GO:0055085	CG7442-PA						PF00083				G3DSA:1.20.1250.20	SSF103473									
aly6687.9	Solute carrier family 22 member 3	GO:0015844,GO:0019534,GO:0051615,GO:0005329,GO:0015697,GO:0032098,GO:0016021,GO:0015695,GO:0015872,GO:0098779,GO:0015101,GO:0005887,GO:0051608,GO:0008513,GO:0055085,GO:0015651	CG7458-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly669.1	Glutathione S-transferase 1	GO:0005737,GO:0022008,GO:0004364,GO:0006749,GO:0005515	CG5224-PA						PF13417,PF00043	PS50405,PS50404			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF52833,SSF47616									
aly669.10	Homocysteine S-methyltransferase 1	GO:0008898,GO:0016205,GO:0005829,GO:0033528,GO:0008270,GO:0047150,GO:0009086	CG10621-PA						PF02574	PS50970			G3DSA:3.20.20.330	SSF82282	346~366,422~442,452~507								
aly669.11	Unknown		n/a												37~57								
aly669.12	WD repeat-containing protein 89	GO:0005515	CG12134-PA				SM00320,SM00320,SM00320,SM00320		PF00400	PS50294,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978									
aly669.13	Cysteine and histidine-rich protein 1 homolog	GO:0016567,GO:0004842,GO:0008270	CG32486-PD						PF13920	PS50089			G3DSA:3.30.40.10	SSF57850,SSF49599									
aly669.14	SAP30-binding protein	GO:0045111,GO:0071011,GO:0071013,GO:0006915,GO:0040029,GO:0000398,GO:0005654,GO:0006355,GO:0010467,GO:0006351,GO:0010942,GO:0022008,GO:0005634,GO:0045814	CG2063-PA						PF07818						199~219								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly669.15	Trafficking protein particle complex subunit 11	GO:0005737,GO:0005794,GO:0016192,GO:0046907,GO:0007616,GO:0007611,GO:0008355	CG17569-PB						PF11817														
aly669.16	Proteasome subunit beta type-1	GO:0005737,GO:0051603,GO:0004175,GO:0005839,GO:0043161,GO:0005634,GO:0010499,GO:0004298,GO:0006511,GO:0000502,GO:0006508	CG4097-PA						PF00227	PS51476			G3DSA:3.60.20.10	SSF56235			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045							
aly669.17	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	GO:0006486,GO:0016021,GO:0006915,GO:0008250,GO:0043066,GO:0004576,GO:0012505,GO:0005886,GO:0004579	CG13393-PA			PIRSF005588			PF02109							00513+2.4.99.18,00510+2.4.99.18			UPA00378				
aly669.18	E3 ubiquitin-protein ligase AMFR	GO:0051087,GO:0005783,GO:0007165,GO:0036503,GO:0005789,GO:0016881,GO:0030176,GO:0008270,GO:0070936,GO:0061630,GO:0000209,GO:0032092,GO:0004842,GO:0016021,GO:0016020,GO:0006511,GO:0032403,GO:0048471,GO:1990381,GO:0051259,GO:0034450,GO:0030433,GO:0006928,GO:0016874,GO:0043234,GO:0000836,GO:0030674,GO:0030968,GO:0051865,GO:0005515,GO:0004872	CG1937-PA				SM00184,SM00546		PF13639,PF02845	PS50089,PS51140			G3DSA:3.30.40.10	SSF57850										
aly669.19	Protein VAC14 homolog	GO:0010008,GO:0070772,GO:0046331,GO:0043550	CG5608-PA						PF11916,PF12755				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly669.2	Glutathione S-transferase 1	GO:0005737,GO:0004364,GO:0006749	CG17523-PA						PF00043,PF13417	PS50405,PS50404			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF47616,SSF52833									
aly669.20	Serine/threonine-protein kinase TBK1	GO:0035160,GO:0010629,GO:0007165,GO:0003676,GO:0008219,GO:0045035,GO:0005737,GO:0000902,GO:0051493,GO:0008407,GO:0004674,GO:0032728,GO:0004672,GO:0008385,GO:0008384,GO:0005524,GO:0043123,GO:0006468,GO:0045087,GO:0016322,GO:0006952,GO:0050830,GO:0032727,GO:0043280,GO:0007015,GO:0051607,GO:0045359,GO:0001578,GO:0005829,GO:0051219,GO:0044565,GO:0002218,GO:0045944,GO:0005515	CG2615-PB				SM00220		PF00069	PS50011		PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112	488~519									
aly669.21	Cactin	GO:0009950,GO:0071013,GO:0000398,GO:0006952,GO:0048812,GO:0007165,GO:0022008	CG1676-PB				SM01050		PF10312,PF09732						176~201,84~111,218~238								
aly669.22	NADH dehydrogenase [ubiqui] iron-sulfur protein 3, mitochondrial	GO:2001243,GO:0072593,GO:0030308,GO:0043209,GO:0008137,GO:0005634,GO:0044237,GO:0006120,GO:0005743,GO:0005739,GO:0021762,GO:0005747,GO:0022904,GO:0031966,GO:0044281,GO:0003954,GO:0055114,GO:0009055	CG12079-PA	MF_01357				TIGR01961	PF00329			PS00542		SSF143243									
aly669.23	Tudor domain-containing protein 5	GO:0030719,GO:0043186,GO:0043046,GO:0071546,GO:0030717,GO:0010529,GO:0007286,GO:0033391	CG8589-PA						PF00567,PF12872,PF12872	PS51644,PS51644			G3DSA:2.30.30.140	SSF63748									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly669.24	Unknown		CG17321-PA																				
aly669.25	Uroporphyrinogen-III synthase	GO:0071418,GO:0006783,GO:0006782,GO:0005829,GO:0006780,GO:0005739,GO:0071243,GO:0033014,GO:0048037,GO:0006778,GO:0046677,GO:0044281,GO:0004852	CG1885-PA						PF02602				G3DSA:3.40.50.10090,G3DSA:3.40.50.10090	SSF69618		00860+4.2.1.75		PWY-5189,PWY-5188	UPA00251				
aly669.26	Unknown		n/a																				
aly669.27	Unknown		n/a																				
aly669.28	Unknown		n/a																				
aly669.29	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly669.3	Glutathione S-transferase 1	GO:0005737,GO:0004364,GO:0006749,GO:0005515	CG16936-PA						PF02798,PF13410	PS50404,PS50405			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF52833,SSF47616									
aly669.4	Esterase FE4	GO:0005575,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135			PS00122,PS01173	G3DSA:3.40.50.1820	SSF53474									
aly669.5	Esterase FE4	GO:0005575,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135			PS00941,PS00122	G3DSA:3.40.50.1820	SSF53474									
aly669.6	Esterase FE4	GO:0005575,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly669.7	Bile salt-activated lipase	GO:0005737,GO:0005794,GO:0004771,GO:0005791,GO:0005615,GO:0043208,GO:0005829,GO:0045121,GO:0052689,GO:0016042,GO:0005575,GO:0032403,GO:0008150,GO:0008152,GO:0042588,GO:0004622,GO:0043234,GO:0042572,GO:0004806,GO:0050253,GO:0043231	CG10175-PD						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly669.8	Esterase FE4	GO:0005575,GO:0007476,GO:0052689	CG1131-PC						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly669.9	Ran-binding protein 10	GO:0005737,GO:0030536,GO:0007010,GO:0008536,GO:0060250,GO:0007259,GO:0007299,GO:0046843	CG42236-PD				SM00757,SM00668,SM00449,SM00667		PF00622,PF08513,PF10607	PS50897,PS50896,PS50188				SSF49899										
aly671.1	Unknown		n/a				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355																
aly671.10	Putative nuclease HARBI1	GO:0005737,GO:0005813,GO:0005634,GO:0046872,GO:0004518	CG43088-PA						PF13359						15~35								
aly671.11	Polycomb group protein Psc	GO:0035102,GO:0005725,GO:0006338,GO:0006342,GO:0005634,GO:0008270,GO:0001047,GO:0003677,GO:0007411,GO:0005704,GO:0035186	CG3886-PA				SM00184		PF00097,PF16207	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850									
aly671.12	Cell division control protein 6 homolog	GO:0008285,GO:0000082,GO:0000083,GO:0007067,GO:0000922,GO:0030071,GO:0051301,GO:0005737,GO:0005634,GO:0000166,GO:0005654,GO:0005656,GO:0006267,GO:0006260,GO:0032467,GO:0005524,GO:0005794,GO:0000278,GO:0019900,GO:0008156,GO:0051984,GO:0051233,GO:0007089,GO:0000076,GO:0000079,G	CG5971-PA			PIRSF001767	SM00382,SM01074		PF09079,PF13401				G3DSA:1.10.10.10,G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540,SSF46785			REACT_152,REACT_383,REACT_1538						
aly671.13	Unknown	GO:0030246	CG6055-PA				SM00034		PF00059	PS50041		PS00615	G3DSA:3.10.100.10	SSF56436									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly671.14	DnaJ homolog subfamily A member 2	GO:0016020,GO:0006457,GO:0070062,GO:0031072,GO:0005829,GO:0051087,GO:0051082,GO:0042026,GO:0009408,GO:0022008,GO:0046872,GO:0005524	CG8863-PA	MF_01152			SM00271		PF00226,PF01556,PF00684	PS51188,PS50076	PR00625,PR00625,PR00625	PS00636	G3DSA:2.60.260.20,G3DSA:2.60.260.20,G3DSA:2.10.230.10,G3DSA:1.10.287.110,G3DSA:2.60.260.20	SSF57938,SSF46565,SSF49493,SSF49493,SSF49493									
aly671.15	Unknown	GO:0006393,GO:0005739,GO:0003677	CG18124-PA																				
aly671.16	U2 small nuclear ribonucleoprotein auxiliary factor 35 kDa subunit-related protein 2	GO:0042060,GO:0030628,GO:0000245,GO:0005634,GO:0000398,GO:0000166,GO:0003723,GO:0005689,GO:0046872,GO:0008380,GO:0005681,GO:0003729	CG3294-PA				SM00356,SM00356,SM00361		PF00642,PF13893	PS50102,PS50103,PS50103	PR01848,PR01848,PR01848,PR01848,PR01848,PR01848		G3DSA:3.30.70.330	SSF54928	90~134								
aly671.17	Unknown		n/a							PS50297,PS50088			G3DSA:1.25.40.20	SSF48403									
aly671.18	Centrosomin	GO:0000242,GO:0007494,GO:0055059,GO:0007279,GO:0000226,GO:0007067,GO:0008356,GO:0005875,GO:0007417,GO:0005737,GO:0031514,GO:0005813,GO:0000280,GO:0005814,GO:0000922,GO:0016459,GO:0051297,GO:0030997,GO:0008017,GO:0016321,GO:0008594,GO:0007052,GO:0007017,GO:0007422,GO:0040016,GO:0007098,GO:0007099,GO:0005515	CG4832-PL						PF07989						193~227,341~368,455~498,139~180,49~69,390~445								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly671.19	Suppressor APC domain-containing protein 2	GO:0005737,GO:0005634,GO:0005730	CG3880-PA						PF11414						318~338,380~407,269~289								
aly671.2	Probable queuine tRNA-ribosyltransferase	GO:0006400,GO:0008616,GO:0046872,GO:0008479	CG4947-PA					TIGR00430,TIGR00449	PF01702				G3DSA:3.20.20.105	SSF51713				PWY-6700	UPA00392				
aly671.20	Unknown		CG18507-PA						PF14800														
aly671.21	Unknown		n/a																				
aly671.22	Glycerophosphocholine phosphodiesterase GPCPD1	GO:0006629,GO:0008889,GO:0005829,GO:0006071,GO:0047389,GO:2001070	CG2818-PA				SM01065		PF03009,PF00686	PS51704			G3DSA:2.60.40.10,G3DSA:3.20.20.190	SSF51695,SSF49452									
aly671.23	Serine/threonine-protein phosphatase 1 regulatory subunit 10	GO:0006909,GO:0019888,GO:0005634,GO:0050790,GO:0006605,GO:0008157,GO:0004864,GO:0006351,GO:0003677,GO:0046872,GO:0035304	CG33526-PD				SM00356		PF00642,PF08711	PS50103,PS51319			G3DSA:4.10.1000.10,G3DSA:1.20.930.10	SSF47676									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly671.24	Transmembrane and coiled-coil domains protein 1	GO:0005789,GO:0016021,GO:0016020,GO:0000139	CG10470-PA			PIRSF023322			PF01956						59~86,30~53								
aly671.25	FAD-dependent oxidoreductase domain-containing protein 1	GO:0032981,GO:0016021,GO:0005739,GO:0005743,GO:0005747,GO:0055114,GO:0016491	CG10655-PA						PF01266				G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.30.9.10,G3DSA:3.30.9.10	SSF51905,SSF51905									
aly671.26	Putative ATP-dependent RNA helicase DHX33	GO:0005737,GO:0033613,GO:0000390,GO:0005730,GO:0006396,GO:0044822,GO:0004004,GO:0004386,GO:0005654,GO:0045943,GO:0005681,GO:0003676,GO:0022008,GO:0005524,GO:0000182	CG4901-PA				SM00847,SM00490,SM00487		PF00271,PF07717,PF04408,PF00270	PS51194,PS51192		PS00690	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									
aly671.27	Neuroligin-1	GO:0050808,GO:0048065,GO:0030425,GO:0030424,GO:0051124,GO:0004872,GO:0002121,GO:0007274,GO:0007416,GO:0016021,GO:0042043,GO:0035176,GO:0009986,GO:0052689,GO:0007628,GO:0046929,GO:0060074,GO:0005887,GO:0005886,GO:0007155,GO:0045433,GO:0045202	CG13772-PA						PF00135			PS00941	G3DSA:3.40.50.1820	SSF53474									
aly671.28	Mitochondrial sodium/hydrogen exchanger 9B2	GO:0006812,GO:0016021,GO:0015299,GO:0003096,GO:0031966,GO:0005903,GO:0015385,GO:0006814,GO:0055085	CG10806-PA						PF00999														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly671.29	Sodium/hydrogen exchanger 9B1	GO:0006812,GO:0016021,GO:0015299,GO:0003096,GO:0005903,GO:0015385,GO:0055085	CG10806-PA						PF00999														
aly671.3	Coiled-coil domain-containing protein 25	GO:0022008	CG4593-PA						PF05670						152~188								
aly671.30	Mitochondrial sodium/hydrogen exchanger 9B2	GO:0005743,GO:0006812,GO:0016021,GO:0015299,GO:0003096,GO:0006814,GO:0034220,GO:0005903,GO:0015385,GO:0055085	CG10806-PA						PF00999														
aly671.31	G-protein coupled receptor Mth2	GO:0004930,GO:0016021,GO:0016020,GO:0006950,GO:0004888,GO:0007166,GO:0005886,GO:0007186	CG31720-PC							PS50261			G3DSA:2.170.180.11										
aly671.32	Protein 60A	GO:0008083,GO:0005615,GO:0005160,GO:0035222,GO:0030707,GO:0007474,GO:0008586,GO:0007528,GO:0030509,GO:0045887,GO:0005576,GO:0007391,GO:0040007,GO:0048636,GO:0007274,GO:0007179,GO:0046928	CG5562-PA				SM00204		PF00019,PF00688	PS51362		PS00250	G3DSA:2.10.90.10	SSF57501										
aly671.33	Protein CWC15 homolog A	GO:0071011,GO:0071013,GO:0000398,GO:0007052,GO:0003674,GO:0003723,GO:0005634,GO:0005681	CG12135-PA						PF04889						125~148								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly671.34	RNA-binding protein 39	GO:0016607,GO:0006351,GO:0000381,GO:0008380,GO:0071011,GO:0005634,GO:0044822,GO:0000398,GO:0000166,GO:0005815,GO:0006355,GO:0003723,GO:0003676,GO:0006397,GO:0071013,GO:0005681,GO:0003729	CG11266-PA				SM00360,SM00360,SM00360	TIGR01622	PF00076,PF00076,PF15519	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928									
aly671.35	Unknown		n/a						PF08547					SSF49785									
aly671.36	Protein FAM210B	GO:0016021	CG17508-PA						PF06916														
aly671.37	2',5'-phosphodiesterase 12	GO:0005759,GO:0046872,GO:0004535,GO:0006397	CG31759-PC						PF03372				G3DSA:3.60.10.10	SSF56219,SSF56219									
aly671.38	Protein transport protein Sec61 subunit beta	GO:0008565,GO:0005784,GO:0016021,GO:0000060,GO:0006886,GO:0044822,GO:0030970,GO:0006616,GO:0048812,GO:0030433,GO:0031205,GO:0043022,GO:0010507	CG10130-PA			PIRSF006398			PF03911														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly671.39	Frizzled-7	GO:0048675,GO:0016318,GO:0008105,GO:0008104,GO:0007166,GO:0035206,GO:0034446,GO:0001944,GO:0014834,GO:0048103,GO:0009790,GO:0007163,GO:0007164,GO:0007165,GO:0030010,GO:0035412,GO:0007298,GO:0001745,GO:0008356,GO:0035317,GO:0032231,GO:0004930,GO:0007435,GO:0006355,GO:0016021,GO:0016020,GO:0007476,GO:0045746,GO:0042666,GO:0035567,GO:0042067,GO:0016360,GO:0007186,GO:0010812,GO:0038031,GO:0033077,GO:0019827,GO:0035159,GO:0060231,GO:0060054,GO:0060070,GO:0030165,GO:0045198,GO:0005938,GO:0005887,GO:0005886,GO:0007156,GO:0001737,GO:0001736,GO:0001738,GO:0007507,GO:0042327,GO:0008406,GO:0032589,GO:0007420,GO:0035320,GO:0016055,GO:0007464,GO:0042813,GO:0005109,GO:0004888,GO:0006357,GO:0017147,GO:0005768,GO:0045893	CG17697-PC				SM00063		PF01534,PF01392	PS50261,PS50038	PR00489,PR00489,PR00489,PR00489,PR00489		G3DSA:1.10.2000.10	SSF63501			REACT_14797						
aly671.4	Protein Dr1	GO:0017055,GO:0017054,GO:0046982,GO:0051123,GO:0006338,GO:0000122,GO:0008134,GO:0004402,GO:0043565,GO:0001075,GO:0005671,GO:0045944,GO:0045893,GO:0016573,GO:0045892,GO:0042766,GO:0005634	CG4185-PA						PF00808				G3DSA:1.10.20.10	SSF47113	126~146								
aly671.40	Anaphase-promoting complex subunit 5	GO:0005737,GO:0045842,GO:0051726,GO:0070979,GO:0007444,GO:0000090,GO:0030162,GO:0090302,GO:0022008,GO:0007067,GO:0051301,GO:0005680	CG10850-PA										G3DSA:1.25.40.10	SSF48452									
aly671.41	Integrator complex subunit 2	GO:0016180,GO:0034472,GO:0016021,GO:0016020,GO:0031965,GO:0032039,GO:0003674,GO:0022008,GO:0005622	CG8211-PA						PF14750		PR02105,PR02105,PR02105,PR02105,PR02105,PR02105,PR02105				127~147								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly671.42	Adenylate cyclase type 3	GO:0045121,GO:0007268,GO:0004016,GO:0007165,GO:0034199,GO:0005929,GO:0035556,GO:0008543,GO:0007143,GO:0005737,GO:0071377,GO:0003091,GO:0016021,GO:0016020,GO:0007189,GO:0006112,GO:0046872,GO:0044281,GO:0006171,GO:0005524,GO:0007608,GO:0045087,GO:0006833,GO:0007173,GO:0045475,G	CG1506-PA				SM00044,SM00044		PF00211,PF00211,PF16214	PS50125,PS50125		PS00452	G3DSA:3.30.70.1230,G3DSA:3.30.70.1230	SSF55073,SSF55073	294~314									
aly671.43	SCO-spondin	GO:0005737,GO:0007424,GO:0030154,GO:0005975,GO:0005615,GO:0007399,GO:0035159,GO:0005770,GO:0003824,GO:0005576,GO:0007155,GO:0008061,GO:0030414,GO:0004099,GO:0006030	CG32209-PB				SM00192,SM00494		PF01607,PF00057,PF01522	PS50068,PS50940		PS01209	G3DSA:2.170.140.10,G3DSA:3.20.20.370,G3DSA:4.10.400.10	SSF88713,SSF57424,SSF57625									
aly671.44	Unknown	GO:0007424,GO:0007632,GO:0005975,GO:0060439,GO:0035159,GO:0016810,GO:0005041,GO:0035001,GO:0008061,GO:0004099,GO:0006030,GO:0005576	CG8756-PI				SM00494,SM00494,SM00192		PF01607,PF00057	PS51257,PS50940,PS50068,PS50940		PS01209	G3DSA:3.20.20.370,G3DSA:4.10.400.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625,SSF88713,SSF57424									
aly671.45	Endoplasmic reticulum-Golgi intermediate compartment protein 3	GO:0005794,GO:0006888,GO:0016192,GO:0016021,GO:0033116,GO:0005789,GO:0003674,GO:0030134	CG7011-PA						PF13850,PF07970														
aly671.46	Transcription termination factor 3, mitochondrial	GO:0044212,GO:0051726,GO:0005739,GO:0006264,GO:0006355,GO:0045892,GO:0006351,GO:0006390,GO:0003690,GO:0032543	CG5047-PA				SM00733,SM00733,SM00733,SM00733,SM00733		PF02536															
aly671.47	Alanine--tRNA ligase, cytoplasmic	GO:0005737,GO:0004813,GO:0000049,GO:0003676,GO:0008270,GO:0006419,GO:0005524	CG13391-PA	MF_00036_B			SM00863	TIGR00344	PF01411,PF07973,PF02272	PS50860	PR00980,PR00980,PR00980,PR00980,PR00980		G3DSA:3.30.930.10	SSF50447,SSF55186,SSF55681,SSF101353	815~842	00970+6.1.1.7	REACT_71						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly671.48	E3 ubiquitin-protein ligase Su(dx)	GO:0005737,GO:0035209,GO:0007219,GO:0048190,GO:0031623,GO:0016874,GO:0005634,GO:0008587,GO:0008586,GO:0016348,GO:0045746,GO:0016567,GO:0042787,GO:0005938,GO:0005515,GO:0019915,GO:0004842,GO:0005112,GO:0019904,GO:0032880	CG4244-PC				SM00456,SM00456,SM00456,SM00456,SM00239,SM00119		PF00397,PF00397,PF00397,PF00397,PF00632,PF00168	PS50020,PS50004,PS50020,PS50020,PS50020,PS50237		PS01159,PS01159,PS01159,PS01159	G3DSA:2.20.70.10,G3DSA:3.30.2160.10,G3DSA:2.20.70.10,G3DSA:2.20.70.10,G3DSA:2.60.40.150,G3DSA:2.20.70.10	SSF51045,SSF49562,SSF56204,SSF51045,SSF51045,SSF51045					UPA00143				
aly671.49	Kinesin-associated protein 3	GO:0019894,GO:0005783,GO:0008285,GO:0007596,GO:1990075,GO:0061024,GO:0015630,GO:0016939,GO:0005488,GO:0005871,GO:0007608,GO:0036064,GO:0072372,GO:0070062,GO:0030951,GO:0005813,GO:0008089,GO:0008104,GO:0043066,GO:0003777,GO:0005794,GO:0032391,GO:0030990,GO:0035058,GO:0019886,GO:0007605,GO:0006461,GO:0046587,GO:0000794,GO:0007288,GO:0005930,GO:0006996,GO:0007017,GO:0005829,GO:0072383,GO:0007018,GO:0097542,GO:0005515,GO:0007165	CG11759-PG				SM00185,SM00185,SM00185,SM00185		PF05804				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371	186~206								
aly671.5	Unknown		n/a																				
aly671.50	Carnitine O-acetyltransferase	GO:0006631,GO:0005783,GO:0006635,GO:0006810,GO:0005777,GO:0005739,GO:0005743,GO:0004092,GO:0016746	CG1041-PA						PF00755			PS00440,PS00439		SSF52777,SSF52777									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly671.51	Ras-related protein Rab-14	GO:0030670,GO:0055037,GO:0009790,GO:0042742,GO:0008543,GO:0032880,GO:0070062,GO:0005770,GO:0090382,GO:0043025,GO:0031901,GO:0005525,GO:0003924,GO:0032482,GO:0045335,GO:0008152,GO:0007264,GO:0031982,GO:0016192,GO:0006895,GO:0005802,GO:0000139,GO:0005765,GO:0019003,GO:0032456,GO:0015031,GO:0045202	CG4212-PB				SM00175,SM00176,SM00174,SM00173	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly671.52	UPF0184 protein C9orf16 homolog	GO:0005575,GO:0003674,GO:0008150	CG14818-PA						PF03670						26~81								
aly671.6	Dolichyldiphosphatase 1	GO:0016021,GO:0006486,GO:0047874,GO:0005789	n/a				SM00014		PF01569				G3DSA:1.20.144.10	SSF48317									
aly671.7	DnaJ homolog subfamily C member 7	GO:0005737,GO:0005856,GO:0006457,GO:0070062,GO:0031072,GO:0034605,GO:0016020,GO:0051082,GO:0005575,GO:1900034,GO:0070389,GO:0005654,GO:0005829	CG4599-PA				SM00271,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF13414,PF13414,PF00515,PF07719,PF00226	PS50076,PS50005,PS50005,PS50005,PS50005,PS50293,PS50005,PS50005,PS50005	PR00625,PR00625,PR00625,PR00625		G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.10.287.110,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF46565	128~148								
aly671.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly671.9	Unknown		n/a						PF13873						254~293								
aly67147.1	Unknown		n/a																				
aly67315.1	Unknown		n/a																				
aly67332.1	Conserved oligomeric Golgi complex subunit 7	GO:0006890,GO:0017119,GO:0006486,GO:0005730,GO:0034067,GO:0006886,GO:0000139,GO:0050821	n/a						PF10191														
aly67376.1	Myosin-IB	GO:0005737,GO:0042623,GO:0007498,GO:0007368,GO:0032528,GO:0003779,GO:0048803,GO:0016459,GO:0042742,GO:0008152,GO:0005903,GO:0003774,GO:0005524,GO:0005938	CG9155-PD																				
aly678.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6781.1	Unknown		n/a												21~55								
aly6781.2	Facilitated trehalose transporter Tret1-2 homolog	GO:0005355,GO:0022891,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0022857,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly6781.3	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	164~184								
aly6781.4	Facilitated trehalose transporter Tret1	GO:0015574,GO:0015771,GO:0016021,GO:0022857,GO:0015749,GO:0005886,GO:0015145,GO:0055085	CG31100-PA						PF00083					SSF103473									
aly6781.5	Unknown		n/a												16~50								
aly6781.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6782.1	Unknown		n/a																				
aly679.1	Unknown		n/a										G3DSA:3.30.40.10	SSF57903	134~161								
aly679.10	Unknown		n/a																				
aly679.11	Senescence-specific cysteine protease SAG39	GO:0010150,GO:0007568,GO:0005615,GO:0051603,GO:0009739,GO:0005811,GO:0009723,GO:0005764,GO:0004197,GO:0010623,GO:0006508,GO:0009737,GO:0010282,GO:0005875	CG8947-PA				SM00848						G3DSA:3.90.70.10	SSF54001									
aly679.12	Digestive cysteine proteinase 2	GO:0005811,GO:0006508,GO:0004197,GO:0008234,GO:0005875	CG8947-PA				SM00645		PF00112			PS00639	G3DSA:3.90.70.10	SSF54001									
aly679.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly679.2	Unknown		n/a							PS50026		PS00022											
aly679.3	Low-density lipoprotein receptor-related protein 1	GO:0006897,GO:0016021,GO:0005041,GO:0005509,GO:0005515,GO:0005905	CG33087-PF				SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192,SM00179,SM00179,SM00181,SM00181,SM00181,SM00135,SM00135,SM00135		PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00057,PF00058,PF00058,PF00058,PF07645	PS50068,PS50068,PS50026,PS50068,PS51120,PS50068,PS51120,PS50026,PS51120,PS50068,PS51120,PS50068,PS50068,PS50068	PR00261,PR00261,PR00261,PR00261,PR00261,PR00261,PR00261,PR00261,PR00261,PR00261,PR00261,PR00261,PR00261,PR00261	PS01209,PS01186,PS01209,PS01209,PS01187,PS01209,PS01209,PS01186,PS01209,PS00010	G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:4.10.1220.10,G3DSA:4.10.1220.10,G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:2.120.10.30,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10	SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57196,SSF57424,SSF57424,SSF63825,SSF57196,SSF57424,SSF57424,SSF57424								
aly679.4	Prolow-density lipoprotein receptor-related protein 1	GO:0007205,GO:0014912,GO:0030425,GO:0043524,GO:0042157,GO:0004872,GO:0051222,GO:0005925,GO:0030178,GO:0030136,GO:0005737,GO:0030666,GO:0005730,GO:0032374,GO:0032370,GO:0001523,GO:0032956,GO:0005509,GO:0097242,GO:0032403,GO:0043025,GO:2000587,GO:0008283,GO:0032429,GO:0070325,GO:0044822,GO:0007603,GO:0010977,GO:0005887,GO:0043277,GO:0005886,GO:0034185,GO:0010875,GO:0043235,GO:0007568,GO:0006898,GO:0005041,GO:0005765,GO:0005515,GO:0042953,GO:0035909,GO:0005768,GO:0042954,GO:0005905	CG33087-PF				SM00135,SM00135,SM00135,SM00135,SM00135,SM00135,SM00135,SM00135,SM00135,SM00192,SM00192,SM00192		PF00057,PF00057,PF00058,PF00058,PF00058	PS50068,PS50068,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120,PS51120	PR00261,PR00261,PR00261	PS01209,PS01209	G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10	SSF57424,SSF57424,SSF63825,SSF63825								
aly679.5	Low-density lipoprotein receptor-related protein 1	GO:0006897,GO:0016021,GO:0005041,GO:0005509,GO:0005515,GO:0005905	CG33087-PF				SM00192,SM00192,SM00192,SM00192,SM00135,SM00135,SM00135,SM00135,SM00181,SM00181,SM00181,SM00181		PF00057,PF00057,PF00057,PF00057,PF00057,PF14670,PF00058	PS50068,PS50068,PS50068,PS51120,PS51120,PS51120,PS50068,PS50068	PR00261,PR00261,PR00261,PR00261,PR00261,PR00261	PS01209,PS01209,PS01209,PS01209	G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.120.25.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.120.10.30,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.10.25.10	SSF63825,SSF63825,SSF57196,SSF57424,SSF57424,SSF57424,SSF57424,SSF57184								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly679.6	Low-density lipoprotein receptor-related protein 1	GO:0006897,GO:0016021,GO:0005041,GO:0005509,GO:0005515,GO:0005905	CG33087-PF				SM00192,SM00192,SM00192,SM00179,SM00135,SM00135,SM00135,SM00135,SM00181,SM00181		PF00058,PF00057,PF00057,PF12662	PS50068,PS51120,PS50068,PS50068,PS51120,PS51120,PS51120	PR00261,PR00261,PR00261	PS01209,PS00010,PS01209,PS01186	G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.120.10.30,G3DSA:2.120.10.30	SSF57424,SSF57424,SSF57424,SSF57196,SSF63825,SSF63825										
aly679.7	NADH dehydrogenase [ubiqui] 1 beta subcomplex subunit 3	GO:0070062,GO:0016021,GO:0005739,GO:0006120,GO:0022900,GO:0005747,GO:0006404,GO:0003954	CG10320-PA						PF08122														
aly679.8	mRNA export factor	GO:0005737,GO:0005730,GO:2000045,GO:0051726,GO:0005643,GO:0071407,GO:0005634,GO:0005635,GO:0045886,GO:0005515,GO:0010506,GO:0051297,GO:0006406	CG9862-PA				SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50082,PS50294,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10	SSF50978										
aly679.9	SOSS complex subunit B homolog	GO:0003677	CG5181-PA										G3DSA:2.40.50.140	SSF50249									
aly67924.1	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A	GO:0030488,GO:0005634,GO:0046331,GO:0016429,GO:0031515	CG14544-PA						PF08704	PS51620,PS51686			G3DSA:3.40.50.150	SSF53335				PWY-6829					
aly681.1	Upstream-binding protein 1	GO:0005737,GO:0043565,GO:0003700,GO:0005634,GO:0005654,GO:0006355,GO:0006357,GO:0006351,GO:0001525	CG30011-PC						PF04516					SSF47769									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6814.1	Unknown	GO:0007157,GO:0005576,GO:0003674	CG10134-PB							PS50835			G3DSA:2.60.40.10	SSF48726									
aly6816.1	Transmembrane and TPR repeat-containing protein 3	GO:0009791,GO:0030324,GO:0016262,GO:0016021,GO:0030154,GO:0048747,GO:0005575,GO:0008150,GO:0048286,GO:0060447,GO:0010468	CG31690-PE																				
aly6826.1	Antithrombin-III	GO:0007584,GO:0050728,GO:0005615,GO:2000266,GO:0002020,GO:0007596,GO:0072562,GO:0005576,GO:0005886,GO:0004867,GO:0010951,GO:0045861,GO:0035009,GO:0008201,GO:0070062	CG6680-PA				SM00093		PF00079			PS00284	G3DSA:2.30.39.10,G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574										
aly6826.2	Antithrombin-III	GO:0007584,GO:0050728,GO:0005615,GO:2000266,GO:0002020,GO:0007596,GO:0072562,GO:0005576,GO:0005886,GO:0004867,GO:0010951,GO:0045861,GO:0035009,GO:0008201,GO:0070062	CG6680-PA				SM00093		PF00079			PS00284	G3DSA:2.30.39.10,G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574										
aly6826.3	Putative ATP-dependent RNA helicase DHX30	GO:0042645,GO:0008026,GO:0004004,GO:0004386,GO:0003723,GO:0003676,GO:0003682,GO:0005524	CG8915-PA				SM00847,SM00487		PF04408	PS51194,PS51192			G3DSA:3.40.50.300	SSF52540	692~712								
aly6831.1	Unknown		n/a										G3DSA:3.40.50.1820										
aly6841.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.10	Zinc finger protein 205	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG9609-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly6841.11	Putative neutral sphingomyelinase	GO:0016021,GO:0046872,GO:0004767,GO:0006665,GO:0006684	CG12034-PA						PF03372				G3DSA:3.60.10.10	SSF56219									
aly6841.12	Transmembrane protein 184C	GO:0016021	CG5850-PG						PF03619														
aly6841.13	DNA-binding protein Ikaros	GO:0005634,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0046872,GO:0007275	CG12769-PC				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF12874	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly6841.14	Liprin-beta-1	GO:0043234,GO:0051124,GO:0005515,GO:0007412,GO:0005925,GO:0042803	CG10743-PB							PS50105			G3DSA:1.10.150.50	SSF47769	240~260,98~167								
aly6841.15	Unknown		n/a																				
aly6841.16	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.17	ER degradation-enhancing alpha-mannosidase-like protein 2	GO:0044267,GO:0006986,GO:0006457,GO:0005783,GO:0030968,GO:0043687,GO:0016020,GO:0005788,GO:0005789,GO:0004571,GO:0005509,GO:0030433,GO:0008340,GO:0018279,GO:0005576	CG3810-PE						PF01532		PR00747,PR00747,PR00747,PR00747,PR00747,PR00747		G3DSA:1.50.10.50,G3DSA:1.50.10.50	SSF48225									
aly6841.18	G2/mitotic-specific cyclin-A	GO:0045841,GO:0055059,GO:0000086,GO:0009794,GO:0007067,GO:0005737,GO:0045170,GO:0005634,GO:0016538,GO:0007088,GO:0045859,GO:0009987,GO:0019901,GO:0046331,GO:0035561,GO:0019908,GO:0022008,GO:0010389,GO:0035186,GO:0000070,GO:0007422,GO:0000079,GO:0045169,GO:0005515,GO:0007096	CG5940-PA			PIRSF001771	SM00385,SM00385		PF02984,PF00134				G3DSA:1.10.472.10,G3DSA:1.10.472.10	SSF47954,SSF47954									
aly6841.19	Unknown	GO:0007166,GO:0072499,GO:0006915,GO:0070050,GO:0005031,GO:0005515,GO:0005887,GO:1900074	CG6531-PA						PF00020	PS50050			G3DSA:2.10.50.10										
aly6841.2	Trypsin-2	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG9564-PC				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly6841.20	Transmembrane protein 41B	GO:0005575,GO:0016021,GO:0032224,GO:0003674,GO:0008045	CG8408-PA						PF09335														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.21	Unknown		CG4558-PB																				
aly6841.22	Monocarboxylate transporter 9	GO:0015718,GO:0015293,GO:0008028,GO:0016021,GO:0034220,GO:0005886,GO:0046415	CG14195-PA										G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	621~622								
aly6841.23	Unknown	GO:0042600,GO:0005201,GO:0031012,GO:0005576,GO:0008061,GO:0006030	CG14796-PA				SM00494,SM00494,SM00494		PF01607,PF01607	PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625									
aly6841.24	Unknown	GO:0006030,GO:0005576,GO:0008061,GO:0016490	CG7017-PA				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly6841.25	Unknown		n/a																				
aly6841.26	Protein PTCD3 homolog, mitochondrial	GO:0005739,GO:0019843,GO:0005575,GO:0043024,GO:0003674,GO:0006417,GO:0008150,GO:0032543	CG4679-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.27	Unknown	GO:0006030,GO:0005576,GO:0008061,GO:0016490	CG7017-PA				SM00494,SM00494		PF01607,PF01607	PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625									
aly6841.28	Unknown	GO:0006030,GO:0005576,GO:0008061	CG31077-PB				SM00494,SM00494,SM00494		PF01607,PF01607	PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625									
aly6841.29	Unknown	GO:0042600,GO:0005201,GO:0031012,GO:0005576,GO:0008061,GO:0006030	CG14796-PA				SM00494,SM00494,SM00494		PF01607,PF01607,PF01607	PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625									
aly6841.3	Unknown		CG16786-PB						PF15950,PF15950														
aly6841.30	Unknown		n/a																				
aly6841.31	Monocarboxylate transporter 9	GO:0015718,GO:0015293,GO:0034220,GO:0008028,GO:0016021,GO:0015355,GO:0005886,GO:0055085,GO:0046415	CG14196-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.32	Monocarboxylate transporter 9	GO:0015355,GO:0016021,GO:0055085,GO:0015293,GO:0005886	CG14196-PA						PF07690,PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	480~500								
aly6841.33	Monocarboxylate transporter 4	GO:0015629,GO:0015129,GO:0016021,GO:0031965,GO:0015293,GO:0044822,GO:0005887,GO:0055085	CG8034-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly6841.34	Unknown	GO:0008028,GO:0016021,GO:0055085	CG8028-PC						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly6841.35	Cytochrome P450 4g15	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0006694,GO:0005506,GO:0055114,GO:0009055	CG11715-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264,SSF48264			REACT_13433						
aly6841.36	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0005215,GO:0016021,GO:0005886,GO:0055085	CG4797-PB						PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00217,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473			REACT_15518						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.37	Achaete-scute complex protein T5	GO:0061331,GO:0043565,GO:0007346,GO:0002805,GO:0007399,GO:0007422,GO:0003700,GO:0005634,GO:0006355,GO:0008407,GO:0007419,GO:0007423,GO:0045893,GO:0005667,GO:0003677,GO:0046983,GO:0046982,GO:0048477,GO:0007417,GO:0061382,GO:0007400	CG3796-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459										
aly6841.38	Achaete-scute complex protein T5	GO:0061331,GO:0043565,GO:0007346,GO:0002805,GO:0007399,GO:0007422,GO:0003700,GO:0005634,GO:0006355,GO:0008407,GO:0007419,GO:0007423,GO:0045893,GO:0005667,GO:0003677,GO:0046983,GO:0046982,GO:0048477,GO:0007417,GO:0061382,GO:0007400	CG3796-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459										
aly6841.39	Achaete-scute complex protein T5	GO:0061331,GO:0043565,GO:0007346,GO:0002805,GO:0007399,GO:0007422,GO:0003700,GO:0005634,GO:0006355,GO:0008407,GO:0007419,GO:0007423,GO:0045893,GO:0005667,GO:0003677,GO:0046983,GO:0046982,GO:0048477,GO:0007417,GO:0061382,GO:0007400	CG3796-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459										
aly6841.4	Signal peptidase complex subunit 3	GO:0005787,GO:0008233,GO:0016021,GO:0006465	CG5677-PB			PIRSF016089			PF04573	PS51257													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.40	Achaete-scute complex protein T4	GO:0007419,GO:0001077,GO:0003677,GO:0061382,GO:0007530,GO:0043565,GO:0007346,GO:0005634,GO:0008407,GO:0043066,GO:0006366,GO:0007417,GO:0005667,GO:0008134,GO:0022416,GO:0007400,GO:0007549,GO:0007423,GO:0007399,GO:0007422,GO:0003700,GO:0007540,GO:0006355,GO:0006357,GO:0045944,GO:0000977,GO:0005515,GO:0046983,GO:0046982	CG3827-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459									
aly6841.41	Protein yellow	GO:0005737,GO:0060179,GO:0016853,GO:0048082,GO:0048065,GO:0048066,GO:0048067,GO:0005576,GO:0042438,GO:0007275,GO:0070451,GO:0006583	CG3757-PA						PF03022		PR01366,PR01366,PR01366,PR01366,PR01366		G3DSA:2.120.10.30										
aly6841.42	Proton-coupled amino acid transporter 1	GO:0016021,GO:0015992,GO:0005783,GO:0035524,GO:1902600,GO:0003333,GO:0005280,GO:0015816,GO:0015193,GO:0005764,GO:0005765,GO:0015078,GO:0015824,GO:0005886,GO:0015180,GO:0015187,GO:0005774,GO:0015808,GO:0015171	CG8785-PB						PF01490														
aly6841.43	Proton-coupled amino acid transporter 4	GO:0003333,GO:0006865,GO:0016021,GO:0015171,GO:0015293	CG8785-PB						PF01490														
aly6841.44	Proton-coupled amino acid transporter 4	GO:0015293,GO:0003333,GO:0015171,GO:0015827,GO:0015824,GO:0005774,GO:0015808,GO:0016021	CG8785-PB						PF01490														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.45	NADH-cytochrome b5 reductase 2	GO:0016126,GO:0004128,GO:0002121,GO:0016021,GO:0055114	CG5946-PA						PF00175,PF00970	PS51384	PR00371,PR00371,PR00371,PR00371,PR00371,PR00371,PR00406,PR00406,PR00406,PR00406,PR00406,PR00406,PR00406		G3DSA:3.40.50.80,G3DSA:2.40.30.10	SSF63380,SSF52343									
aly6841.46	Unknown		n/a																				
aly6841.47	Unknown	GO:0035002,GO:0035151,GO:0019991,GO:0003674,GO:0005918	CG6038-PA																				
aly6841.48	Calmodulin	GO:0051383,GO:0042052,GO:0046716,GO:0031476,GO:0031475,GO:0005875,GO:0005737,GO:0016028,GO:0016062,GO:0016061,GO:0016060,GO:0005814,GO:0000922,GO:0005509,GO:0007099,GO:0032036,GO:0006468,GO:0007605,GO:0072499,GO:0030048,GO:0007052,GO:0005819,GO:2001020,GO:0031489,GO:0070855,GO:0016059,GO:0016056,GO:0030496,GO:0051533,GO:0005513,GO:0046331,GO:0005516,GO:0005515	CG8472-PA						PF13833	PS50222,PS50222,PS50222,PS50222		PS00018	G3DSA:1.10.238.10	SSF47473	83~118								
aly6841.49	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.5	FGFR1 oncogene partner 2 homolog	GO:0005575,GO:0008150,GO:0003674,GO:0005737	CG10158-PA						PF05769						85~112								
aly6841.50	Unknown	GO:0035158,GO:0008362,GO:0035152,GO:0007424,GO:0006031	CG1397-PA										G3DSA:2.10.60.10										
aly6841.51	Protein lin-9 homolog	GO:0005737,GO:0031523,GO:0071897,GO:0017053,GO:0000122,GO:0005634,GO:0003677,GO:0005700,GO:0005654,GO:0007052,GO:0000785,GO:0006351,GO:0007307,GO:0051297,GO:0007049	CG3480-PA						PF06584						571~574,437~457								
aly6841.52	Nuclear pore complex protein Nup50	GO:0006909,GO:0046907,GO:0005643,GO:0031965,GO:0005515,GO:0015031,GO:0022008,GO:0051028,GO:0007184	CG2158-PA				SM00160		PF00638,PF08911	PS50196			G3DSA:2.30.29.30	SSF50729									
aly6841.53	Unknown		n/a												31~58,63~83								
aly6841.54	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.55	LIM domain only protein 3	GO:0045475,GO:0006909,GO:0005634,GO:0007476,GO:0036011,GO:0035218,GO:0022416,GO:0008270,GO:0005515,GO:0042220,GO:0002121,GO:0045893	CG44425-PD				SM00132,SM00132		PF00412,PF00412	PS50023,PS50023		PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716,SSF57716										
aly6841.56	Unknown		n/a						PF00089				G3DSA:2.40.10.10	SSF50494									
aly6841.57	Unknown		n/a																				
aly6841.58	Unknown		n/a						PF16009														
aly6841.59	Histidine--tRNA ligase, cytoplasmic	GO:0005737,GO:0006427,GO:0004821,GO:0005739,GO:0032543,GO:0005524	CG6335-PA				SM00991		PF03129,PF13393				G3DSA:3.40.50.800,G3DSA:3.30.930.10,G3DSA:3.30.930.10,G3DSA:1.10.287.10	SSF55681,SSF52954	114~134		REACT_71						
aly6841.6	Epoxide hydrolase 3	GO:0016787,GO:0006482,GO:0016021,GO:0052689	CG5068-PA						PF12697		PR00412,PR00412,PR00412		G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.60	Vacuolar protein-sorting associated protein 36	GO:0007224,GO:0000814,GO:0043162,GO:0008283,GO:0032266,GO:0043130,GO:0003730,GO:0008593,GO:0015031,GO:0051028,GO:0042981,GO:0005768	CG10711-PA						PF04157,PF11605	PS51495			G3DSA:1.10.10.10,G3DSA:1.10.10.10	SSF46785,SSF50729,SSF46785									
aly6841.61	Exonuclease 3' 5' domain-containing protein 1	GO:0008408,GO:0003676	CG11263-PA						PF01612				G3DSA:3.30.420.10	SSF53098									
aly6841.62	Unknown		n/a																				
aly6841.63	Cytosolic carboxypeptidase NnaD	GO:0004181,GO:0005739,GO:0002164,GO:0003407,GO:0008270,GO:0017076,GO:0006508,GO:0007005	CG44533-PH						PF00246				G3DSA:3.40.630.10	SSF53187	1017~1037,882~909								
aly6841.64	Probable glutamine-dependent NAD(+) synthetase	GO:0009435,GO:0016810,GO:0003952,GO:0005524	CG9940-PC			PIRSF006630		TIGR00552	PF02540,PF00795	PS50263			G3DSA:3.60.110.10,G3DSA:3.40.50.620	SSF56317,SSF52402,SSF52402		00760+6.3.1.5,00760+6.3.5.1		PWY-5381,PWY-5653	UPA00253				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.65	Protein ovo	GO:0048067,GO:0003700,GO:0003676,GO:0003677,GO:0035316,GO:0005737,GO:0043565,GO:0042335,GO:0000122,GO:0005634,GO:0006366,GO:0046872,GO:0048477,GO:0000981,GO:0019099,GO:0016348,GO:0008360,GO:0070896,GO:0045893,GO:0035017,GO:0008343,GO:0007010,GO:0018992,GO:0009913,GO:0006355,GO:0042810,GO:0045944,GO:0045892	CG6824-PB				SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly6841.66	Unknown	GO:0005575,GO:0003674,GO:0008150	CG17233-PC																				
aly6841.67	Unknown	GO:0005575,GO:0003674,GO:0008150	CG17233-PC																				
aly6841.68	Caprin homolog	GO:0005737,GO:0005829,GO:0005811,GO:0007349,GO:0030529,GO:0003723,GO:0045571,GO:0009794	CG18811-PA																				
aly6841.69	Single-stranded DNA binding protein, mitochondrial	GO:0000002,GO:0000262,GO:0005739,GO:0006264,GO:0006260,GO:0003697	CG4337-PA	MF_00984				TIGR00621	PF00436	PS50935			G3DSA:2.40.50.140	SSF50249									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.7	Leucine-rich repeat-containing protein 56		CG14185-PA										G3DSA:3.80.10.10	SSF52058									
aly6841.70	Ets DNA-binding protein pokkuri	GO:0048749,GO:0008406,GO:0003705,GO:0045467,GO:0007298,GO:0030178,GO:0005737,GO:0043565,GO:0007254,GO:0000122,GO:0005634,GO:0001709,GO:0000165,GO:0005654,GO:0048666,GO:0035155,GO:0050767,GO:0060233,GO:0009987,GO:0007517,GO:0048747,GO:0045596,GO:0045892,GO:0046580,GO:0008340,GO:0045316,GO:0001751,GO:0006897,GO:0090175,GO:0003700,GO:0005829,GO:0007464,GO:0007391,GO:0006355,GO:0048813,GO:0046533,GO:0006351,GO:0005515,GO:0045610,GO:0035157,GO:0045678,GO:0019904	CG3166-PB				SM00251,SM00413		PF00178,PF02198	PS50061,PS51433	PR00454,PR00454,PR00454	PS00346,PS00345	G3DSA:1.10.150.50,G3DSA:1.10.10.10	SSF47769,SSF46785									
aly6841.71	Unknown		n/a																				
aly6841.72	Gamma-tubulin complex component 2	GO:0000086,GO:0008275,GO:0007067,GO:0005815,GO:0051225,GO:0007020,GO:0007126,GO:0072686,GO:0030953,GO:0005813,GO:0016020,GO:0000922,GO:0005654,GO:0005875,GO:0051011,GO:0051297,GO:0015631,GO:0000278,GO:0008017,GO:0006461,GO:0005881,GO:0007052,GO:0007017,GO:0051726,GO:0005829,GO:0007283,GO:0043015	CG3917-PA						PF04130,PF04130						484~484		REACT_152						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.73	Dynamin-1-like protein	GO:0016020,GO:0006921,GO:0051289,GO:0000266,GO:0090200,GO:0061025,GO:1903578,GO:0060047,GO:0010821,GO:0005905,GO:0001836,GO:0005874,GO:0005875,GO:0030054,GO:0005737,GO:0090149,GO:0030382,GO:0016185,GO:0016559,GO:0043653,GO:0090141,GO:0005777,GO:0000281,GO:0005739,GO:0043065,GO:1900063,GO:0005741,GO:0007005,GO:2001244,GO:0048471,GO:0042802,GO:0005525,GO:0048312,GO:0005794,GO:0070266,GO:0030672,GO:0070585,GO:0006915,GO:0003924,GO:0008289,GO:0012501,GO:0008152,GO:0051646,GO:0043234,GO:0070584,GO:0003374,GO:0031625,GO:0006897,GO:0043231,GO:0050714,GO:0005829,GO:0016050,GO:0005903,GO:0032459,GO:0042803,GO:1903146	CG3210-PA				SM00302,SM00053		PF01031,PF00350,PF02212	PS51718,PS51388	PR00195,PR00195,PR00195,PR00195,PR00195,PR00195		G3DSA:3.40.50.300	SSF52540									
aly6841.74	TIP41-like protein	GO:0005737	CG9578-PA						PF04176														
aly6841.75	Unknown		n/a				SM00409,SM00409,SM00409						G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly6841.76	Circadian clock-controlled protein	GO:0007623,GO:0005615,GO:0032504	CG10407-PA				SM00700		PF06585														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.77	TWiK family of potassium channels protein 7	GO:0005267,GO:0016020,GO:0016021,GO:0005252,GO:0071805	CG43155-PC						PF07885,PF07885		PR01095,PR01095,PR01095,PR01333,PR01333		G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324,SSF81324									
aly6841.78	Unknown	GO:0005515	n/a							PS50005,PS50293			G3DSA:1.25.40.10	SSF48452	103~123								
aly6841.79	Cytochrome P450 4g15	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0006694,GO:0005506,GO:0055114,GO:0009055	CG11715-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264,SSF48264			REACT_13433						
aly6841.8	Thymidylate synthase	GO:0019088,GO:0060574,GO:0051384,GO:0048589,GO:0008144,GO:0004799,GO:0046653,GO:0014070,GO:0005737,GO:0005730,GO:0006206,GO:0005542,GO:0009636,GO:0005739,GO:0000166,GO:0005759,GO:0046683,GO:0042803,GO:0007623,GO:0034097,GO:0031100,GO:0045471,GO:0009263,GO:0048037,GO:0046078,GO:0022008,GO:0006235,GO:0051216,GO:0007568,GO:0006231,GO:0051593,GO:0019860,GO:0042493,GO:0005743,GO:0033189,GO:0032570,GO:0005634,GO:0003729	CG3181-PA	MF_00008				TIGR03284	PF00303		PR00108,PR00108,PR00108,PR00108,PR00108	PS00091	G3DSA:3.30.572.10	SSF55831		00670+2.1.1.45,00240+2.1.1.45		PWY-7210,PWY-7198,PWY-7199,PWY-3841,PWY-7184,PWY-7187	UPA00575				
aly6841.80	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.81	Unknown		n/a																				
aly6841.82	DENN domain-containing protein 5B	GO:0005794,GO:0043547,GO:0005262,GO:0050982,GO:0016021,GO:0016020,GO:0070588,GO:0017112,GO:0032483,GO:0005515	CG7852-PB				SM00801,SM00799,SM00593,SM00593,SM00800		PF03456,PF01477,PF02759,PF02759,PF02141,PF03455	PS50211,PS50095,PS50947,PS50826,PS50946,PS50826			G3DSA:2.60.60.20	SSF49723,SSF140741,SSF140741,SSF140741,SSF140741										
aly6841.83	Beta-1,4-mannosyltransferase egh	GO:0016333,GO:0033227,GO:0007293,GO:0007411,GO:0001744,GO:0008049,GO:0007298,GO:0007299,GO:0016021,GO:0030720,GO:0030707,GO:0019187,GO:0006688,GO:0048477,GO:0016325,GO:0007281,GO:0005887,GO:0046662,GO:0045434,GO:0042248,GO:0045165,GO:0097502,GO:0048935	CG9659-PC						PF13632					SSF53448										
aly6841.84	Unknown		n/a																				
aly6841.85	Eye-specific diacylglycerol kinase	GO:0006654,GO:0016310,GO:0003951,GO:0035556,GO:0005875,GO:0019992,GO:0016020,GO:0046834,GO:0006661,GO:0046872,GO:0004143,GO:0005524,GO:0007608,GO:0007605,GO:0007601,GO:0007602,GO:0008152,GO:0007015,GO:0016059,GO:0016056,GO:0043052,GO:0007205,GO:0045494	CG42667-PH																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.86	Unknown		n/a										G3DSA:3.30.40.10	SSF57903									
aly6841.87	Unknown		n/a																				
aly6841.88	Unknown		n/a																				
aly6841.89	Unknown		n/a																				
aly6841.9	Uncharacterized protein C6orf106 homolog		CG5445-PB						PF07705,PF16158,PF14555				G3DSA:1.10.8.10	SSF46934									
aly6841.90	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6841.91	Liprin-beta-2	GO:0043234,GO:0051124,GO:0005615,GO:0005515,GO:0007412,GO:0042803	CG10743-PB				SM00454		PF07647				G3DSA:1.10.150.50	SSF47769									
aly6841.92	Transient receptor potential cation channel protein painless	GO:0050960,GO:0007631,GO:0050965,GO:0045924,GO:0005262,GO:0007638,GO:0005227,GO:0034704,GO:0008049,GO:0048266,GO:0050966,GO:0016021,GO:0009612,GO:0048060,GO:0019233,GO:0050974,GO:0007620,GO:0042048,GO:0005216,GO:0008016,GO:0006816,GO:0009408,GO:0043052,GO:0070588	CG15860-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796,PF00520	PS50297,PS50088,PS50088			G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403									
aly6841.93	cAMP-dependent protein kinase catalytic subunit	GO:0007228,GO:0008103,GO:0048149,GO:0007615,GO:0007612,GO:0007613,GO:0030425,GO:0007611,GO:0008359,GO:0019933,GO:0004691,GO:0042981,GO:0040040,GO:0008355,GO:0005737,GO:0007476,GO:0004674,GO:0004672,GO:0048477,GO:0005524,GO:0048749,GO:0006468,GO:0007622,GO:0007480,GO:0044297,GO:0045879,GO:0007317,GO:0007314,GO:0045475,GO:0005886,GO:0005952,GO:0050804,GO:0007448,GO:0045187,GO:0005515	CG4379-PB				SM00220,SM00220		PF00069,PF00069	PS50011,PS50011,PS51285		PS00108,PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF56112									
aly6847.1	Elongation of very long chain fatty acids protein 6	GO:0005783,GO:0016021,GO:0030497,GO:0005789,GO:0009922,GO:0007283,GO:0030176,GO:0016740,GO:0042759,GO:0019367	CG3971-PA						PF01151			PS01188				00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					
aly6847.2	Uracil phosphoribosyltransferase homolog	GO:0005737,GO:0005634,GO:0004845	CG5537-PA						PF14681				G3DSA:3.40.50.2020	SSF53271									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6847.3	Four and a half LIM domains protein 2	GO:0005737,GO:0060347,GO:0055015,GO:0055014,GO:0015629,GO:0000122,GO:0003700,GO:0009725,GO:0005634,GO:0005654,GO:0050832,GO:0043066,GO:0008270,GO:0005925,GO:0008134,GO:0001649,GO:0006351	CG32171-PC				SM00132,SM00132,SM00132,SM00132,SM00132,SM00132		PF00412,PF00412,PF00412,PF00412,PF00412,PF06297	PS50023,PS50023,PS50023,PS50023,PS50023,PS50023		PS00478,PS00478,PS00478,PS00478,PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716,SSF57716,SSF57716,SSF57716									
aly6847.4	Unknown		n/a												42~62								
aly6847.5	Unknown	GO:0003700,GO:0050832,GO:0005634,GO:0008270	CG42679-PK																				
aly685.1	Protein dachsous	GO:0016318,GO:0018149,GO:0016337,GO:0004871,GO:0016339,GO:0035222,GO:0045198,GO:0007164,GO:0004872,GO:0030010,GO:0007157,GO:0016020,GO:0000904,GO:0016021,GO:0007480,GO:0007476,GO:0050839,GO:0005509,GO:0035159,GO:0008283,GO:0042067,GO:0048592,GO:0005887,GO:0005886,GO:0044331,GO:0045317,GO:0007156,GO:0001737,GO:0001736,GO:0090176,GO:0090175,GO:0045296,GO:0007165	CG17941-PA				SM00112,SM00112		PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028	PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49313									
aly685.2	Excitatory amino acid transporter	GO:0089711,GO:0042995,GO:0005313,GO:0016020,GO:0015734,GO:0015501,GO:0005369,GO:0006835,GO:0005886,GO:0017153,GO:0016021,GO:0015183	CG3159-PC						PF00375		PR00173,PR00173,PR00173,PR00173,PR00173,PR00173,PR00173,PR00173	PS00713	G3DSA:1.10.3860.10,G3DSA:1.10.3860.10	SSF118215,SSF118215			REACT_19419,REACT_15518						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6858.1	Lateral signaling target protein 2 homolog	GO:0046872	CG6051-PB						PF01363				G3DSA:3.30.40.10	SSF57903									
aly6858.2	Unknown		n/a						PF03221	PS51253													
aly6858.3	Pro-corazonin	GO:0045823,GO:0007218,GO:0005576,GO:0005184	n/a																				
aly6858.4	Unknown		n/a																				
aly686.1	Unknown		n/a																				
aly686.10	Unknown		n/a						PF15999														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly686.11	Unknown		n/a																				
aly686.12	Unknown		n/a																				
aly686.13	Unknown		n/a																				
aly686.14	Cuticle protein 6	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG3672-PA						PF00379	PS51155													
aly686.15	Unknown		n/a																				
aly686.16	Unknown	GO:0008157,GO:0005874,GO:0030071,GO:0000776	CG15415-PB												236~277,105~132,147~213,297~317,73~100								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly686.17	Exocyst complex component 4	GO:0050803,GO:0006904,GO:0007286,GO:0007009,GO:0003674,GO:0007298,GO:0005737,GO:0016028,GO:0000145,GO:0016020,GO:0000916,GO:0043147,GO:0009925,GO:0016324,GO:0000910,GO:0016081,GO:0016080,GO:0007269,GO:0005886,GO:0016192,GO:0007111,GO:0007110,GO:0090522,GO:0046907,GO:0015031	CG2095-PA													258~278,32~63							
aly686.18	Unknown		n/a													99~119							
aly686.19	Rap1 GTPase-GDP dissociation stimulator 1-A	GO:0005737,GO:0005856,GO:0017160,GO:0015991,GO:0005096,GO:0046716,GO:0043547,GO:0006099,GO:0000221,GO:0046961,GO:1901216,GO:0007264,GO:0042052	CG3572-PA						PF03224				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371										
aly686.2	Unknown	GO:0016747	CG4576-PA																				
aly686.20	Uncharacterized protein ZK1073.1		CG2082-PG						PF03096				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly686.21	Tubulin alpha chain	GO:0045298,GO:0051258,GO:0005200,GO:0019730,GO:0007017,GO:0005813,GO:0009987,GO:0003924,GO:0005737,GO:0007052,GO:0005819,GO:0000235,GO:0007094,GO:0006184,GO:0005874,GO:0005525	CG1913-PA				SM00864,SM00865		PF00091,PF03953		PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01162,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161	PS00227	G3DSA:3.40.50.1440,G3DSA:3.30.1330.20,G3DSA:1.10.287.600	SSF52490,SSF55307	455~475								
aly686.22	Basic helix-loop-helix neural transcription factor TAP	GO:0007399,GO:0007423,GO:0003700,GO:0005634,GO:0030154,GO:0006355,GO:0006357,GO:0006351,GO:0003677,GO:0046983	CG7659-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459	143~163								
aly686.23	Acetylcholinesterase	GO:0042135,GO:0052689,GO:0005576,GO:0045202,GO:0005886,GO:0003990,GO:0030054,GO:0031225	CG6018-PA						PF00135,PF00135				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474									
aly686.24	Carboxylesterase 4A	GO:0005575,GO:0005576,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly686.25	Unknown	GO:0052689	CG1082-PA						PF00135				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly686.26	Acetylcholinesterase	GO:0042135,GO:0052689,GO:0005575,GO:0005576,GO:0008150,GO:0045202,GO:0008152,GO:0005886,GO:0003990,GO:0030054	CG10175-PD						PF00135,PF00135				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474									
aly686.27	Acetylcholinesterase	GO:0042135,GO:0052689,GO:0005575,GO:0008150,GO:0045202,GO:0008152,GO:0003990,GO:0030054	CG10175-PD						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly686.28	Retinol dehydrogenase 12	GO:0016614,GO:0050896,GO:0007601,GO:0005622,GO:0008152,GO:0042572,GO:0004745	CG7675-PB						PF00106		PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									
aly686.29	Dehydrogenase/reductase SDR family member 13	GO:0016020,GO:0005576,GO:0016614,GO:0008152,GO:0016491	CG7675-PB						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly686.3	Elongation of very long chain fatty acids protein AAEL008004	GO:0006633,GO:0009922,GO:0016021,GO:0030497,GO:0005575,GO:0016740,GO:0030176,GO:0022008	CG5326-PA						PF01151							00062+2.3.1.199	REACT_22258	PWY-7619,PWY-6433,PWY-7602,PWY-7601,PWY-5972,PWY-7036,PWY-5080,PWY-6598					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly686.30	Cadherin-23	GO:0016339,GO:0005902,GO:0016021,GO:0016020,GO:0007605,GO:0005509,GO:0042803,GO:0032420,GO:0016324,GO:0050957,GO:0007601,GO:0006816,GO:0050953,GO:0005887,GO:0005886,GO:0044331,GO:0007156,GO:0051480,GO:0050896,GO:0005829,GO:0045494,GO:0046843	CG6445-PB				SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112		PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028	PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00232,PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313										
aly686.31	Unknown		n/a																				
aly686.32	Unknown		n/a																				
aly686.33	Alcohol dehydrogenase 2	GO:0045735,GO:0005811,GO:0004022,GO:0055114	CG3763-PA						PF00106		PR00081,PR00081,PR00080,PR00080		G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735									
aly686.34	Unknown		n/a								PR01217,PR01217,PR01217,PR01217												

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly686.35	Unknown		n/a																				
aly686.36	Unknown		n/a																				
aly686.37	Unknown		n/a												257~277,156~176								
aly686.38	Protein spaetzle	GO:0005125,GO:0019732,GO:0008592,GO:0005121,GO:0021556,GO:0006967,GO:0006965,GO:0043523,GO:0000578,GO:0008063,GO:0007411,GO:0010941,GO:0031637,GO:0008083,GO:0042803,GO:0007310,GO:0045087,GO:0031334,GO:0006952,GO:0050830,GO:0008045,GO:0007311,GO:0006955,GO:0005615,GO:0043234,GO:0050832,GO:0009953,GO:0007399,GO:0009950,GO:0009620,GO:0031640,GO:0005576,GO:0016015	CG42576-PF						PF16077				G3DSA:2.10.90.10	SSF57501										
aly686.39	Tyrosine kinase receptor Cad96Ca	GO:0006468,GO:0045792,GO:0016339,GO:0016020,GO:0045177,GO:0042060,GO:0018108,GO:0004714,GO:0090303,GO:0004713,GO:0005887,GO:0004672,GO:0007156,GO:0007030,GO:0005524,GO:0005509	CG10244-PA				SM00219		PF07714	PS50011	PR00109,PR00109,PR00109,PR00109,PR00109	PS00107,PS00109	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly686.4	Unknown		n/a																				
aly686.40	THAP domain containing protein 2	GO:0005730,GO:0003700,GO:0005634,GO:0048813,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG10431-PA				SM00692,SM00980		PF05485	PS50950				SSF57716	140~160								
aly686.41	PIH1 domain-containing protein 2	GO:0005549,GO:0007608,GO:0016020,GO:0005575,GO:0003674,GO:0004984,GO:0046427	CG4022-PA						PF02949														
aly686.42	Histone H2A	GO:0005634,GO:0000786,GO:0006333,GO:0003677,GO:0046982,GO:0006334	CG33865-PA				SM00414		PF16211,PF00125		PR00620,PR00620,PR00620,PR00620,PR00620	PS00046	G3DSA:1.10.20.10	SSF47113									
aly686.43	Pseudouridylate synthase 7 homolog	GO:0008033,GO:0044822,GO:0019899,GO:0009451,GO:0009982,GO:0003723,GO:0001522	CG6745-PA			PIRSF037016		TIGR00094	PF01142	PS50984				SSF55120,SSF55120,SSF55120,SSF55120									
aly686.44	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly686.45	Unknown		n/a																				
aly686.46	Unknown		n/a																				
aly686.47	Silk gland factor 3	GO:0007425,GO:0043565,GO:0006351,GO:0030154,GO:0007420,GO:0007399,GO:0007422,GO:0003700,GO:0005634,GO:0003677,GO:0001228,GO:0006355,GO:0048813,GO:0001077,GO:0045944,GO:0048814,GO:0008045,GO:0000980,GO:0035284,GO:0002807,GO:0000977	CG10037-PC				SM00389,SM00352		PF00046,PF00157	PS51179,PS50071	PR00028,PR00028,PR00028,PR00028,PR00028	PS00035,PS00465,PS00027	G3DSA:1.10.260.40,G3DSA:1.10.10.60	SSF47413,SSF46689									
aly686.48	Unknown	GO:0008270,GO:0003676	n/a				SM00343,SM00343			PS50158			G3DSA:4.10.60.10	SSF57756									
aly686.49	Unknown		n/a										G3DSA:3.60.10.10	SSF56219									
aly686.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly686.50	Unknown		n/a																				
aly686.51	Flagellar radial spoke protein 3	GO:0005856,GO:0007017,GO:0031514,GO:0008017,GO:2000155,GO:0001534,GO:0005875	CG32392-PB						PF06098														
aly686.52	PR domain zinc finger protein 13	GO:0046872,GO:0000122,GO:0005634,GO:0042054,GO:0000977,GO:0003676,GO:0022008,GO:0003682,GO:0006351	CG13296-PA				SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667										
aly686.53	Retinol dehydrogenase 13	GO:0042462,GO:0016614,GO:0010842,GO:0005743,GO:0008152,GO:0009644,GO:0016491	CG7675-PB						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly686.54	Palmitoyltransferase ZDHHC22	GO:0005794,GO:0018345,GO:0016021,GO:0008270,GO:0019706,GO:0072659,GO:0005783	CG10344-PB						PF01529	PS50216													
aly686.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly686.7	Glutamate receptor-interacting protein 1	GO:0008022,GO:0050808,GO:0005783,GO:0055037,GO:0016358,GO:0030425,GO:0031594,GO:0008104,GO:0030054,GO:0016023,GO:0000060,GO:0043005,GO:0048644,GO:0016203,GO:0035259,GO:0016204,GO:0005798,GO:0045211,GO:0005886,GO:0043195,GO:0045121,GO:0005515,GO:0005102	CG14447-PA				SM00228,SM00228,SM00228,SM00228,SM00228,SM00228,SM00228		PF00595,PF00595,PF00595,PF00595	PS50106,PS50106,PS50106,PS50106,PS50106,PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156,SSF50156,SSF50156,SSF50156,SSF50156,SSF50156										
aly686.8	Unknown		n/a																				
aly686.9	Unknown	GO:0005875	CG11905-PA						PF15999,PF15999														
aly68643.1	Unknown		n/a																				
aly6885.1	Unknown		n/a						PF10179														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6885.2	Zinc finger protein 277	GO:0000979,GO:0005634,GO:0070301,GO:0006355,GO:0006351,GO:0046872,GO:2000772	CG9890-PA				SM00355,SM00355,SM00355,SM00355		PF12756,PF12756	PS50157		PS00028,PS00028		SSF57667,SSF57667									
aly689.1	Unknown		n/a																				
aly689.10	Zinc finger protein PLAG1	GO:0005737,GO:0005819,GO:0035264,GO:0003700,GO:0005634,GO:0060252,GO:0060736,GO:0010629,GO:0001077,GO:0008270,GO:0003676,GO:0022612,GO:0000978,GO:0046872,GO:0005876,GO:0000981	CG8474-PA				SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly689.2	Endoribonuclease Dcr-1	GO:0033227,GO:0042078,GO:0030422,GO:0007279,GO:0070883,GO:0031054,GO:0007294,GO:0005737,GO:0007367,GO:0004525,GO:0005634,GO:0030727,GO:0035087,GO:0006309,GO:0016246,GO:0046872,GO:0005524,GO:0004386,GO:0090502,GO:0090501,GO:0042594,GO:0035195,GO:0035196,GO:0004530,GO:0003727,GO:0048813,GO:0003725,GO:0005515,GO:0016443,GO:0016442,GO:0045448	CG4792-PA				SM00949		PF00271,PF02170	PS51194,PS50821			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:2.170.260.10,G3DSA:2.170.260.10	SSF101690,SSF52540,SSF52540	867~887,283~303									
aly689.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly689.4	Adenylyltransferase and sulfurtransferase MOCS3	GO:0006777,GO:0016779,GO:0046872,GO:0070733,GO:0016783,GO:0061605,GO:0005829,GO:0018117,GO:0042292,GO:0032447,GO:0008265,GO:0002143,GO:0034227,GO:0018192,GO:0004792,GO:0061604,GO:0005524,GO:0002098	CG13090-PC						PF00899				G3DSA:3.40.50.720	SSF69572	4~31								
aly689.5	Unknown		n/a												42~66								
aly689.6	Adenylyltransferase and sulfurtransferase MOCS3	GO:0006777,GO:0061605,GO:0005829,GO:0008641,GO:0018192,GO:0008265,GO:0002143,GO:0046872,GO:0004792,GO:0061604,GO:0005524	CG13090-PC				SM00450		PF00581	PS50206			G3DSA:3.40.250.10	SSF52821									
aly689.7	Transmembrane protein 26	GO:0016021	CG14238-PA						PF09772														
aly689.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly689.9	Neuroligin-3	GO:0048675,GO:0050808,GO:0008152,GO:0060024,GO:0007612,GO:0061002,GO:0030425,GO:0050804,GO:0030139,GO:0060080,GO:0004872,GO:0002087,GO:0005887,GO:0008542,GO:0030054,GO:0045202,GO:2000331,GO:0097105,GO:0097104,GO:0060999,GO:0007416,GO:2000310,GO:0043025,GO:0071625,GO:2000463,GO:0042043,GO:0097151,GO:0035176,GO:0009986,GO:1902474,GO:0048709,GO:0052689,GO:0008150,GO:0007158,GO:0060077,GO:0060076,GO:2000969,GO:0050839,GO:0030534,GO:1900271,GO:0090394,GO:0060291,GO:0006898,GO:0005575,GO:0097110,GO:0051965,GO:0051968,GO:2000809	CG10175-PD						PF00135,PF00135				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474										
aly691.1	Krueppel-like factor 3	GO:0043565,GO:0006351,GO:0050774,GO:0003700,GO:0005634,GO:1901653,GO:0003677,GO:0046872,GO:0007275,GO:0048814	CG12029-PB				SM00355,SM00355,SM00355		PF00096	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly691.10	NADH dehydrogenase [ubiqui] iron-sulfur protein 2, mitochondrial	GO:0046872,GO:0051539,GO:0048812,GO:0008137,GO:0005739,GO:0006120,GO:0005654,GO:0046331,GO:0016651,GO:0006979,GO:0051287,GO:0048038,GO:0003954,GO:0055114,GO:0005747	CG1970-PA	MF_01358				TIGR01962	PF00346			PS00535	G3DSA:1.10.645.10	SSF56762									
aly691.11	Unknown		n/a												17~44,187~210,78~98								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly691.12	Kanadaptin	GO:0005737,GO:0017107,GO:0043231,GO:0005634,GO:0005654,GO:0005515,GO:0005886	CG7706-PA				SM00240		PF00498	PS50006			G3DSA:2.60.200.20	SSF49879									
aly691.2	Leucine-rich repeat neuronal protein 1	GO:0016021,GO:0051965	CG5096-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly691.3	Leucine-rich repeat neuronal protein 3	GO:0016021,GO:0051965,GO:0005515	CG5096-PA				SM00082,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly691.4	Brain-specific homeobox protein homolog	GO:0005737,GO:0007626,GO:0006351,GO:0007420,GO:0043565,GO:0003700,GO:0005634,GO:0006366,GO:0060056,GO:0006355,GO:0001077,GO:0000976,GO:0042755,GO:0005667,GO:0003677,GO:0045944,GO:0000978,GO:0048663	CG10604-PB				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly691.5	Ankyrin repeat domain-containing protein 50	GO:1990126,GO:0005575,GO:0008150,GO:0015031,GO:0003674,GO:0005768	CG10011-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796,PF12796,PF12796,PF12796,PF13637	PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50297,PS50088,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403									
aly691.6	Ankyrin repeat domain-containing protein 50	GO:1990126,GO:0005575,GO:0008150,GO:0015031,GO:0003674,GO:0005768	CG10011-PA						PF13191														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly691.7	U6 snRNA-associated Sm-like protein LSm2	GO:0005737,GO:0046540,GO:0000381,GO:0017160,GO:0030532,GO:0071011,GO:0005634,GO:0044822,GO:0000398,GO:0006402,GO:0005654,GO:0019901,GO:0005688,GO:0000244,GO:0022008,GO:0071013,GO:0005681	CG10418-PA			PIRSF016394	SM00651		PF01423				G3DSA:2.30.30.100	SSF50182										
aly691.8	Protein suppressor of forked	GO:0016070,GO:0005847,GO:0003729,GO:0005634,GO:0005848,GO:0031123,GO:0006379,GO:1903220,GO:0006397	CG17170-PF				SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386		PF05843					SSF48452	474~494									
aly691.9	Unknown		n/a																				
aly69165.1	NEDD8 ultimate buster 1	GO:0005737,GO:0032436,GO:0005730,GO:0005634,GO:0034341,GO:0016567,GO:0006511,GO:0034612	CG5111-PA																				
aly69170.1	Unknown		n/a																				
aly6920.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6925.1	Eukaryotic translation initiation factor 2D	GO:0005737,GO:0022627,GO:0032790,GO:0005654,GO:0002192,GO:0001731,GO:0006413,GO:0003743	CG31426-PA										G3DSA:2.30.130.10	SSF88697									
aly6927.1	Unknown		CG8929-PB																				
aly6927.2	Unknown		n/a																				
aly694.1	Unknown	GO:0008150,GO:0003674,GO:0005887	CG31561-PA						PF07898														
aly694.10	Unknown	GO:0003674,GO:0008150,GO:0005887	CG15593-PA																				
aly694.11	Unknown	GO:0003674,GO:0008150,GO:0005887	CG15591-PA						PF07898														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly694.12	Unknown	GO:0003674,GO:0007476,GO:0005887	CG15592-PA						PF07898						124~144								
aly694.13	Unknown	GO:0003674,GO:0007476,GO:0005887	CG15592-PA						PF07898														
aly694.14	Unknown	GO:0003674,GO:0007476,GO:0005887	CG15592-PA						PF07898,PF07898														
aly694.15	Unknown	GO:0003674,GO:0007476,GO:0005887	CG15592-PA						PF07898														
aly694.16	Unknown	GO:0003674,GO:0007476,GO:0005887	CG15592-PA						PF07898						120~140								
aly694.17	Unknown	GO:0046331,GO:0003674,GO:0005887	CG1153-PA						PF07898														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly694.18	Unknown	GO:0003674,GO:0008150,GO:0005887	CG15590-PA						PF07898														
aly694.19	Unknown		n/a																				
aly694.2	Unknown	GO:0008150,GO:0003674,GO:0005887	CG31561-PA						PF07898														
aly694.20	Unknown		n/a																				
aly694.21	Unknown	GO:0008150,GO:0003674,GO:0005887	CG1150-PA																				
aly694.22	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly694.3	Unknown	GO:0008150,GO:0003674,GO:0005887	CG31561-PA						PF07898														
aly694.4	Unknown	GO:0008150,GO:0003674,GO:0005887	CG1155-PA							PS51257													
aly694.5	Unknown		n/a																				
aly694.6	Unknown	GO:0008150,GO:0003674,GO:0005887	CG15596-PA																				
aly694.7	Unknown		CG15594-PB																				
aly694.8	Unknown	GO:0003674,GO:0008150,GO:0005887	CG1154-PA						PF07898														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly694.9	Unknown	GO:0008150,GO:0003674,GO:0005887	CG15596-PA						PF07898														
aly6940.1	Unknown		CG17264-PA						PF00431	PS01180			G3DSA:2.60.120.290	SSF49854									
aly6940.2	Insulin receptor substrate 1-B	GO:0004871,GO:0030307,GO:0042169,GO:0048009,GO:0007296,GO:0042594,GO:0007295,GO:0008355,GO:0005737,GO:0000902,GO:0005634,GO:0005159,GO:0008286,GO:0046620,GO:0035159,GO:0046622,GO:0005158,GO:0060250,GO:0008361,GO:0007285,GO:0008152,GO:0008340,GO:0034059,GO:0045793,GO:0007568,GO:0040014,GO:0040018,GO:0050778,GO:0043231,GO:0043548,GO:0048133	CG5686-PA				SM00310,SM00233		PF02174,PF00169	PS51064,PS50003	PR00628,PR00628,PR00628,PR00628,PR00628,PR00628		G3DSA:2.30.29.30,G3DSA:2.30.29.30	SSF50729,SSF50729									
aly6940.3	Disks large homolog 5	GO:0016337,GO:0030159,GO:0045197,GO:0007165,GO:0007298,GO:0042981,GO:0035556,GO:0005737,GO:0045176,GO:0019730,GO:0072205,GO:0060441,GO:0030859,GO:0008285,GO:0006461,GO:0008013,GO:0045186,GO:0046331,GO:0005913,GO:0005886,GO:0008092,GO:0030901,GO:0071896	CG6509-PB				SM00228,SM00228,SM00228		PF00625,PF00595,PF00595,PF00595	PS50106,PS50106,PS50052,PS50106			G3DSA:3.40.50.300,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF52540,SSF90257,SSF50156,SSF50156,SSF50156	323~343,180~200,407~441,81~115,137~164,208~242,449~483,281~315									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6940.4	Nucleosomal histone kinase 1	GO:0018107,GO:0018105,GO:0000785,GO:0007143,GO:0051301,GO:0005737,GO:0007126,GO:0035184,GO:0005634,GO:0004674,GO:0004672,GO:0005524,GO:0005730,GO:0006468,GO:0016572,GO:0007052,GO:0035405,GO:2001020,GO:0022008,GO:0007130,GO:0036098,GO:0036099,GO:0097150,GO:0000070,GO:0006897,GO:0016055,GO:0030717,GO:0008360	CG6386-PA				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112										
aly6940.5	Protein aveugle	GO:0005737,GO:0007601,GO:0046579,GO:0001754,GO:0042675,GO:0007173,GO:0007165,GO:0005515,GO:0005886,GO:0003674,GO:0070374,GO:0001751	CG30476-PA				SM00454		PF07647	PS50105			G3DSA:1.10.150.50	SSF47769									
aly6940.6	Unknown		n/a																				
aly69527.1	Unknown		n/a																				
aly6954.1	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246	n/a				SM00034,SM00034		PF00059,PF00059	PS50041,PS50041			G3DSA:3.10.100.10,G3DSA:3.10.100.10	SSF56436,SSF56436									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6954.10	Myosin heavy chain, non-muscle	GO:0031036,GO:0032027,GO:0035277,GO:0007496,GO:0008258,GO:0007443,GO:0008152,GO:0007297,GO:0045200,GO:0007298,GO:0009653,GO:0035317,GO:0030018,GO:0035072,GO:0005856,GO:0007435,GO:0042623,GO:0045179,GO:0000281,GO:0016459,GO:0003774,GO:0005524,GO:0016203,GO:0000910,GO:0032507,GO:0006936,GO:0030239,GO:0035159,GO:0031252,GO:0042060,GO:0032154,GO:0045214,GO:0005938,GO:0035017,GO:0046664,GO:0022008,GO:0001736,GO:0046663,GO:0051259,GO:0051726,GO:0007391,GO:0007395,GO:0070986,GO:0016461,GO:0016460,GO:0005829	CG15792-PA				SM00242,SM00015		PF02736,PF00612,PF01576,PF00063	PS50096,PS51456	PR00193,PR00193,PR00193,PR00193,PR00193		G3DSA:4.10.270.10,G3DSA:1.20.5.340	SSF90257,SSF90257,SSF52540,SSF90257,SSF90257	1784~1864,1742~1776,1390~1452,1657~1705,1039~1098,1713~1740,1113~1382,836~1031,1460~1649									
aly6954.11	Inositol monophosphatase 1	GO:0005737,GO:0008934,GO:0000287,GO:0046855,GO:0016311,GO:0031403,GO:0052833,GO:0030145,GO:0052834,GO:0052832,GO:0046854,GO:0006021	CG9391-PA						PF00459		PR00378,PR00378,PR00378,PR00378,PR00378,PR00377,PR00377,PR00377,PR00377,PR00377,PR00377,PR00377	PS00629,PS00630	G3DSA:3.40.190.80,G3DSA:3.30.540.10	SSF56655		00562+3.1.3.25,00521+3.1.3.25		PWY-4702,PWY-2301,PWY-6363	UPA00823				
aly6954.12	Chorion peroxidase	GO:0005615,GO:0020037,GO:0030707,GO:0006979,GO:0004666,GO:0001516,GO:0042744,GO:0007304,GO:0007306,GO:0042743,GO:0046872,GO:0004601,GO:0055114,GO:0005875	CG42331-PB						PF03098	PS50292	PR00457,PR00457,PR00457,PR00457,PR00457,PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									
aly6954.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6954.2	Sucrose-6-phosphate hydrolase	GO:0005737,GO:0005985,GO:0005975,GO:0004564,GO:0004575	n/a				SM00640	TIGR01322	PF00251			PS00609	G3DSA:2.115.10.20,G3DSA:2.60.120.560	SSF49899,SSF75005		00500+3.2.1.26,00052+3.2.1.26		PWY-621	UPA00238				
aly6954.3	Lipase 1	GO:0004806,GO:0006629,GO:0007586,GO:0016788,GO:0016042,GO:0048812,GO:0005576	CG31871-PA						PF12146,PF04083				G3DSA:3.40.50.1820	SSF53474									
aly6954.4	Forkhead box protein K2	GO:0043565,GO:0051090,GO:0005667,GO:0007389,GO:0003700,GO:0006355,GO:0005634,GO:0000122,GO:0003705,GO:0009888,GO:0009790,GO:0008301,GO:0006351,GO:0005515,GO:0003677,GO:0000287,GO:0003690,GO:0008134	CG11799-PN				SM00339,SM00240		PF00498,PF00250	PS50006,PS50039	PR00053,PR00053,PR00053	PS00658	G3DSA:2.60.200.20,G3DSA:1.10.10.10	SSF49879,SSF46785									
aly6954.5	Dynein heavy chain 3, axonemal	GO:0036156,GO:0042623,GO:0007018,GO:0000166,GO:0005875,GO:0005524,GO:0030286,GO:0005874,GO:0003774,GO:0003777	CG17150-PD				SM00382,SM00382,SM00382		PF12781,PF12780,PF03028,PF08393,PF12777,PF12774,PF12775				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540	150~170,812~832,2881~2946,197~229,4111~4116,3261~3281								
aly6954.6	Transmembrane channel-like protein 5	GO:0006811,GO:0016021,GO:0070062	CG3280-PC						PF07810														
aly6954.7	Protein C10	GO:0005737	CG15387-PB						PF14974														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly6954.8	Beta-1,3-galactosyltransferase brn	GO:0016333,GO:0005795,GO:0042248,GO:0007219,GO:0006486,GO:0006688,GO:0047915,GO:0016021,GO:0016020,GO:0030707,GO:0000139,GO:0007293,GO:0005576,GO:0008378,GO:0046981,GO:0008375,GO:0001744,GO:0007299,GO:0048477,GO:0007298	CG4934-PA						PF01762										UPA00378				
aly6954.9	Probable low-specificity L-threonine aldolase 2	GO:0006567,GO:0006545,GO:0016829,GO:0006520,GO:0004793,GO:0030170,GO:0008732,GO:0005829	CG10184-PA			PIRSF017617			PF01212				G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383										
aly696.1	Glycerol-3-phosphate acyltransferase 1, mitochondrial	GO:0004366,GO:0005783,GO:0008654,GO:0016021,GO:0005886,GO:0031667,GO:0005739,GO:0045169,GO:0046686,GO:0007009,GO:0005741,GO:0035324,GO:0032869,GO:0016024,GO:0031966,GO:0034587,GO:0014823,GO:0010867,GO:0009750	CG5508-PA				SM00563		PF01553				G3DSA:3.40.1130.10	SSF69593										
aly696.2	Probable RNA directed DNA polymerase from transposon X-element	GO:0003964,GO:0006278,GO:0006313	n/a						PF00078														
aly696.3	Charged multivesicular body protein 3	GO:0006909,GO:0007034,GO:0000815,GO:0005829,GO:0003674,GO:0015031,GO:0070676,GO:0031902	CG9779-PA						PF03357						144~164,30~57								
aly696.4	Xenotropic and polytropic retrovirus receptor 1	GO:0005737,GO:0005794,GO:0004930,GO:0009615,GO:0016021,GO:0001618,GO:0004888,GO:0004872,GO:0005887,GO:0005886,GO:0007186	CG7536-PB						PF03105,PF03124	PS51380,PS51382													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly696.5	Exosome complex component CSL4	GO:0005737,GO:0000178,GO:0005730,GO:0005634,GO:0000176,GO:0000177,GO:0000175,GO:0005654,GO:0006364,GO:0035327,GO:0003723,GO:0010468,GO:0006396,GO:0006397	CG6249-PA						PF14382,PF10447					SSF110324,SSF50249									
aly696.6	Coatomer subunit alpha	GO:0005737,GO:0006890,GO:0006909,GO:0016192,GO:0005615,GO:0070062,GO:0006886,GO:0016020,GO:0048205,GO:0005198,GO:0061024,GO:0048812,GO:0010883,GO:0005515,GO:0007112,GO:0030126,GO:0005829,GO:0030157,GO:0000902	CG7961-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF04053,PF04053,PF06957	PS50082,PS50082,PS50082,PS50082,PS50082,PS50294,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10	SSF50978,SSF50978,SSF51004,SSF51004			REACT_11123							
aly696.7	Unknown		n/a																				
aly697.1	Connectin	GO:0016200,GO:0007156,GO:0009986,GO:0044295,GO:0031594,GO:0005515,GO:0005886,GO:0007155,GO:0007413,GO:0031225	CG7503-PA				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly697.2	Unknown		n/a																				
aly6975.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly69960.1	DNA-binding protein Ets97D	GO:0043565,GO:0003700,GO:0005634,GO:0030154,GO:0006355,GO:0006357,GO:0010821,GO:0003677,GO:0000981,GO:0045451	CG6338-PB				SM00251		PF02198	PS51433			G3DSA:1.10.150.50	SSF47769									
aly6997.1	Cytochrome P450 6k1	GO:0004497,GO:0016020,GO:0043231,GO:0020037,GO:0016705,GO:0005789,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG8859-PA						PF00067,PF00067		PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433					
aly6997.2	Cytochrome P450 6k1	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG8859-PA						PF00067		PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433					
aly7001.1	Sphingolipid delta(4)-desaturase DES1	GO:0006633,GO:0030148,GO:0016020,GO:0005783,GO:0042284,GO:0016006,GO:0005739,GO:0005789,GO:0007283,GO:0007053,GO:0006665,GO:0070938,GO:0005887,GO:0005886,GO:0006636,GO:0004768,GO:0044281,GO:0016021,GO:0055114,GO:0009055	CG9078-PA						PF08557								REACT_22258					
aly7001.2	40S ribosomal protein S3a	GO:0022626,GO:0022627,GO:0005622,GO:0003735,GO:0007052,GO:0000022,GO:0048477,GO:0006412,GO:0005840	CG2168-PA	MF_03122					PF01015			PS01191											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7001.3	Scavenger receptor class B member 1	GO:0034375,GO:0015914,GO:0043691,GO:0005901,GO:0051000,GO:0070328,GO:0032497,GO:0010867,GO:0070062,GO:0010886,GO:0016020,GO:0043654,GO:0035461,GO:0010899,GO:0008035,GO:0006707,GO:0035071,GO:0015920,GO:0006952,GO:0043534,GO:0005887,GO:0007155,GO:0042632,GO:0001530,GO:0030169,GO:0048102,GO:0005044,GO:0044406,GO:0034384,GO:0005765,GO:0033344,GO:0034383,GO:0001875,GO:0070506,GO:0001935	CG3829-PA						PF01130		PR01609,PR01609,PR01609,PR01609,PR01609												
aly7003.1	Membrane alanyl aminopeptidase (Fragment)	GO:0004177,GO:0033227,GO:0008270,GO:0005886,GO:0006508,GO:0008237,GO:0031225	CG8773-PB						PF01433,PF11838				G3DSA:1.10.390.10	SSF55486,SSF63737									
aly7003.2	Membrane alanyl aminopeptidase	GO:0004177,GO:0008270,GO:0005886,GO:0006508,GO:0008237,GO:0031225	CG14516-PB						PF11838,PF01433				G3DSA:1.10.390.10	SSF63737,SSF55486,SSF63737									
aly7003.3	Aminopeptidase N	GO:0004177,GO:0016021,GO:0008270,GO:0005886,GO:0006508,GO:0008237,GO:0031225	CG31445-PA						PF01433,PF01433,PF11838		PR00756,PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF63737,SSF55486									
aly7003.4	Probable muscarinic acetylcholine receptor gar-2	GO:0004930,GO:0007213,GO:0016021,GO:0005887,GO:0016907,GO:0007186,GO:0008227	CG7918-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7003.5	Unknown	GO:0003676	n/a										G3DSA:3.30.420.10	SSF53098									
aly7003.6	Unknown		n/a																				
aly7032.1	Uncharacterized protein C9orf78	GO:0005737,GO:0005654	CG7974-PA						PF07052						138~158								
aly7032.2	Malate synthase, glyoxysomal	GO:0003824,GO:0006099,GO:0009514,GO:0006097,GO:0004474	n/a			PIRSF001363			PF01274				G3DSA:1.20.1220.12,G3DSA:3.20.20.360	SSF51645		00620+2.3.3.9,00630+2.3.3.9		PWY-7118,PWY-7295,PWY-6969,PWY-6728,PWY-7294	UPA00703				
aly7032.3	AN1-type zinc finger protein 2B	GO:0005783,GO:0008270,GO:0006616	CG12795-PB				SM00154,SM00154		PF01428,PF01428,PF02809	PS51039			G3DSA:4.10.1110.10,G3DSA:4.10.1110.10	SSF118310,SSF118310									
aly7032.4	Probable pyruvate dehydrogenase E1 component subunit alpha, mitochondrial	GO:0045254,GO:0004739,GO:0005739,GO:0005759,GO:0006090,GO:0006096,GO:0055114	CG7010-PC					TIGR03182	PF00676				G3DSA:3.40.50.970	SSF52518		00620+1.2.4.1,00020+1.2.4.1,00010+1.2.4.1							
aly7032.5	Multidrug resistance protein homolog 49	GO:0015893,GO:0006855,GO:0005887,GO:0042623,GO:0016021,GO:0031427,GO:0042626,GO:0015238,GO:0008559,GO:0008354,GO:0016887,GO:0005886,GO:0001666,GO:0055085,GO:0005524	CG3879-PA				SM00382,SM00382		PF00005,PF00005,PF00664,PF00664	PS50893,PS50893,PS50929,PS50929		PS00211,PS00211	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.20.1560.10,G3DSA:1.20.1560.10	SSF52540,SSF52540,SSF90123,SSF90123,SSF90123									
aly70327.1	Unknown		CG14446-PE						PF15706														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7037.1	Serine/threonine-protein kinase 10	GO:0032147,GO:0010800,GO:0042981,GO:0046777,GO:0007049,GO:0005737,GO:0007346,GO:0000902,GO:2000401,GO:0000281,GO:0004674,GO:0023014,GO:0004672,GO:0042801,GO:0005524,GO:0042803,GO:0033109,GO:0006468,GO:0008283,GO:0032154,GO:1990023,GO:0007052,GO:0005938,GO:0005886,GO:0032879,GO:0000132,GO:0031098,GO:0004702,GO:0007091	CG4527-PD				SM00220		PF00069	PS50011		PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112										
aly70389.1	Unknown		n/a																				
aly704.1	Dedicator of cytokinesis protein 2	GO:0019897,GO:0043547,GO:0016020,GO:0061327,GO:0046633,GO:0030036,GO:0032863,GO:0001766,GO:0001768,GO:0007298,GO:0007417,GO:0005737,GO:0001726,GO:0045059,GO:0000902,GO:0042608,GO:0042098,GO:0007519,GO:0050766,GO:0016203,GO:0005856,GO:0035022,GO:0035212,GO:0046631,GO:0006935,GO:0005096,GO:0007264,GO:0042110,GO:0001771,GO:0007520,GO:0007523,GO:0070062,GO:0030676,GO:0045060,GO:0007010,GO:0002277,GO:0044351,GO:0007391,GO:0005515,GO:0012505	CG10379-PB				SM00326		PF14429,PF06920,PF16172	PS50002,PS51650,PS51651			G3DSA:2.30.30.40	SSF50044	550~550									
aly704.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly704.3	Dedicator of cytokinesis protein 1	GO:0019897,GO:0061327,GO:0007596,GO:0005085,GO:0030036,GO:0032863,GO:0007165,GO:0007411,GO:0007298,GO:0007417,GO:0005737,GO:0001726,GO:0007264,GO:0000902,GO:0005634,GO:0016020,GO:0007519,GO:0005654,GO:0002244,GO:0016477,GO:0016203,GO:0038096,GO:0035212,GO:0045087,GO:0006915,GO:0005096,GO:0006911,GO:0007520,GO:0048010,GO:0007523,GO:0043547,GO:0030676,GO:0007010,GO:0005829,GO:0007391,GO:0005515,GO:0007229	CG10379-PB										G3DSA:1.25.10.10	SSF48371,SSF48371	324~351								
aly704.4	Dedicator of cytokinesis protein 1	GO:0019897,GO:0006909,GO:0061327,GO:0005085,GO:0030036,GO:0032863,GO:0007298,GO:0007417,GO:0005737,GO:0001726,GO:0007264,GO:0000902,GO:0005634,GO:0016020,GO:0007519,GO:0005654,GO:0002244,GO:0016477,GO:0016203,GO:0035212,GO:0006915,GO:0005096,GO:0007520,GO:0030676,GO:0007010,GO:0007391,GO:0005515	CG10379-PB						PF06920	PS51651													
aly70422.1	Unknown		n/a																				
aly70571.1	GPI transamidase component PIG-S	GO:0006501,GO:0016020,GO:0044267,GO:0043687,GO:0003923,GO:0005789,GO:0005575,GO:0042996,GO:0042765,GO:0016255,GO:0045313	CG44255-PC						PF10510										UPA00196				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly706.1	Dual specificity mitogen-activated protein kinase kinase dSOR1	GO:0000187,GO:0046579,GO:0007165,GO:0007298,GO:0007362,GO:0045500,GO:0000165,GO:0004674,GO:0004713,GO:0004672,GO:0005524,GO:0042386,GO:0006468,GO:0008595,GO:0007173,GO:0008592,GO:0005622,GO:0004707,GO:0004702,GO:0008293,GO:0070374,GO:0004708	CG15793-PA				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112										
aly706.2	Chromatin assembly factor 1 subunit A	GO:0034728,GO:0031497,GO:0000724,GO:0006334,GO:0010332,GO:0042023,GO:0006260,GO:0035264,GO:0033186,GO:0006281,GO:0007444,GO:0005634,GO:0007049	CG12109-PA						PF12253						289~423								
aly706.3	Unknown	GO:0005743,GO:0005747,GO:0042773,GO:0008137	CG6914-PA						PF07347														
aly706.4	Unknown		CG9368-PA												31~57								
aly706.5	G patch domain and KOW motifs-containing protein	GO:0022008,GO:0005634,GO:0003676	CG10324-PA						PF12656				G3DSA:2.30.30.30	SSF50104									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7069.1	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG3466-PA						PF00067		PR00463,PR00463,PR00463		G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly7069.10	Uncharacterized protein C45G9.7	GO:0007266,GO:0030111,GO:0005622	CG3402-PA			PIRSF037712	SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156									
aly7069.11	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 5	GO:0008137,GO:0006120,GO:0005575,GO:0005743,GO:0008150,GO:0016651,GO:0022904,GO:0003674,GO:0070469,GO:0003954,GO:0005747	CG6463-PA						PF04716						73~93								
aly7069.12	E3 ubiquitin-protein ligase Topors	GO:0008270,GO:0061630,GO:0000209,GO:0007140,GO:0016874,GO:0005634,GO:0007060,GO:0071763,GO:0042787,GO:0005652,GO:0005521,GO:0051299,GO:0004842,GO:0010032,GO:0006997,GO:0044547,GO:0005700,GO:0006355,GO:0006511,GO:0006351,GO:0007095,GO:0016568	CG15104-PA				SM00184		PF00097	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850									
aly7069.13	Mitogen-activated protein kinase 14B	GO:0048082,GO:0003007,GO:0000165,GO:0038001,GO:0071243,GO:0008340,GO:0042742,GO:0042594,GO:0016909,GO:0009651,GO:0005634,GO:0009617,GO:0007476,GO:0004674,GO:0005524,GO:0006468,GO:0007623,GO:0045088,GO:2000331,GO:0034614,GO:0072593,GO:0071276,GO:0006952,GO:0006955,GO:0009408,GO:0007179,GO:0030510,GO:0050832,GO:0045793,GO:1900407,GO:0042542,GO:0040018,GO:0004707,GO:0001934	CG7393-PA				SM00220		PF00069	PS50011	PR01773,PR01773,PR01773,PR01773,PR01773	PS00107,PS01351	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112			REACT_11061						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7069.14	Unknown	GO:0006120,GO:0003954,GO:0005747	CG13240-PA						PF09782														
aly7069.15	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG3466-PA						PF00067				G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly7069.16	Unknown		n/a																				
aly7069.2	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly7069.3	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264	130~150		REACT_13433						
aly7069.4	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7069.5	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232		PR00131,PR00131,PR00131,PR00131,PR00131	PS00653,PS00572	G3DSA:3.20.20.80	SSF51445										
aly7069.6	Transcriptional coactivator YAP1	GO:0003714,GO:0016020,GO:0045927,GO:0071480,GO:0090263,GO:0060242,GO:0035019,GO:0001076,GO:2001237,GO:0030054,GO:2000737,GO:0005737,GO:0000902,GO:0072091,GO:0044212,GO:0031410,GO:0005634,GO:0005770,GO:0003713,GO:0005654,GO:0043066,GO:0005667,GO:0030857,GO:0006366,GO:0060449,G	CG4005-PG				SM00456,SM00456		PF00397,PF00397	PS50020,PS50020		PS01159,PS01159	G3DSA:2.20.70.10,G3DSA:2.20.70.10	SSF51045,SSF51045	279~309									
aly7069.7	Zinc finger protein 234	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF00096,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57716,SSF57667										
aly7069.8	Ornithine aminotransferase, mitochondrial	GO:0006591,GO:0005739,GO:0008483,GO:0005759,GO:0030170,GO:0004587,GO:0022008,GO:0055129	CG8782-PA					TIGR01885	PF00202			PS00600	G3DSA:3.40.640.10,G3DSA:3.90.1150.10,G3DSA:3.90.1150.10	SSF53383		00330+2.6.1.13		PWY-6922,PWY-6344,PWY-4981,PWY-3341	UPA00098				
aly7069.9	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	GO:0047115,GO:0047837,GO:0055114,GO:0016491	CG3609-PA						PF01408				G3DSA:3.30.360.10,G3DSA:3.40.50.720	SSF55347,SSF51735									
aly707.1	Antichymotrypsin-2	GO:0005615,GO:0032504,GO:0050829,GO:0030162,GO:0004867,GO:0010951,GO:0045861	CG9334-PA				SM00093		PF00079,PF00079				G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly707.10	E3 ubiquitin-protein ligase Hakai	GO:0040003,GO:0007427,GO:0060429,GO:0007494,GO:0003676,GO:0007015,GO:0016023,GO:0007391,GO:0008258,GO:0030335,GO:0045296,GO:0045807,GO:0016567,GO:0007162,GO:0004842,GO:0008270,GO:0005515,GO:0005886,GO:0048471,GO:0016874,GO:0035282	CG10263-PF							PS50089		PS00518	G3DSA:3.30.40.10,G3DSA:3.30.160.60	SSF57850	44~64								
aly707.11	Transmembrane protein 115	GO:0005794,GO:0006890,GO:0006486,GO:0008285,GO:0016021,GO:0015031,GO:0032580,GO:0005634,GO:0042802	CG9536-PA						PF08551					SSF144091									
aly707.12	Proliferating cell nuclear antigen	GO:0030337,GO:0019730,GO:0006272,GO:0005634,GO:0007307,GO:0006298,GO:0006275,GO:0006289,GO:0007052,GO:0006260,GO:0006261,GO:0003677,GO:0043626,GO:0022008,GO:0005875	CG9193-PA	MF_00317,MF_01966				TIGR00197,TIGR00590	PF00705,PF03853,PF02747	PS51385	PR00339,PR00339,PR00339,PR00339,PR00339,PR00339	PS01251,PS00293	G3DSA:3.40.50.10260,G3DSA:3.70.10.10	SSF55979,SSF55979,SSF64153				PWY-6938					
aly707.13	Protein bric-a-brac 2	GO:0007478,GO:0003700,GO:0007455,GO:0005634,GO:0005700,GO:0006355,GO:0061040,GO:0006351,GO:0003680,GO:0046872	CG6765-PA				SM00355,SM00355,SM00355,SM00355,SM00225		PF00651,PF00096,PF12874	PS50097,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.710.10,G3DSA:3.30.160.60	SSF57667,SSF54695									
aly707.14	Integrator complex subunit 5	GO:0016180,GO:0034472,GO:0005634,GO:0016020,GO:0032039,GO:0022008,GO:0016021	CG9591-PA						PF14837,PF14838														
aly707.15	GPN-loop GTPase 1	GO:0005737,GO:0017076,GO:0005634,GO:0003924,GO:0005525	CG3704-PA						PF03029				G3DSA:3.40.50.300	SSF52540	264~291								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly707.16	FAD synthase	GO:0005737,GO:0003824,GO:0008152,GO:0005886,GO:0006747,GO:0003919,GO:0005524	CG4407-PA						PF01507,PF01507				G3DSA:3.40.50.620	SSF52402									
aly707.17	tRNA (guanine(37)-N1)-methyltransferase	GO:0030488,GO:0005634,GO:0006555,GO:0005759,GO:0008175,GO:0006400,GO:0052906,GO:0009019	CG32281-PA	MF_03152					PF02475	PS51684			G3DSA:3.40.50.150,G3DSA:3.30.300.110	SSF53335				PWY-7286,PWY-7285,PWY-6829					
aly707.18	Leucine-rich repeat-containing protein 74A		n/a				SM00368,SM00368,SM00368,SM00368,SM00368,SM00368		PF00560		PR00019,PR00019		G3DSA:3.80.10.10	SSF52047									
aly707.19	Proton-coupled folate transporter	GO:0016021,GO:0005542,GO:0055085	CG15890-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly707.2	Netrin receptor UNC5C	GO:0007432,GO:0016021,GO:0005043,GO:0005042,GO:0007165,GO:0008045,GO:0007411,GO:0007275,GO:0008347	CG8166-PA				SM00005,SM00408,SM00409,SM00409,SM00218,SM00209		PF00531,PF00791,PF07679	PS51145,PS50835,PS50092,PS50092			G3DSA:1.10.533.10,G3DSA:2.60.40.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10	SSF82895,SSF47986,SSF48726,SSF82895									
aly707.20	Proton-coupled folate transporter	GO:0016021,GO:0005542,GO:0055085	CG15890-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly707.21	Proton-coupled folate transporter	GO:0016021,GO:0005542,GO:0055085	CG15890-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly707.22	Proton-coupled folate transporter	GO:0016021,GO:0005542,GO:0055085	CG15890-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly707.23	Proton-coupled folate transporter	GO:0016021,GO:0005542,GO:0055085	CG15890-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473	485~517								
aly707.24	Solute carrier family 46 member 3	GO:0016021,GO:0055085	CG15890-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly707.25	Unknown	GO:0007157,GO:0005576,GO:0003674,GO:0031225	CG14064-PA										G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly707.26	Protein transport protein Sec24B	GO:0048208,GO:0005789,GO:0060088,GO:0061024,GO:0016192,GO:0008270,GO:0030134,GO:0048471,GO:0003151,GO:0002474,GO:0006888,GO:1901301,GO:0006886,GO:0016020,GO:0001843,GO:0061156,GO:0060463,GO:0019886,GO:0044267,GO:0005215,GO:0043687,GO:0012507,GO:0021747,GO:0030127,GO:0090110,GO:0005048,GO:0005829,GO:0090178,GO:0000139,GO:0018279,GO:0035909,GO:0060982,GO:0044281	CG1472-PA						PF04811				G3DSA:3.40.50.410	SSF53300			REACT_11123						
aly707.27	Unknown		n/a																				
aly707.3	Dual specificity protein phosphatase 14	GO:0005737,GO:0008138,GO:0006470,GO:0004725,GO:0044822,GO:0017017,GO:0000188,GO:0005575,GO:0035335,GO:0005634	CG15528-PB				SM00195		PF00782	PS50054,PS50056			G3DSA:3.90.190.10	SSF52799									
aly707.4	Cytochrome P450 6B6	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG13977-PA						PF00067		PR00464,PR00464,PR00464,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly707.5	Cytochrome P450 6B6	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG13977-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00465,PR00465,PR00465	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly707.6	Cytochrome P450 6B6	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0070330,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA						PF00067,PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086,PS00086	G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264,SSF48264			REACT_13433						
aly707.7	UPF0728 protein C10orf53 homolog		n/a						PF15092														
aly707.8	Protein transport protein Sec24A	GO:0006888,GO:0005048,GO:0050714,GO:0005789,GO:0005215,GO:0006886,GO:2000189,GO:0030134,GO:0045714,GO:0008270,GO:0048471,GO:0000139,GO:0030127,GO:0090110	CG1472-PA						PF08033,PF04810,PF04815,PF04811				G3DSA:2.60.40.1670,G3DSA:3.40.50.410,G3DSA:3.40.20.10	SSF81995,SSF81995,SSF82919,SSF81811,SSF53300,SSF82754			REACT_11123						
aly707.9	MAP kinase-interacting serine/threonine-protein kinase 1	GO:0005737,GO:0006468,GO:0007017,GO:0005813,GO:0040008,GO:0005635,GO:0051019,GO:0004674,GO:0046580,GO:0016301,GO:0004672,GO:0006417,GO:0005874,GO:0005524	CG17342-PA				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112	45~65								
aly708.1	Motor neuron and pancreas homeobox protein 1	GO:0021520,GO:0043565,GO:0006959,GO:0031018,GO:0021904,GO:0007399,GO:0006357,GO:0003700,GO:0005634,GO:0008045,GO:0021675,GO:0009791,GO:0006355,GO:0046331,GO:0001764,GO:0006351,GO:0003677,GO:0060539,GO:0007412,GO:0009653,GO:0007417	CG8254-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly708.2	Ras-related protein RABF2b	GO:0006897,GO:0031982,GO:0007422,GO:0005768,GO:0055037,GO:0003924,GO:0005774,GO:0030139,GO:0032482,GO:0045202,GO:0008152,GO:0005886,GO:0015031,GO:0006886,GO:0005525,GO:0005783,GO:0005769,GO:0031901,GO:0016192	CG3870-PA				SM00174,SM00173,SM00175		PF00071,PF00071	PS51419	PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540			REACT_11044						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly708.3	Protein canopy homolog 1	GO:0070613,GO:0050708,GO:0005783,GO:0009951,GO:0003674,GO:0007311,GO:0007275	CG12918-PA						PF11938														
aly708.4	Unknown		n/a																				
aly708.5	Paired amphipathic helix protein Sin3b	GO:0035206,GO:0035220,GO:0000785,GO:0044281,GO:0030178,GO:0001741,GO:0005737,GO:0070822,GO:0007346,GO:0000122,GO:0000806,GO:0005634,GO:0000805,GO:0007519,GO:0003712,GO:0016575,GO:0048666,GO:0017053,GO:0007517,GO:0001106,GO:0000791,GO:0045892,GO:0008340,GO:0044255,GO:0010633,GO:0003682,GO:0016580,GO:0010631,GO:0007422,GO:0003700,GO:0031647,GO:0005700,GO:0048738,GO:0006355,GO:0048813,GO:0006351,GO:0030849,GO:0046982,GO:0005654	CG8815-PG				SM00761		PF16879,PF02671,PF02671,PF08295	PS51477,PS51477,PS51477			G3DSA:1.20.1160.11,G3DSA:1.20.1160.11,G3DSA:1.20.1160.11	SSF47762,SSF47762,SSF47762			REACT_22258							
aly708.6	3-hydroxy-3-methylglutaryl coenzyme A reductase	GO:0004420,GO:0007626,GO:0050661,GO:0005778,GO:0035232,GO:0018990,GO:0015936,GO:0016021,GO:0008406,GO:0035050,GO:0005622,GO:0007280,GO:0008299,GO:0008354,GO:0005789,GO:0055114	CG10367-PA					TIGR00533	PF12349,PF00368	PS50156,PS50065,PS51257	PR00071,PR00071,PR00071,PR00071,PR00071,PR00071	PS01192,PS00318,PS00066	G3DSA:1.10.3270.10,G3DSA:1.20.1640.10,G3DSA:3.90.770.10,G3DSA:3.90.770.10,G3DSA:3.30.70.420	SSF55035,SSF56542,SSF56542		00900+1.1.1.34		PWY-922,PWY-6174,PWY-7391,PWY-7524	UPA00058				
aly709.1	Unknown		n/a												683~708								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly709.10	Unknown		n/a												80~100								
aly709.11	Dystrophin, isoform D	GO:0005200,GO:0008586,GO:0046716,GO:0008270,GO:0030010,GO:0007274,GO:0005856,GO:0007517,GO:0007474,GO:0005198,GO:0003779,GO:0005509,GO:0005737,GO:0042383,GO:0050699,GO:0008307,GO:0046928,GO:0048172,GO:0005938,GO:0008092,GO:0016010,GO:0045202	CG31175-PH				SM00456,SM00150,SM00150,SM00291		PF00569,PF09068,PF00435,PF09069,PF00397	PS50020,PS50135		PS01357	G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.20.58.60,G3DSA:2.20.70.10,G3DSA:1.20.58.60	SSF46966,SSF46966,SSF46966,SSF47473,SSF47473,SSF51045,SSF57850	809~839,740~774,111~135									
aly709.12	Cyclin-dependent kinases regulatory subunit 1	GO:0007113,GO:0000278,GO:0016538,GO:0019005,GO:0051301,GO:0007067,GO:0007049	CG9790-PA				SM01084		PF01111		PR00296,PR00296,PR00296	PS00945	G3DSA:3.30.170.10	SSF55637									
aly709.13	Cyclin-dependent kinases regulatory subunit 1	GO:0007113,GO:0000278,GO:0016538,GO:0019005,GO:0051301,GO:0007067,GO:0007049	CG9790-PA				SM01084		PF01111		PR00296,PR00296,PR00296,PR00296	PS00944,PS00945	G3DSA:3.30.170.10	SSF55637									
aly709.14	Unknown	GO:0016772	CG14314-PA				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112	207~227								
aly709.15	Inverted formin-2	GO:0003779,GO:0007424,GO:0030036,GO:0016043,GO:0035147	CG33556-PB				SM00498		PF02181,PF06367	PS51444,PS51232				SSF48371,SSF101447	1137~1138,862~882,543~563,673~693								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly709.16	Unknown		CG13699-PA																				
aly709.17	Unknown		n/a																				
aly709.2	Unknown	GO:0003677	CG8359-PA				SM00595		PF10545,PF02944	PS51029,PS51031													
aly709.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly709.4	Dystrophin	GO:0042391,GO:0005200,GO:0014819,GO:0021629,GO:0014809,GO:0007519,GO:0033137,GO:0008586,GO:0046716,GO:0030175,GO:0008065,GO:0017166,GO:0014904,GO:0008270,GO:0030010,GO:0045202,GO:0060048,GO:0030018,GO:0030055,GO:0005856,GO:0007517,GO:0044306,GO:0086001,GO:0007274,GO:0005634,GO:0043043,GO:0007474,GO:0005198,GO:0003779,GO:0002027,GO:0045666,GO:0060857,GO:0005509,GO:1901385,GO:0010468,GO:0016203,GO:0005737,GO:0042383,GO:0010881,GO:0050699,GO:0009986,GO:0034613,GO:1902083,GO:0090287,GO:0048747,GO:0060314,GO:0045211,GO:0008307,GO:0046928,GO:0048172,GO:0017022,GO:0005886,GO:0051647,GO:0043623,GO:0043234,GO:0050998,GO:0008092,GO:2000651,GO:0045121,GO:0031527,GO:0006355,GO:0016010,GO:0045213,GO:0010976,GO:0010880,GO:0035994,GO:0001954,GO:0070373,GO:0043034,GO:0002162	CG31175-PH				SM00150,SM00150,SM00150,SM00150,SM00150,SM00033,SM00033		PF00307,PF00307,PF00435	PS50021,PS50021		PS00020	G3DSA:1.10.418.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.10.418.10,G3DSA:1.20.58.60	SSF46966,SSF46966,SSF46966,SSF46966,SSF47576	609~629,1853~1873,1252~1272,711~741,1106~1126,833~864,1307~1327,680~700,965~985									
aly709.5	Dystrophin, isoforms A/C/F/G/H	GO:0005200,GO:0008586,GO:0046716,GO:0045202,GO:0030010,GO:0007274,GO:0005856,GO:0007517,GO:0007474,GO:0005198,GO:0003779,GO:0005509,GO:0005737,GO:0042383,GO:0050699,GO:0008307,GO:0046928,GO:0048172,GO:0005938,GO:0008092,GO:0016010,GO:0008270	CG34157-PI				SM00150,SM00150		PF00435,PF00435				G3DSA:1.20.58.60,G3DSA:1.20.58.60	SSF46966,SSF46966	293~327,84~118									
aly709.6	Dystrophin, isoform D	GO:0005737,GO:0005856,GO:0007517,GO:0042383,GO:0008092,GO:0008307,GO:0050699,GO:0008270,GO:0008586,GO:0007474,GO:0005198,GO:0003779,GO:0016010,GO:0046928,GO:0048172,GO:0005938,GO:0030010,GO:0007274,GO:0046716,GO:0045202	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly709.7	Unknown		n/a																				
aly709.8	Unknown		n/a																				
aly709.9	Unknown		n/a																				
aly7098.1	Lachesin	GO:0007424,GO:0016331,GO:0035151,GO:0050767,GO:0009986,GO:0019991,GO:0035160,GO:0042803,GO:0005918,GO:0061343,GO:0043005,GO:0005886,GO:0016337,GO:0007156,GO:0043025,GO:0031225	CG31646-PA				SM00408,SM00408,SM00409,SM00409,SM00409		PF07679,PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly7098.2	Unknown		n/a																				
aly7098.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly71.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0022857,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly714.1	Xaa-Pro aminopeptidase 1	GO:0005737,GO:0004177,GO:0005829,GO:0010815,GO:0030145,GO:0070006,GO:0006508	CG6291-PA						PF00557,PF16188				G3DSA:3.90.230.10	SSF55920									
aly714.2	Unknown	GO:0004129,GO:0005751,GO:0006123	CG7181-PB						PF02285				G3DSA:4.10.81.10										
aly714.3	Leucyl-cystinyl aminopeptidase	GO:0004177,GO:0005765,GO:0060395,GO:0016021,GO:0016020,GO:0030163,GO:0005622,GO:0030659,GO:0008270,GO:0005886,GO:0006508,GO:0048471,GO:0008237,GO:0012505	CG14516-PB						PF01433		PR00756,PR00756,PR00756,PR00756		G3DSA:1.10.390.10	SSF55486,SSF63737									
aly714.4	Probable Xaa-Pro aminopeptidase P	GO:0004177,GO:0005829,GO:0034396,GO:0070006,GO:0006508,GO:0046872,GO:0005634,GO:0008237	CG6291-PA						PF16189,PF01321				G3DSA:3.40.350.10	SSF53092									
aly7149.1	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7149.2	Transmembrane protease serine 9	GO:0004252,GO:0005887,GO:0009950,GO:0031639,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly7149.3	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0035007,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG6361-PB				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly7149.4	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly7149.5	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly71490.1	Splicing factor 3A subunit 1	GO:0044822,GO:0071004,GO:0000381,GO:0071011,GO:0005634,GO:0000389,GO:0000398,GO:0005654,GO:0007052,GO:0003723,GO:0005686,GO:0007067,GO:0005684,GO:0071013,GO:0005681	CG16941-PA																				
aly71644.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly71712.1	Unknown		n/a																				
aly718.1	Glutathione S-transferase 1	GO:0005737,GO:0004364,GO:0006749	CG17530-PA						PF02798,PF00043	PS50404,PS50405			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF47616,SSF52833									
aly718.2	Antichymotrypsin-2	GO:0010951,GO:0045861,GO:0030162,GO:0005615,GO:0004867	CG9460-PA				SM00093		PF00079			PS00284	G3DSA:2.30.39.10,G3DSA:2.30.39.10,G3DSA:3.30.497.10,G3DSA:3.30.497.10	SSF56574										
aly718.3	Unknown	GO:0007157,GO:0005576,GO:0003674,GO:0005515	CG10152-PB							PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726									
aly7186.1	CDK5 regulatory subunit-associated protein 3	GO:0044389,GO:0003674,GO:0071901,GO:0044818,GO:0005737,GO:0007346,GO:0097371,GO:0005634,GO:0016020,GO:0031398,GO:1901798,GO:0030332,GO:0008283,GO:1903363,GO:0051059,GO:0019901,GO:0012505,GO:0043234,GO:1900182,GO:0000079,GO:0032088,GO:0005575,GO:0045944,GO:0005813,GO:0071569,GO:0007095,GO:0001933	CG30291-PA						PF05600														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7186.2	Eukaryotic translation initiation factor 4E type 2	GO:0005737,GO:0005845,GO:0001701,GO:0031370,GO:0016281,GO:0007476,GO:0000340,GO:0031625,GO:0044822,GO:0005515,GO:0017148,GO:0030371,GO:0022008,GO:0006413,GO:0002121,GO:0003743	CG33100-PB						PF01652			PS00813	G3DSA:3.30.760.10	SSF55418										
aly7186.3	Activin receptor type-2B	GO:0032924,GO:0042078,GO:0008258,GO:0017002,GO:0005026,GO:0010629,GO:0007411,GO:0001745,GO:0016021,GO:0004675,GO:0004672,GO:0046872,GO:0005524,GO:0045705,GO:0048666,GO:0006468,GO:0030718,GO:0005886,GO:0022008,GO:0007179,GO:0048179,GO:0007443,GO:0007424,GO:0009953,GO:0007428,GO:0007391,GO:0005024,GO:0048813,GO:0004702,GO:0048185	CG7904-PB						PF01064,PF00069	PS50011	PR00653,PR00653,PR00653	PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:2.10.60.10	SSF57302,SSF56112										
aly7186.4	DNA primase large subunit	GO:0000278,GO:0005634,GO:1990077,GO:0003887,GO:0006260,GO:0006261,GO:0003896,GO:0003677,GO:0046872,GO:0005658,GO:0006269,GO:0051539	CG5553-PA						PF04104														
aly7186.5	Fatty acid 2-hydroxylase	GO:0006633,GO:0042127,GO:0006631,GO:0032286,GO:0005783,GO:0020037,GO:0001949,GO:0016021,GO:0080132,GO:0032287,GO:0006665,GO:0052722,GO:0005789,GO:0030258,GO:0005506,GO:0055114,GO:0042634	CG30502-PB			PIRSF005149			PF04116,PF00173	PS50255		PS00191	G3DSA:3.10.120.10	SSF55856										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7186.6	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098	PS50292	PR00457,PR00457,PR00457,PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									
aly7186.7	Leucine-rich repeat-containing protein C10orf11 homolog	GO:0005575,GO:0003674,GO:0046579,GO:0030318	CG31447-PA							PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									
aly7190.1	Dihydrofolate reductase	GO:0006139,GO:0050661,GO:0006760,GO:0006545,GO:0006730,GO:0009165,GO:0006189,GO:0005515,GO:0015955,GO:0004146,GO:0046654,GO:0055114	CG14887-PA						PF00186	PS51330	PR00070,PR00070,PR00070	PS00075	G3DSA:3.40.430.10	SSF53597		00790+1.5.1.3,00670+1.5.1.3		PWY-6614,PWY-3841	UPA00077				
aly7192.1	Anoctamin-4	GO:0005229,GO:0017128,GO:0061589,GO:0061591,GO:0061590,GO:0016021,GO:0005886,GO:0005622,GO:0034220,GO:0006821,GO:1902476,GO:0055085	CG6938-PC						PF16178,PF04547														
aly7192.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7193.1	Unknown		n/a																				
aly7193.2	Protein FAM98A	GO:0044822,GO:0072669	CG5913-PA						PF10239														
aly7193.3	BUD13 homolog	GO:0071013,GO:0000398	CG13625-PA						PF09736						104~124								
aly72.1	GMP reductase 1	GO:0046872,GO:0006909,GO:0003938,GO:0003920,GO:0005829,GO:0030554,GO:0043101,GO:0055086,GO:0009117,GO:1902560,GO:0006164,GO:0009409,GO:0007411,GO:0006177,GO:0048477,GO:0006144,GO:0055114,GO:0044281	CG1799-PC					TIGR01305	PF00478			PS00487	G3DSA:3.20.20.70	SSF51412		00230+1.7.1.7	REACT_1698						
aly72.10	Exportin-2	GO:0005737,GO:0005635,GO:0006909,GO:0006611,GO:0006606,GO:0005634,GO:0006915,GO:0008536,GO:0051533,GO:0005654,GO:0008262,GO:0005515,GO:0022008,GO:0005829	CG13281-PA				SM00913		PF03378,PF03810,PF08506	PS50166			G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371	965~969								
aly72.11	Ornithine decarboxylase	GO:0005737,GO:0008284,GO:0009615,GO:0005829,GO:0009446,GO:0006596,GO:0001822,GO:0006595,GO:0003824,GO:0042176,GO:0033387,GO:0004586,GO:0048471,GO:0042803	CG8721-PA						PF00278,PF02784		PR01179,PR01179,PR01179,PR01179,PR01179,PR01182,PR01182,PR01182,PR01182,PR01182,PR01182,PR01182,PR01182	PS00878,PS00879	G3DSA:2.40.37.10,G3DSA:3.20.20.10	SSF51419,SSF50621			REACT_13							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly72.12	Unknown		n/a						PF08524						144~182								
aly72.13	Vacuolar amino acid transporter 3	GO:0006995,GO:0016021,GO:0005783,GO:0005789,GO:0005774,GO:1902475,GO:0000329,GO:0015171,GO:0030435,GO:0015807,GO:0032974,GO:0003333,GO:0034639	CG13646-PA						PF01490														
aly72.14	Acyl-CoA synthetase family member 3, mitochondrial	GO:0006631,GO:0005739,GO:0004467,GO:0008152,GO:0016874,GO:0005524	CG18155-PB						PF13193,PF00501,PF00501			PS00455	G3DSA:2.30.38.10,G3DSA:2.30.38.10,G3DSA:3.30.300.30,G3DSA:3.40.50.980,G3DSA:3.40.50.980,G3DSA:3.40.50.980	SSF56801,SSF56801									
aly72.15	Transmembrane protein 68	GO:0016021,GO:0016746,GO:0008152	CG34348-PA						PF01553					SSF69593									
aly72.16	Mediator of RNA polymerase II transcription subunit 25	GO:0002805,GO:0007399,GO:0001104,GO:0006357,GO:0006367,GO:0016592	CG12254-PA						PF11232,PF11265						623~658,586~620								
aly72.17	Deleted in autism protein 1 homolog	GO:0014066,GO:0060038,GO:0030137,GO:0005615	CG11170-PB						PF12260														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly72.18	G patch domain-containing protein 1 homolog	GO:0071011,GO:0071013,GO:0003676,GO:0000398	CG8833-PA						PF01585,PF07713	PS50174					457~477								
aly72.19	UPF0183 protein CG7083	GO:0005575,GO:0003674,GO:0008150	CG7083-PA						PF03676														
aly72.2	Unknown	GO:0030414	n/a						PF05375					SSF57283,SSF57283									
aly72.20	UPF0183 protein CG7083	GO:0005575,GO:0003674,GO:0008150	CG7083-PA						PF03676														
aly72.21	Ceramide glucosyltransferase	GO:0016021,GO:0016020,GO:0008120,GO:0005789,GO:1903955,GO:0043066,GO:0006679,GO:0000139	CG6437-PA						PF13506				G3DSA:3.90.550.10	SSF53448		00600+2.4.1.80		PWY-5129	UPA00222				
aly72.22	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly72.23	Unknown		n/a												885~905,1266~1286								
aly72.24	Nuclear transcription factor Y subunit gamma	GO:0043565,GO:0008589,GO:0016602,GO:0032993,GO:0003700,GO:0005634,GO:0009987,GO:0035222,GO:0006366,GO:0005654,GO:0006355,GO:0001077,GO:0045944,GO:0045893,GO:0005667,GO:0003677,GO:0007411,GO:0000978,GO:0046982	CG3075-PA						PF00808				G3DSA:1.10.20.10	SSF47113									
aly72.25	Zinc finger protein ubi-d4	GO:0005737,GO:0007517,GO:0043231,GO:0003700,GO:0005813,GO:0005634,GO:0006915,GO:0000790,GO:0005654,GO:0006355,GO:0048813,GO:0008270,GO:0090544,GO:0000978,GO:0006351	CG2682-PA						PF14051	PS50157		PS00028		SSF57667									
aly72.26	Unknown		n/a																				
aly72.27	RNA-binding protein fusilli	GO:0005634,GO:0043484,GO:0000166,GO:0007173,GO:0003676,GO:0003729,GO:0008380,GO:0006397	CG8205-PE				SM00360,SM00360,SM00360		PF14259,PF14259,PF14259	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928									
aly72.28	Unknown	GO:0030414	n/a			PIRSF001625			PF05375,PF05375	PS51446,PS51446				SSF57283,SSF57283									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly72.3	Unknown	GO:0030414	n/a						PF05375	PS51446,PS51446,PS51446,PS51446,PS51446,PS51446,PS51446,PS51446				SSF57283,SSF57283,SSF57283,SSF57283	930~950								
aly72.4	Unknown	GO:0030414	n/a						PF05375	PS51446,PS51446,PS51446				SSF57283,SSF57283									
aly72.5	Pacifastin-like protease inhibitor cvp4	GO:0005576,GO:0030414,GO:0004867	n/a						PF05375,PF05375,PF05375	PS51446,PS51446,PS51446,PS51446,PS51446				SSF57283,SSF57283,SSF57283,SSF57283									
aly72.6	Protein TSSC1	GO:0005515	CG10646-PA				SM00320,SM00320,SM00320,SM00320,SM00320			PS50294,PS50082			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978									
aly72.7	RNA-binding protein pno1	GO:0022008,GO:0003729,GO:0003723,GO:0005730	CG11738-PA				SM00322						G3DSA:3.30.1370.10	SSF54791									
aly72.8	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 10, mitochondrial	GO:0006139,GO:0019206,GO:0016773,GO:0008137,GO:0005811,GO:0055114,GO:0005739,GO:0006120,GO:0005747,GO:0005759,GO:0070469,GO:0003954,GO:0005524	CG6343-PA			PIRSF000543			PF01712				G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly72.9	Glutathione synthetase	GO:0004363,GO:0000287,GO:0071722,GO:0006974,GO:0006750,GO:0042803,GO:0005524,GO:0043295	CG6835-PH			PIRSF001558			PF03199,PF03917,PF03917				G3DSA:3.30.470.20,G3DSA:3.30.1490.80,G3DSA:1.10.1080.10,G3DSA:3.40.50.1760	SSF56059,SSF56059		00480+6.3.2.3			UPA00142				
aly72062.1	Calcineurin-binding protein cabin-1	GO:0005737,GO:0006336,GO:0060548,GO:0016235,GO:0005654,GO:0004864,GO:0007166,GO:0043086,GO:0016568	n/a																				
aly72093.1	Unknown		n/a																				
aly72266.1	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG3466-PA						PF00067				G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly7236.1	Gastrulation defective protein 1 homolog	GO:0005575,GO:0022008,GO:0003674,GO:0005515	CG5543-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400	PS50082,PS50294,PS50082,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978	78~105								
aly7236.2	Counting factor associated protein D	GO:1903665,GO:0005615,GO:0051603,GO:0031410,GO:0005811,GO:0031288,GO:0005875,GO:0005764,GO:0030435,GO:0004197,GO:0006508,GO:1903669,GO:0008234,GO:0005576	CG8947-PA				SM00645,SM00848		PF08246,PF00112,PF00112		PR00705,PR00705,PR00705	PS00640,PS00639,PS00139	G3DSA:3.90.70.10	SSF54001									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7239.1	Nose resistant to fluoxetine protein 6	GO:0040003,GO:0022600,GO:0006869,GO:0007586,GO:0016021,GO:0008289,GO:0007275,GO:0016747,GO:0009651,GO:0048477,GO:0030421	CG32589-PA						PF01757														
aly7239.2	Unknown		n/a																				
aly7240.1	Metal transporter CNNM2	GO:0030554,GO:0016021,GO:0006873,GO:0016323,GO:0005575,GO:0015693,GO:0003674,GO:0010960	CG42595-PE						PF01595														
aly7244.1	Unknown		n/a																				
aly725.1	Peroxidase	GO:0042600,GO:0046872,GO:0006909,GO:0020037,GO:0004601,GO:0045471,GO:0005576,GO:0042744,GO:0007306,GO:0022008,GO:0005506,GO:0006979,GO:0055114	CG3477-PA						PF03098	PS50292	PR00457,PR00457,PR00457,PR00457		G3DSA:1.10.640.10,G3DSA:1.10.640.10	SSF48113									
aly725.10	Glutathione S-transferase 1, isoform C	GO:0005737,GO:0004364,GO:0018833,GO:0005515,GO:0006749	CG10045-PA						PF13417,PF00043	PS50404,PS50405			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF52833,SSF47616									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly725.11	Glutathione S-transferase 1, isoform C	GO:0005737,GO:0004364,GO:0018833,GO:0005515,GO:0006749	CG10045-PA						PF13417,PF00043	PS50404,PS50405			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF47616,SSF52833									
aly725.12	Ras-related protein Rab-11A	GO:0008103,GO:0019730,GO:0030424,GO:0007165,GO:0007298,GO:0001745,GO:0055038,GO:0031982,GO:0005771,GO:0016020,GO:0000922,GO:0007080,GO:2000039,GO:0005794,GO:0003924,GO:0032154,GO:0010971,GO:0042998,GO:0072659,GO:0010634,GO:0070732,GO:0000916,GO:0043025,GO:0005828,GO:0032794,GO:0031175,GO:1990182,GO:0051223,GO:0048169,GO:0006886,GO:0006887,GO:0007349,GO:0016360,GO:0048471,GO:0048477,GO:0005525,GO:0030140,GO:0032482,GO:0045335,GO:0046664,GO:0007112,GO:0006897,GO:0030670,GO:0010796,GO:0030866,GO:0045169,GO:0000910,GO:0042078,GO:0055037,GO:0050807,GO:0005737,GO:0030953,GO:0031410,GO:0005635,GO:0005739,GO:0032403,GO:0032402,GO:0060187,GO:0072594,GO:0060627,GO:0048137,GO:0030718,GO:0005515,GO:0005802,GO:0042052,GO:0034334,GO:0090307,GO:0045202,GO:0030133,GO:0070062,GO:0031532,GO:0005813,GO:0005811,GO:0030723,GO:0048749,GO:0048599,GO:0036258,GO:0048210,GO:0007317,GO:0022416,GO:0005886,GO:0045478,GO:0051642,GO:0043195,GO:0090150,GO:0007394,GO:0045773,GO:0007391,GO:0005768	CG5771-PB				SM00173,SM00174,SM00175,SM00176	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly725.13	39S ribosomal protein L1, mitochondrial	GO:0005654,GO:0015934,GO:0044822,GO:0003735,GO:0005743,GO:0003723,GO:0005762,GO:0006412	CG7494-PA						PF00687				G3DSA:3.30.190.20,G3DSA:3.30.190.20,G3DSA:3.40.50.790	SSF56808									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly725.14	Probable G-protein coupled receptor 158	GO:0004930,GO:0016021,GO:0005575,GO:0008277,GO:0003674,GO:0005886,GO:0008150,GO:0072659	CG31195-PB										G3DSA:2.170.300.10,G3DSA:2.170.300.10										
aly725.15	Mitochondrial pyruvate carrier 1	GO:0050833,GO:0016021,GO:0006850,GO:0005739,GO:0031305,GO:0005743,GO:0006090	CG14290-PB						PF03650														
aly725.16	Glandular kallikrein-12, submandibular/renal	GO:0004252,GO:0006508	CG17477-PA				SM00020		PF00089	PS50240		PS00135	G3DSA:2.40.10.10	SSF50494									
aly725.17	Ras-related protein Rab-18	GO:0005794,GO:0007420,GO:0071782,GO:0031982,GO:0070062,GO:0006886,GO:0071786,GO:0003924,GO:0034389,GO:0032482,GO:0008360,GO:0007155,GO:0008152,GO:0019003,GO:0015031,GO:0001654,GO:0005525,GO:0043025,GO:0005769,GO:0016192	CG3129-PA				SM00176,SM00175,SM00174,SM00177,SM00173	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449	PS00675	G3DSA:3.40.50.300	SSF52540			REACT_11044							
aly725.18	Unknown		n/a																				
aly725.19	Unknown	GO:0007415,GO:0005515,GO:0016198,GO:0005576,GO:0003674,GO:0005887,GO:0007155,GO:0007157,GO:0007275	CG14334-PA				SM00409,SM00409		PF13927	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly725.2	Unknown		n/a												278~305								
aly725.20	Unknown		n/a																				
aly725.21	Transmembrane protein 135	GO:0016021	CG11737-PA																				
aly725.22	Tissue factor pathway inhibitor	GO:0005201,GO:0005604,GO:0004222,GO:0005615,GO:0009986,GO:0007596,GO:0030198,GO:0008270,GO:0004867,GO:0005578	CG33103-PE				SM00131,SM00131		PF00014,PF00014	PS50279,PS50279	PR00759,PR00759,PR00759		G3DSA:4.10.410.10,G3DSA:4.10.410.10	SSF57362,SSF57362									
aly725.3	Mitotic-spindle organizing protein 1	GO:0005813,GO:0005819,GO:0033566,GO:0008274	n/a						PF12554														
aly725.4	Mitochondrial import inner membrane translocase subunit Tim17 B	GO:0015450,GO:0006626,GO:0005739,GO:0031305,GO:0005743,GO:0005744,GO:0006886	CG40451-PA						PF02466														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly725.5	Trafficking protein particle complex subunit 1	GO:0005794,GO:0006888,GO:0016192,GO:0005801,GO:0017112,GO:0043547,GO:0030008,GO:0005783	CG1359-PA						PF04099				G3DSA:3.30.450.70	SSF64356									
aly725.6	Unknown	GO:0003674,GO:0031024,GO:0007099,GO:0005814,GO:0071539	CG5690-PA												453~498,627~647,401~421,513~596,675~709,48~68								
aly725.7	WD repeat-containing protein 44	GO:0005794,GO:0005829,GO:0048471,GO:0005515,GO:0010008	CG34133-PC				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400	PS50082,PS50294,PS50082,PS50294			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978									
aly725.8	Unknown		CG34133-PC																				
aly725.9	Glutathione S-transferase D1	GO:0005737,GO:0004364,GO:0018833,GO:0006749	CG10045-PA						PF13417,PF00043	PS50404,PS50405			G3DSA:1.20.1050.10,G3DSA:3.40.30.10	SSF47616,SSF52833									
aly7261.1	Fatty acyl-CoA reductase 1	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0046474,GO:0035336,GO:0008611	CG4020-PA						PF07993				G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735,SSF51735			REACT_22258						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7261.2	Putative fatty acyl-CoA reductase CG8306	GO:0080019,GO:0006629,GO:0016021,GO:0005777,GO:0012505,GO:0050062,GO:0010025,GO:0035336	CG14893-PB						PF03015														
aly7261.3	Fatty acyl-CoA reductase 1	GO:0016021,GO:0005778,GO:0080019,GO:0006629,GO:0008611	CG5065-PA						PF07993				G3DSA:3.40.50.720				REACT_22258						
aly7261.4	Unknown		n/a																				
aly7263.1	Sex peptide receptor	GO:0045434,GO:0008528,GO:0016021,GO:0048042,GO:0005886,GO:0007186	CG16752-PA						PF10324	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly727.1	E3 ubiquitin-protein ligase RNF25	GO:0051092,GO:0061630,GO:0005829,GO:0051059,GO:0016567,GO:0004842,GO:0008270,GO:0005515,GO:0016874,GO:0005634	CG13344-PC				SM00591,SM00184		PF05773,PF13639	PS50089,PS50908			G3DSA:3.30.40.10,G3DSA:3.10.110.10	SSF54495,SSF57850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly727.10	MutS protein homolog 4	GO:0006298,GO:0030983,GO:0007292,GO:0051026,GO:0003677,GO:0000228,GO:0010165,GO:0043570,GO:0006302,GO:0006301,GO:0005634,GO:0032138,GO:0032137,GO:0005524,GO:0031573,GO:0000403,GO:0045143,GO:0008094,GO:0000400,GO:0007283,GO:0001541,GO:0000795,GO:0007131,GO:0010224,GO:0042771,GO:0006311,GO:0045128,GO:0000406,GO:0000404,GO:0000710,GO:0032301,GO:0032302,GO:0003684	CG4215-PA				SM00534,SM00533		PF00488,PF05188			PS00486	G3DSA:3.40.50.300,G3DSA:1.10.1420.10	SSF48334,SSF52540	284~304									
aly727.11	Phosphoserine phosphatase	GO:0005737,GO:0006564,GO:0006563,GO:0048149,GO:0045433,GO:0016311,GO:0007422,GO:0004647,GO:0005509,GO:0007411,GO:0000287	CG3705-PA					TIGR00338,TIGR01488	PF00702				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000,G3DSA:1.10.150.210	SSF56784		00260+3.1.3.3,00680+3.1.3.3			UPA00135				
aly727.12	Sterile alpha motif domain-containing protein 11	GO:0042731,GO:0032093,GO:0000122,GO:0005634,GO:0007283,GO:0031935,GO:0005515,GO:0040008,GO:0043621	CG31868-PA				SM00454		PF00536	PS50105			G3DSA:1.10.150.50	SSF47769									
aly727.13	UNC93-like protein	GO:0016021,GO:0003009,GO:0005886	CG2121-PB						PF05978				G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly727.14	UNC93-like protein	GO:0016021,GO:0003009,GO:0005886	CG2121-PB						PF05978				G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly727.15	Transcription elongation factor SPT6	GO:0008023,GO:0050684,GO:0035101,GO:0042393,GO:0051147,GO:0003677,GO:0051028,GO:0032968,GO:0045191,GO:0006355,GO:0005634,GO:0006366,GO:0008380,GO:0006351,GO:0002805,GO:0044822,GO:0035363,GO:0016788,GO:0035327,GO:0006338,GO:0003700,GO:0005705,GO:0000176,GO:0005703,GO:0061086,GO:0003723,GO:0016032,GO:0010793,GO:0003682,GO:0006397	CG12225-PA				SM00316,SM00252		PF14639,PF14633,PF14635,PF14878,PF14632,PF14641,PF00575	PS50001,PS50126			G3DSA:1.10.10.650,G3DSA:3.30.505.10,G3DSA:1.10.3500.10,G3DSA:1.10.3500.10,G3DSA:1.10.3500.10,G3DSA:2.40.50.140,G3DSA:3.30.420.140,G3DSA:1.10.150.310,G3DSA:3.30.505.10	SSF55550,SSF47781,SSF55550,SSF47781,SSF158832,SSF158832,SSF53098,SSF50249	469~496		REACT_216						
aly727.16	AH receptor-interacting protein	GO:0005737,GO:0016020,GO:0006457,GO:0036004,GO:0008134,GO:0005829,GO:0017162,GO:0003713,GO:0051082,GO:0010738,GO:0005654,GO:0006805,GO:0022417,GO:0007165,GO:0004871,GO:0034751,GO:0006626,GO:0051344	CG1847-PC				SM00028,SM00028,SM00028		PF13414,PF00254	PS50293			G3DSA:1.25.40.10,G3DSA:3.10.50.40,G3DSA:3.10.50.40	SSF54534,SSF54534,SSF48452	185~205									
aly727.17	tRNA (uracil-5-)-methyltransferase homolog A	GO:0044822,GO:0000166,GO:0008173,GO:0003676,GO:0006396,GO:0003729	CG3808-PA						PF05958	PS51687		PS01230,PS01231	G3DSA:3.30.70.330,G3DSA:3.40.50.150	SSF53335,SSF53335,SSF54928	168~188								
aly727.18	Tyramine beta-hydroxylase	GO:0006589,GO:0040011,GO:0005507,GO:0030728,GO:0071927,GO:0048149,GO:0043059,GO:0016715,GO:0002118,GO:0004500,GO:0007612,GO:0007613,GO:0050795,GO:0005575,GO:0048047,GO:0007629,GO:0002121,GO:0008049,GO:0008345,GO:0016021,GO:0055114	CG1543-PB				SM00664		PF03712,PF03351,PF01082	PS50836	PR00767,PR00767,PR00767,PR00767,PR00767,PR00767	PS00084	G3DSA:2.60.120.310,G3DSA:2.60.120.230	SSF49742,SSF49742									
aly727.19	Cold shock domain-containing protein CG9705	GO:0005575,GO:0006355,GO:0048813,GO:0003677	CG9705-PB				SM00357		PF00313				G3DSA:2.40.50.140	SSF50249									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly727.2	Switch-associated protein 70	GO:0005856,GO:0008064,GO:0032233,GO:0030835,GO:0030027,GO:1902309,GO:0005829,GO:0045190,GO:0051017,GO:0007204,GO:0016444,GO:0005575,GO:0003674,GO:0005886,GO:0003677,GO:0060754,GO:0008150,GO:0033633,GO:0005634,GO:0005524,GO:0032880	CG43867-PK				SM00233		PF00169	PS50003			G3DSA:2.30.29.30	SSF50729	400~477,342~382								
aly727.20	Huntingtin-interacting protein 1	GO:0016020,GO:0030154,GO:0097190,GO:0072583,GO:0048268,GO:0005200,GO:0048260,GO:0042981,GO:0030136,GO:0030665,GO:0005634,GO:0005543,GO:0003779,GO:0005794,GO:0006919,GO:0006915,GO:0030276,GO:0007010,GO:0043231,GO:0035091,GO:0005856,GO:0005737,GO:0006355,GO:0006351	CG10971-PA				SM00273		PF07651,PF01608	PS50942,PS50945			G3DSA:1.25.40.90	SSF48464	498~549,600~659,355~375,771~791,554~595,387~414								
aly727.21	FACT complex subunit Ssrp1	GO:0005730,GO:0051101,GO:0035101,GO:0006281,GO:0000217,GO:0006355,GO:0003697,GO:0003727,GO:0031492,GO:0006260,GO:0003723,GO:0005515,GO:0003677,GO:0005694,GO:0022008,GO:0001672,GO:0005634,GO:0043621,GO:0006351	CG4817-PA				SM00398		PF03531,PF00505,PF08512	PS50118	PR00887,PR00887,PR00887,PR00887,PR00887,PR00887,PR00887,PR00887,PR00887		G3DSA:1.10.30.10,G3DSA:2.30.29.30	SSF50729,SSF47095	621~641,594~614								
aly727.22	Mobility group protein 1A	GO:0005634,GO:0005694,GO:0003677	CG17921-PB				SM00398		PF00505	PS50118			G3DSA:1.10.30.10	SSF47095	53~73								
aly727.23	Target of rapamycin complex subunit lst8	GO:0005737,GO:0045793,GO:0005834,GO:0031929,GO:0003924,GO:0005515	CG3004-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50082,PS50294,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly727.24	ADP-ribosylation factor-binding protein GGA1	GO:0005737,GO:0006892,GO:0016020,GO:0016192,GO:0005794,GO:0006886,GO:0005802,GO:0032050,GO:0043231,GO:0005654,GO:0045732,GO:1901998,GO:0005515,GO:0030131,GO:0048471,GO:0010008,GO:0008565,GO:0005829,GO:0030136	CG3002-PB				SM00809,SM00288		PF00790,PF03127,PF02883	PS50909,PS50180,PS50179			G3DSA:1.20.5.170,G3DSA:2.60.40.1230,G3DSA:1.20.58.160,G3DSA:1.25.40.90	SSF48464,SSF49348,SSF89009	192~212								
aly727.25	Protein EMRE homolog, mitochondrial	GO:0050829,GO:0016021,GO:0045089,GO:0005739	CG17680-PA						PF10161														
aly727.26	Protein flightless-1	GO:0030239,GO:0007629,GO:0051014,GO:0003779,GO:0010004,GO:0005509,GO:0005515,GO:0007527	CG1484-PA				SM00262,SM00262,SM00262,SM00262,SM00262,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00364,SM00364,SM00364,SM00364,SM00364,SM00364		PF13855,PF13855,PF00626,PF00626,PF00626,PF00626	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR00597,PR00597,PR00597,PR00597		G3DSA:3.80.10.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10	SSF55753,SSF55753,SSF52058,SSF55753,SSF55753,SSF55753,SSF55753,SSF52058	58~78								
aly727.27	Mitochondrial import receptor subunit TOM22 homolog	GO:0015450,GO:0045040,GO:0006886,GO:0005739,GO:0008320,GO:0005742,GO:0005743,GO:0005741,GO:0016021	CG14981-PA						PF04281														
aly727.28	Inositol hexakisphosphate kinase 2	GO:0005737,GO:0006468,GO:0000832,GO:0008440,GO:0000828,GO:0005634,GO:0006817,GO:0045111,GO:0043065,GO:0030308,GO:0046488,GO:0046854,GO:0052723,GO:0052724,GO:0005524	CG10082-PA						PF03770					SSF56104,SSF56104,SSF56104									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly727.29	Unknown		n/a												196~223,153~173,59~79								
aly727.3	IQ domain-containing protein D		n/a							PS50096					70~122,268~288,185~226								
aly727.30	Unknown		n/a												29~49								
aly727.31	Ribonuclease P protein subunit p20	GO:0005737,GO:0030677,GO:0008033,GO:0005515,GO:0005730,GO:0005634,GO:0004526,GO:0030678,GO:0090502,GO:0003676,GO:0044822	CG33931-PA			PIRSF036572			PF12328				G3DSA:3.30.110.20	SSF82704										
aly727.32	Unknown		n/a																				
aly727.33	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly727.34	Unknown		n/a																				
aly727.35	Unknown		n/a																				
aly727.36	Unknown		n/a																				
aly727.37	Unknown		n/a																				
aly727.38	Huntingtin-interacting protein 1	GO:0016020,GO:0030154,GO:0097190,GO:0072583,GO:0048268,GO:0005200,GO:0048260,GO:0042981,GO:0030136,GO:0030665,GO:0005634,GO:0005543,GO:0003779,GO:0005794,GO:0006919,GO:0006915,GO:0030276,GO:0007010,GO:0043231,GO:0035091,GO:0005856,GO:0005737,GO:0006355,GO:0006351	CG10971-PA				SM00307		PF01608	PS50945			G3DSA:1.20.1410.10	SSF109885										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly727.39	Unknown		n/a												250~376,381~408,431~458,130~160,49~108,179~206,6~26								
aly727.4	Unknown		n/a																				
aly727.5	Coiled-coil domain-containing protein 65		CG30259-PA						PF14772						129~149								
aly727.6	General odorant-binding protein 71	GO:0005549,GO:0006810,GO:0007608,GO:0050896,GO:0007606,GO:0005576	CG13517-PB						PF01395				G3DSA:1.10.238.20	SSF47565									
aly727.7	Unknown		n/a												51~71,115~142								
aly727.8	Unknown		n/a						PF08661				G3DSA:2.40.50.140	SSF50249									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly727.9	Pre-mRNA-processing-splicing factor 8	GO:0016607,GO:0000386,GO:0000244,GO:0030619,GO:0097157,GO:0071011,GO:0030620,GO:0030623,GO:0016020,GO:0044822,GO:0000398,GO:0005682,GO:0070530,GO:0022008,GO:0005634,GO:0071013,GO:0005681,GO:0017070	CG8877-PA				SM00232		PF08083,PF10598,PF01398,PF08084,PF08082,PF12134,PF10596,PF10597					SSF53098,SSF53098	1419~1439								
aly72758.1	Zinc finger protein 706	GO:0005737,GO:0005634,GO:1902455,GO:0045892,GO:0006417,GO:0046872	CG15715-PA						PF04419				G3DSA:4.10.1050.10	SSF118359									
aly72758.2	Unknown		n/a																				
aly728.1	Protocadherin Fat 4	GO:0048565,GO:0016339,GO:0072307,GO:0007155,GO:0007009,GO:0004872,GO:0050829,GO:0005925,GO:0021987,GO:0045177,GO:0007156,GO:0070062,GO:0007431,GO:0016021,GO:0001822,GO:0022008,GO:0005509,GO:0009925,GO:0048477,GO:0043931,GO:0045089,GO:0007442,GO:0035329,GO:0003007,GO:0060122,GO:0005887,GO:0005886,GO:0001658,GO:0007157,GO:0050839,GO:0001736,GO:0007424,GO:0007440,GO:0030950,GO:0042247,GO:0005622,GO:0045571	CG7749-PD							PS50268		PS00232	G3DSA:2.60.40.60	SSF49313									
aly728.10	UPF0691 protein C9orf116	GO:0005575,GO:0032313,GO:0003674,GO:0008150,GO:0005097	CG12816-PA						PF14892														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly728.11	Synapsin	GO:0008021,GO:0008049,GO:0043195,GO:0048149,GO:0051124,GO:0016079,GO:0030054,GO:0007613,GO:0003824,GO:0008306,GO:0045202,GO:0007269,GO:0009408,GO:0071632,GO:0072553,GO:0005524,GO:0008355	CG3985-PD						PF02078,PF02750	PS50975	PR01368,PR01368,PR01368,PR01368,PR01368,PR01368		G3DSA:3.30.470.20,G3DSA:3.30.470.20,G3DSA:3.40.50.20,G3DSA:3.30.1490.20	SSF56059,SSF52440			REACT_13685						
aly728.12	Unknown		CG12814-PE				SM00241		PF00100	PS51034													
aly728.13	Carboxypeptidase E	GO:0004181,GO:0004185,GO:0030658,GO:0005576,GO:0008270,GO:0006508	CG4678-PE				SM00631		PF13620,PF00246		PR00765,PR00765,PR00765	PS00132,PS00133	G3DSA:3.40.630.10,G3DSA:2.60.40.1120	SSF53187,SSF49464									
aly728.14	Glutamate receptor ionotropic, delta-2	GO:0045211,GO:0009593,GO:0008328,GO:0035235,GO:0016021,GO:0015276,GO:0005234,GO:0034220,GO:0030054,GO:0005886,GO:0030425,GO:0035249,GO:0004970	CG33492-PC						PF10613				G3DSA:1.10.287.70,G3DSA:3.40.190.10	SSF53850,SSF53850									
aly728.15	Protein THEM6	GO:0005575,GO:0008150,GO:0005576,GO:0003674	CG4666-PA						PF13279,PF13279				G3DSA:3.10.129.10,G3DSA:3.10.129.10	SSF54637,SSF54637									
aly728.16	Doublesex- and mab-3-related transcription factor A2	GO:0003700,GO:0006355,GO:0005634,GO:0046872,GO:0043565	CG5737-PA				SM00301		PF00751,PF03474	PS50809		PS40000	G3DSA:4.10.1040.10	SSF82927,SSF46934									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly728.17	Integrator complex subunit 12	GO:0016180,GO:0022008,GO:0008270,GO:0034472,GO:0032039	CG5491-PA				SM00249		PF00628	PS50016		PS01359	G3DSA:3.30.40.10	SSF57903									
aly728.18	Unknown		n/a																				
aly728.19	GTP-binding protein Di-Ras2	GO:0016020,GO:0003924,GO:0005622,GO:0005575,GO:0005886,GO:0006184,GO:0007264,GO:0005525	CG8500-PA				SM00175,SM00173,SM00174	TIGR00231	PF00071	PS51421	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly728.2	Circumsporozoite protein	GO:0009986,GO:0042302	CG10625-PH						PF00379	PS51155		PS00233			1449~1449,754~774								
aly728.20	Constitutive coactivator of PPAR-gamma-like protein 2	GO:0044822	n/a											SSF88723									
aly728.21	GPN-loop GTPase 2	GO:0016787,GO:0022008,GO:0005525,GO:0000166	CG10222-PA						PF03029				G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly728.22	PDZ domain-containing protein GIPC1	GO:0008021,GO:0031647,GO:0032435,GO:0030139,GO:0048167,GO:0005903,GO:0031987,GO:0031982,GO:0009966,GO:0016020,GO:0001965,GO:0032467,GO:0043542,GO:0006605,GO:0014047,GO:0030165,GO:0005938,GO:0012506,GO:0007268,GO:0008340,GO:0001736,GO:0030511,GO:0070062,GO:0043197,GO:0043198,GO:0005829,GO:0016055,GO:0005515	CG11546-PA			PIRSF038083	SM00228			PS50106			G3DSA:2.30.42.10	SSF50156										
aly728.23	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	GO:0035774,GO:0007507,GO:0008152,GO:0042594,GO:0042182,GO:0008410,GO:0014823,GO:0042493,GO:0005739,GO:0009725,GO:0045471,GO:0044281,GO:0008260,GO:0060612,GO:0005759,GO:0044255,GO:0042803,GO:0046952,GO:0007584,GO:0046950,GO:0007420	CG1140-PA			PIRSF000858	SM00882,SM00882	TIGR02429,TIGR02428	PF01144,PF01144			PS01274,PS01273	G3DSA:3.40.810.20,G3DSA:3.40.1080.10	SSF100950,SSF100950		00650+2.8.3.5,00280+2.8.3.5,00072+2.8.3.5			UPA00929				
aly728.24	Unknown		n/a																				
aly728.25	39S ribosomal protein L20, mitochondrial	GO:0005840,GO:0005739,GO:0019843,GO:0003735,GO:0005762,GO:0006412	CG11258-PA					TIGR01032	PF00453		PR00062,PR00062,PR00062		G3DSA:1.10.1900.20	SSF74731									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly728.26	Protein PET117 homolog, mitochondrial	GO:0005739	CG11562-PA						PF15786														
aly728.27	Pancreatic triacylglycerol lipase (Fragment)	GO:0004806,GO:0007476,GO:0016042,GO:0005575,GO:0005576,GO:0046872,GO:0016298	CG5966-PA			PIRSF000865			PF00151		PR00823,PR00823,PR00823,PR00823,PR00823,PR00821,PR00821,PR00821,PR00821,PR00821,PR00821		G3DSA:2.60.60.20,G3DSA:3.40.50.1820	SSF53474		00561+3.1.1.3		PWY-6857					
aly728.28	Unknown		n/a																				
aly728.29	Translation initiation factor eIF-2B subunit gamma	GO:0005737,GO:0051716,GO:0005851,GO:0005829,GO:0032057,GO:0005085,GO:0016779,GO:0009749,GO:0006417,GO:0071456,GO:0014003,GO:0009408,GO:0043434,GO:0006413,GO:0006412,GO:0003743	CG8190-PA						PF00483,PF00132				G3DSA:2.160.10.10,G3DSA:3.90.550.10	SSF53448,SSF53448,SSF53448			REACT_17015						
aly728.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly728.30	Cell surface glycoprotein 1	GO:0007424,GO:0005201,GO:0051539,GO:0040005,GO:0005618,GO:0000272,GO:0030246,GO:0007475,GO:0008362,GO:0046331,GO:0005509,GO:0030115,GO:0031012,GO:0005578,GO:0005576	CG33196-PQ						PF16043														
aly728.31	Unknown	GO:0006030,GO:0005576,GO:0008061	CG13643-PD				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625	223~243								
aly728.32	Unknown		n/a																				
aly728.33	Unknown		CG10476-PA											SSF55729									
aly728.34	Glutamate receptor ionotropic, NMDA 3A	GO:0005262,GO:0007616,GO:0016358,GO:0030425,GO:0045202,GO:0060134,GO:0004972,GO:0035249,GO:0030054,GO:0016594,GO:0045471,GO:0072375,GO:0042331,GO:0016021,GO:0016020,GO:0007476,GO:0043005,GO:0008355,GO:0043025,GO:0042802,GO:0050975,GO:0008328,GO:0035235,GO:0006811,GO:0006816,GO:0005234,GO:0034220,GO:0008306,GO:0014069,GO:0005886,GO:0051721,GO:0045211,GO:0017146	CG2902-PA				SM00079,SM00918		PF00060,PF00497				G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.190.10,G3DSA:3.40.50.2300,G3DSA:1.10.287.70	SSF53850,SSF53850										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly728.35	Multiple inositol polyphosphate phosphatase 1	GO:0008969,GO:0005783,GO:0043647,GO:0016311,GO:0052826,GO:0004721,GO:0006797,GO:0001503,GO:0005788,GO:0034417,GO:0044281,GO:0030282,GO:0003993,GO:0070062	CG4123-PB						PF00328				G3DSA:3.40.50.1240	SSF53254									
aly728.36	Multiple inositol polyphosphate phosphatase 1	GO:0016791,GO:0052826,GO:0005788,GO:0004721,GO:0034417,GO:0003993	CG4123-PB			PIRSF000894			PF00328				G3DSA:3.40.50.1240	SSF53254									
aly728.37	Ras-related protein Rab-3	GO:0008021,GO:0007269,GO:0006904,GO:0007165,GO:0030054,GO:0030667,GO:0048789,GO:0031982,GO:0006886,GO:0048786,GO:0017157,GO:0009306,GO:0003924,GO:0006913,GO:0032482,GO:0048172,GO:0008152,GO:0005886,GO:0031630,GO:0016192,GO:0016079,GO:0048790,GO:0015031,GO:0005525,GO:0005768,GO:0045202	CG7576-PA				SM00176,SM00175,SM00173,SM00174	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly728.38	SH3 and cysteine-rich domain-containing protein 3	GO:0045793,GO:0019992,GO:0007519,GO:0005622,GO:0005575,GO:0046331,GO:0035556,GO:0046872,GO:0007274,GO:0003009	CG43729-PJ				SM00326,SM00109		PF00018,PF00130	PS50081,PS50002		PS00479	G3DSA:3.30.60.20,G3DSA:2.30.30.40	SSF57889,SSF103657,SSF50044	556~583,292~312								
aly728.39	Transcription cofactor vestigial-like protein 4	GO:0006355,GO:0005634,GO:0006351	n/a				SM00711,SM00711,SM00711		PF15245														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly728.4	Unknown	GO:0002009,GO:0005605,GO:0007507,GO:0035088,GO:0007508,GO:0061343,GO:0016477,GO:0005578	CG5700-PB																				
aly728.40	Calcium/calmodulin-dependent protein kinase type II alpha chain	GO:0007619,GO:0007616,GO:0008582,GO:0007268,GO:0030425,GO:0007611,GO:0008049,GO:0005737,GO:0048786,GO:0004674,GO:0004672,GO:0005524,GO:0006468,GO:0060278,GO:0007528,GO:0045211,GO:0005886,GO:0030424,GO:0005954,GO:0051489,GO:0004683,GO:0005516	CG18069-PJ				SM00220		PF00069,PF08332	PS50011		PS00108,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:3.10.450.50	SSF54427,SSF56112			REACT_13685						
aly728.41	Torsin-2A	GO:0051085,GO:0005788,GO:0005524	CG4880-PA										G3DSA:3.40.50.300	SSF52540									
aly728.42	Protein aurora borealis	GO:0005737,GO:0045167,GO:0007422,GO:0005634,GO:0032147,GO:0005515,GO:0007067,GO:0051301	CG6897-PA						PF15280		PR02038,PR02038,PR02038,PR02038,PR02038												
aly728.43	Pancreatic triacylglycerol lipase	GO:0004806,GO:0007476,GO:0016042,GO:0005575,GO:0005576,GO:0046872,GO:0016298	CG5966-PA			PIRSF000865			PF00151		PR00821,PR00821,PR00821,PR00821,PR00823,PR00823,PR00823		G3DSA:3.40.50.1820	SSF53474		00561+3.1.1.3		PWY-6857					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly728.44	THUMP domain-containing protein 1 homolog	GO:0005575,GO:0008150,GO:0003674,GO:0003723	CG15014-PA				SM00981		PF02926	PS51165				SSF143437	262~282								
aly728.45	Unknown		n/a																				
aly728.46	Unknown		n/a																				
aly728.47	Metalloproteinase inhibitor 3	GO:0035202,GO:0007426,GO:0042331,GO:0007472,GO:0060232,GO:0030425,GO:0046872,GO:0005576,GO:0071711,GO:0007155,GO:0008191,GO:0048526,GO:0005578	CG6281-PB				SM00206		PF00965	PS50189			G3DSA:2.40.50.120,G3DSA:3.90.370.10	SSF50242									
aly728.48	Fas-associated death domain protein	GO:0005737,GO:0045089,GO:0005123,GO:0006919,GO:0006963,GO:0006915,GO:0050700,GO:0006952,GO:0007291,GO:0007165,GO:0005515,GO:0006955,GO:0050829,GO:0002230,GO:0061057,GO:0042981	CG12297-PA						PF01335,PF00531	PS50017			G3DSA:1.10.533.10,G3DSA:1.10.533.10	SSF47986,SSF47986,SSF47986									
aly728.49	Sodium channel protein Nach	GO:0035002,GO:0016021,GO:0005272,GO:0035725,GO:0006814	CG33508-PA						PF00858				G3DSA:2.60.470.10,G3DSA:2.60.470.10,G3DSA:1.10.287.770										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly728.5	Serine/arginine repetitive matrix protein 1	GO:0035145,GO:0071011,GO:0071013,GO:0000398,GO:0005634,GO:0008380,GO:0006397	CG11274-PA				SM00311		PF01480	PS51025			G3DSA:1.20.1390.10	SSF101233	266~309,821~841								
aly728.50	Unknown		n/a																				
aly728.6	Phosphoribosylformylglycinamidine synthase	GO:0005737,GO:0009156,GO:0004642,GO:0006541,GO:0006189,GO:0006164,GO:0046872,GO:0005524	CG9127-PA	MF_00419				TIGR01735	PF13507,PF02769,PF02769,PF00586	PS51273			G3DSA:3.30.1330.10,G3DSA:3.30.1330.10,G3DSA:3.40.50.880	SSF109736,SSF52317,SSF56042,SSF55326,SSF56042,SSF55326,SSF82697		00230+6.3.5.3	REACT_1698	PWY-6121,PWY-6122,PWY-6277	UPA00074				
aly728.7	Fas-associated death domain protein	GO:0005737,GO:0045089,GO:0005123,GO:0006919,GO:0006963,GO:0006915,GO:0050700,GO:0006952,GO:0007291,GO:0007165,GO:0005515,GO:0006955,GO:0050829,GO:0061057,GO:0002230	CG12297-PA						PF01335,PF00531	PS50017			G3DSA:1.10.533.10,G3DSA:1.10.533.10	SSF47986,SSF47986,SSF47986	157~184								
aly728.8	Glycine dehydrogenase (decarboxylating), mitochondrial	GO:0005960,GO:0004375,GO:0019464,GO:0006546,GO:0005739,GO:0030170,GO:0016829,GO:0055114,GO:0042803	CG3999-PA	MF_00711				TIGR00461	PF01212,PF02347				G3DSA:3.40.640.10,G3DSA:3.40.640.10	SSF53383,SSF53383,SSF53383	1000~1003	00260+1.4.4.2							
aly728.9	TBC1 domain family member 30	GO:0032313,GO:0005097	CG42795-PG				SM00164		PF00566,PF15733	PS50086			G3DSA:1.10.8.270	SSF47923,SSF47923	127~147								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7286.1	Low-density lipoprotein receptor-related protein	GO:0030334,GO:0006897,GO:0042395,GO:0040017,GO:0016324,GO:0040018,GO:0016021,GO:0002119,GO:0005041,GO:0015918,GO:0030139,GO:0048812,GO:0005509,GO:0005515,GO:0005886,GO:0015248,GO:0005905	CG31092-PE				SM00192		PF00057	PS50068			G3DSA:4.10.400.10	SSF57424										
aly731.1	Inactive pancreatic lipase-related protein 1	GO:0051384,GO:0004806,GO:0005615,GO:0031016,GO:0005509,GO:0043434,GO:0016298,GO:0006629	CG17292-PA						PF00151		PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly731.10	Protein FAM89A		n/a																				
aly731.11	Protein dpy-30 homolog	GO:0016197,GO:0005794,GO:0030317,GO:0005802,GO:0035097,GO:0005654,GO:0006355,GO:0048188,GO:0006351,GO:0051568,GO:0005634,GO:0042802,GO:0042803	CG11591-PA						PF05186														
aly731.12	Radial spoke head 1 homolog	GO:0035082,GO:0031514,GO:0005829,GO:0051321,GO:0005634	CG5458-PA				SM00698,SM00698,SM00698,SM00698,SM00698,SM00698		PF02493,PF02493,PF02493,PF02493,PF02493,PF02493,PF02493				G3DSA:2.20.110.10	SSF82185									
aly731.13	Coiled-coil domain-containing protein 85C	GO:0016246,GO:0007275	CG17265-PA						PF10226						317~337,228~262,168~202								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly731.14	Pancreatic triacylglycerol lipase (Fragment)	GO:0004806,GO:0006629,GO:0052689,GO:0016042,GO:0005576,GO:0046872	CG6431-PC						PF00151		PR00821,PR00821,PR00821		G3DSA:3.40.50.1820	SSF53474									
aly731.15	RNA-binding protein 42	GO:0005737,GO:0071011,GO:0071013,GO:0000398,GO:0000166,GO:0003723,GO:0003676,GO:0022008,GO:0005634,GO:0003729	CG2931-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928									
aly731.16	Protein YIPF6	GO:0016021,GO:0016020	CG3652-PA						PF04893														
aly731.17	Alpha,alpha-trehalose-phosphate synthase [UDP-forming]	GO:0036168,GO:0034605,GO:0005811,GO:0005992,GO:0003825,GO:0036180,GO:0009405,GO:0030447	CG4104-PA					TIGR00685	PF02358,PF00982				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000,G3DSA:3.40.50.2000,G3DSA:3.40.50.2000	SSF56784,SSF53756									
aly731.18	Androgen-dependent TFPI-regulating protein	GO:0016021,GO:0005886	CG3625-PB						PF04750														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly731.19	ATP-binding cassette sub-family G member 1	GO:0009897,GO:0034375,GO:0034374,GO:0006909,GO:0055099,GO:0055037,GO:0017127,GO:0030301,GO:0034041,GO:0016887,GO:0042987,GO:1901998,GO:0055091,GO:0005548,GO:0042626,GO:0033993,GO:0016021,GO:0005739,GO:0005654,GO:0034436,GO:0034437,GO:0010745,GO:0010875,GO:0005524,GO:0033700,GO:0005794,GO:0005215,GO:0042803,GO:0043531,GO:0005886,GO:0010872,GO:0042632,GO:0043691,GO:0010033,GO:0008203,GO:0043190,GO:0019534,GO:0043231,GO:0032367,GO:0006355,GO:0033344,GO:0045542,GO:0046982,GO:0005768,GO:0010888	CG5853-PA				SM00382		PF01061,PF00005	PS50893		PS00211	G3DSA:3.40.50.300	SSF52540	623~627								
aly731.2	Ankyrin-1	GO:0045199,GO:0005200,GO:0005261,GO:0005262,GO:0007638,GO:0010638,GO:0072661,GO:0030425,GO:0034703,GO:0005929,GO:0007411,GO:0030506,GO:0030507,GO:0005856,GO:0031430,GO:0006888,GO:0005634,GO:0006887,GO:0005198,GO:0001964,GO:0030018,GO:0006812,GO:0010996,GO:0008381,GO:0050975,GO:0050974,GO:0042383,GO:0007605,GO:0050954,GO:0005216,GO:0006816,GO:0016323,GO:0014731,GO:0045211,GO:0019899,GO:0005886,GO:0040011,GO:0008093,GO:0007010,GO:0030673,GO:0051117,GO:0008092,GO:0043025,GO:0005829,GO:0070588,GO:0016529,GO:0007165	CG11020-PF				SM00248,SM00248		PF00520,PF00023,PF12796,PF12796,PF12796,PF12796,PF12796,PF12796,PF12796,PF13606	PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50297,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088	PR01415,PR01415,PR01097,PR01097,PR01097		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403,SSF48403,SSF48403			REACT_18266						
aly731.20	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly731.21	Unknown	GO:0005261,GO:0005262,GO:0007638,GO:0030425,GO:0034703,GO:0005929,GO:0030506,GO:0016020,GO:0001964,GO:0006812,GO:0010996,GO:0043025,GO:0006811,GO:0050975,GO:0050974,GO:0007605,GO:0050954,GO:0005216,GO:0006816,GO:0055085,GO:0040011,GO:0008092,GO:0008381,GO:0070588	CG11020-PF						PF00520														
aly731.3	Unknown		n/a																				
aly731.4	Acyl-CoA synthetase family member 2, mitochondrial	GO:0006631,GO:0005777,GO:0005739,GO:0004467,GO:0008152,GO:0016874,GO:0005875,GO:0005524	CG12512-PA						PF00501,PF13193			PS00455	G3DSA:2.30.38.10,G3DSA:3.30.300.30,G3DSA:3.40.50.980,G3DSA:3.40.50.980	SSF56801									
aly731.5	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463		G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly731.6	RNA-binding protein 7	GO:0003729,GO:0051321,GO:0003723,GO:0003676,GO:0000166	CG11454-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly731.7	Transmembrane protein 136	GO:0016021	n/a				SM00724		PF03798	PS50922													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly731.8	Protein FAM179B	GO:0005575,GO:0003674,GO:0008150	CG42399-PB						PF02985				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371										
aly731.9	Anaphase-promoting complex subunit 11	GO:0005737,GO:0045842,GO:0090302,GO:0070979,GO:0000151,GO:0031145,GO:0000090,GO:0008270,GO:0005515,GO:0007067,GO:0004842,GO:0051301,GO:0005680	CG34440-PC						PF12861	PS50089			G3DSA:3.30.40.10	SSF57850					UPA00143				
aly73144.1	GDNF-inducible zinc finger protein 1	GO:0005737,GO:0005794,GO:0006351,GO:0000122,GO:0005634,GO:0005730,GO:0043565,GO:0005654,GO:0045892,GO:0008270,GO:0003677,GO:0001658,GO:0001206,GO:0000978,GO:0046872,GO:0001078,GO:0000980	CG14711-PA				SM00355,SM00355,SM00355,SM00868		PF07776	PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57716									
aly73225.1	V-type proton ATPase subunit B	GO:0016820,GO:0015992,GO:0007035,GO:0046034,GO:0015991,GO:0033181,GO:0033180,GO:0000221,GO:0046961,GO:0005886,GO:0005903,GO:0048471,GO:0005769,GO:0005524	CG17369-PC						PF00006				G3DSA:3.40.50.300	SSF52540		00195+3.6.3.14,00190+3.6.3.14		PWY-7219					
aly73254.1	Unknown	GO:0003824,GO:0008152	CG6236-PB						PF02995				G3DSA:3.40.720.10	SSF53649,SSF53649									
aly7329.1	Myrosinase 1	GO:0019137,GO:0046872,GO:0005975,GO:0004553	CG9701-PA						PF00232				G3DSA:3.20.20.80	SSF51445									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7341.1	Rho-related BTB domain-containing protein 1	GO:0005575,GO:0003924,GO:0005622,GO:0035011,GO:0005515,GO:0007264,GO:0005525	CG5701-PB				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695									
aly7341.2	H/ACA ribonucleoprotein complex subunit 2-like protein	GO:0005732,GO:0005730,GO:0031118,GO:0030559,GO:0006364,GO:0009267,GO:0030515	CG5258-PB						PF01248		PR00881,PR00881,PR00881		G3DSA:3.30.1330.30	SSF55315									
aly7341.3	H/ACA ribonucleoprotein complex subunit 2-like protein	GO:0005732,GO:0005730,GO:0031118,GO:0030559,GO:0006364,GO:0030515	CG5258-PB																				
aly7341.4	ADP-ribosylation factor-like protein 3	GO:0035147,GO:0042073,GO:0015630,GO:0005876,GO:0005737,GO:0042461,GO:0070062,GO:0005813,GO:0005634,GO:0001822,GO:0005525,GO:0005794,GO:0032391,GO:0042384,GO:0060271,GO:0008017,GO:0003924,GO:0005881,GO:0072372,GO:0007264,GO:0000910,GO:0006892,GO:0007224,GO:0030496,GO:0000139,GO:0019003,GO:0015031	CG6560-PA				SM00177,SM00178	TIGR00231	PF00025	PS51417	PR00328,PR00328,PR00328,PR00328		G3DSA:3.40.50.300	SSF52540									
aly7341.5	Unknown	GO:0003674,GO:0005615,GO:0032504	CG8420-PA												474~475								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7349.1	AT-rich interactive domain-containing protein 5B	GO:0044212,GO:0005634,GO:0006351,GO:0051091,GO:0060612	n/a																				
aly736.1	Protein G12		CG4398-PA						PF06757						142~162								
aly736.2	Unknown		CG4398-PA						PF06757						142~162								
aly736.3	Phosphatidylinositol N-acetylglucosaminyltransferase subunit H	GO:0017176,GO:0000506,GO:0006506	n/a						PF10181							00563+2.4.1.198			UPA00196				
aly736.4	Cilia- and flagella-associated protein 36	GO:0005737,GO:0042995,GO:0042384,GO:0005634	CG14367-PA						PF11527				G3DSA:1.20.1520.10										
aly736.5	Serine/threonine-protein phosphatase 4 regulatory subunit 3	GO:0005737,GO:0008105,GO:0006909,GO:0030289,GO:0016601,GO:0006281,GO:0005634,GO:0016020,GO:0055059,GO:0007391,GO:0005515,GO:0007405,GO:0000775	CG9351-PB						PF04802	PS50229			G3DSA:2.30.29.30	SSF50729,SSF48371,SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly736.6	INO80 complex subunit D	GO:0006310,GO:0006355,GO:0005634,GO:0006351,GO:0006281	n/a						PF13891														
aly736.7	Unknown		n/a																				
aly73680.1	Unknown		n/a						PF00431	PS01180			G3DSA:2.60.120.290	SSF49854									
aly7376.1	Unknown	GO:0000381,GO:0005634,GO:0007283,GO:0005515,GO:0048024,GO:0048025,GO:0005685,GO:0003729,GO:0006397	CG8912-PC						PF09005,PF09005						24~44								
aly7376.10	Eukaryotic translation initiation factor 2 subunit 1	GO:0043614,GO:0000049,GO:0005840,GO:0005850,GO:0005851,GO:0005829,GO:0044822,GO:0007052,GO:0043022,GO:0033290,GO:0001677,GO:0000022,GO:0005525,GO:0006413,GO:0005875,GO:0003743	CG9946-PB				SM00316		PF00575,PF07541	PS50126			G3DSA:3.30.70.1130,G3DSA:1.10.150.190,G3DSA:2.40.50.140	SSF110993,SSF116742,SSF50249	273~293								
aly7376.11	Collagen alpha 1(XXI) chain	GO:0005737,GO:0005201,GO:0005587,GO:0005581,GO:0007391,GO:0005604,GO:0005578,GO:0035848	CG4145-PC				SM00210		PF01391,PF01391,PF01391,PF01391					SSF49899										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7376.2	Transient receptor potential cation channel subfamily V member 6	GO:0016020,GO:0005261,GO:0005262,GO:0048060,GO:0034703,GO:0040040,GO:0070062,GO:0035898,GO:0048148,GO:0017158,GO:0001964,GO:0010996,GO:0006811,GO:0007608,GO:0007605,GO:0006812,GO:0005216,GO:0006816,GO:0007629,GO:0034220,GO:0005887,GO:0005886,GO:0009408,GO:0055085,GO:0043052,GO:0070588,GO:0005516,GO:0055074	CG4536-PA				SM00248,SM00248,SM00248,SM00248,SM00248		PF00520	PS50297,PS50088,PS50088			G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403	657~657								
aly7376.3	Unknown		n/a												624~644								
aly7376.4	Probable phenylalanine-tRNA ligase, mitochondrial	GO:0004826,GO:0000049,GO:0008033,GO:0006432,GO:0000287,GO:0005739,GO:0005759,GO:0005524	CG13348-PA					TIGR00469	PF01409,PF01409	PS50862			G3DSA:3.30.930.10,G3DSA:3.30.930.10	SSF54991,SSF55681,SSF55681		00970+6.1.1.20	REACT_71						
aly7376.5	Endonuclease G, mitochondrial	GO:0090502,GO:0043565,GO:0006915,GO:0000001,GO:0035234,GO:0000737,GO:0004521,GO:0004520,GO:0005739,GO:0005743,GO:0006261,GO:0003676,GO:0007286,GO:0006401,GO:0046872,GO:0006309,GO:0042803,GO:0004519	CG8862-PA				SM00477,SM00892		PF01223			PS01070	G3DSA:3.40.570.10	SSF54060									
aly7376.6	Unknown	GO:0003676	n/a				SM00980		PF05485	PS50950				SSF57716	673~693								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7376.7	Unknown		n/a																				
aly7376.8	Unknown		n/a																				
aly7376.9	Unknown		n/a						PF14214						824~844								
aly73793.1	Phosphoglucomutase-2	GO:0008973,GO:0005975,GO:0004614,GO:0005980,GO:0070062,GO:0005829,GO:0000287,GO:0016052,GO:0071704,GO:0005978,GO:0044281,GO:0004615,GO:0016868,GO:0006006,GO:0019388,GO:0046386	CG8073-PA						PF00408				G3DSA:3.30.310.50	SSF55957		00520+5.4.2.10		PWY-6749					
aly74.1	LIM and SH3 domain protein Lasp	GO:0070864,GO:0045856,GO:0015629,GO:0005829,GO:0031672,GO:0071689,GO:0003779,GO:0007279,GO:0007283,GO:0007291,GO:0045214,GO:0008270,GO:0005925,GO:0014881,GO:0030018	CG3849-PB				SM00132		PF00412	PS50023		PS00478	G3DSA:2.10.110.10	SSF57716									
aly74.2	Coiled-coil domain-containing protein 13	GO:0030030,GO:0005737,GO:0042995,GO:0005815	CG13032-PA												131~158,370~411,450~491,175~202,80~107,546~573,289~337								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly74.3	WD repeat-containing protein 7	GO:0008021,GO:0007035,GO:0005834,GO:0003924,GO:0002244,GO:0005515,GO:0008593,GO:0007186	CG17766-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400	PS50294,PS50294,PS50082,PS50082		PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50969,SSF50969,SSF50969,SSF50978,SSF50978,SSF50978									
aly74.4	Unknown	GO:0005834,GO:0007186,GO:0007035,GO:0003924,GO:0008593	CG17766-PA																				
aly74.5	Cuticle protein 1	GO:0005576	n/a																				
aly7429.1	Protein takeout	GO:0007631,GO:0007623,GO:0005615,GO:0007617,GO:0005576,GO:0042594,GO:0042595,GO:0008343,GO:0008049,GO:0007622	CG11854-PB				SM00700		PF06585														
aly74334.1	Cullin-1	GO:1990452,GO:0009887,GO:0031625,GO:0008283,GO:0006915,GO:0031146,GO:0016322,GO:0046627,GO:0006513,GO:0006511,GO:0019005,GO:0031461,GO:0032007,GO:0007095,GO:0000152	CG1877-PC						PF00888				G3DSA:1.20.1310.10	SSF74788									
aly74489.1	PiggyBac transposable element-derived protein 3		n/a						PF13843														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7450.1	Unknown		n/a																				
aly7450.2	Insulin-degrading enzyme	GO:0005737,GO:0048638,GO:0004222,GO:0005777,GO:0090062,GO:0045089,GO:0002021,GO:1901143,GO:0008270,GO:0005886,GO:0008340,GO:0050829,GO:0045926,GO:0014067,GO:0046872,GO:0006508,GO:0046662	CG5517-PB						PF05193				G3DSA:3.30.830.10	SSF63411									
aly74519.1	Unknown		n/a																				
aly74580.1	Unknown	GO:0033109,GO:0007443,GO:0007427,GO:0007494,GO:0008258,GO:0007424,GO:0008289,GO:0007391,GO:0005622,GO:0035024,GO:0008586,GO:0007173,GO:0005938,GO:0035277,GO:0035160,GO:0005100,GO:0007266,GO:0016323,GO:0007274,GO:0048814	CG31319-PA																				
aly74585.1	PiggyBac transposable element-derived protein 4		n/a						PF13843														
aly74675.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly747.1	Regulator of G protein signaling loco	GO:0055059,GO:0010001,GO:0005886,GO:0008105,GO:0007419,GO:0008277,GO:0007303,GO:0003015,GO:0000578,GO:0008069,GO:0007049,GO:0005737,GO:0043547,GO:0005057,GO:0019991,GO:0045179,GO:0016324,GO:0001965,GO:0060857,GO:0007186,GO:0038032,GO:0032291,GO:0005092,GO:0050790,GO:0005096,GO:0050832,GO:0014045,GO:0009786,GO:0007310,GO:0009408,GO:0006979,GO:0042594,GO:0030866,GO:0005515	CG43707-PE				SM00228,SM00233,SM00233		PF00595,PF00169,PF00169	PS50106,PS50003			G3DSA:2.30.29.30,G3DSA:2.30.42.10,G3DSA:2.30.29.30	SSF50156,SSF50729,SSF50729										
aly747.2	Protein bowel	GO:0007362,GO:0007442,GO:0006351,GO:0048617,GO:0009880,GO:0007480,GO:0005634,GO:0000122,GO:0016348,GO:0045944,GO:0046331,GO:0045892,GO:0035220,GO:0003676,GO:0007366,GO:0046872,GO:0048619,GO:0000981,GO:0045893	CG10021-PB				SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667	720~726									
aly747.3	Protein odd-skipped	GO:0007443,GO:0007389,GO:0007350,GO:0007366,GO:0000122,GO:0003700,GO:0005634,GO:0016348,GO:0006357,GO:0045944,GO:0045893,GO:0003676,GO:0003677,GO:0045892,GO:0046872,GO:0006351	CG3851-PA				SM00355,SM00355,SM00355,SM00355		PF13912,PF00096,PF00096	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly747.4	Protein odd-skipped	GO:0007443,GO:0007389,GO:0007350,GO:0007366,GO:0000122,GO:0003700,GO:0005634,GO:0016348,GO:0006357,GO:0045944,GO:0045893,GO:0003676,GO:0003677,GO:0045892,GO:0046872,GO:0006351	CG3851-PA				SM00355,SM00355		PF13912	PS50157,PS50157		PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667	14~34									
aly747.5	Protein drumstick	GO:0007442,GO:0007440,GO:0048617,GO:0048619,GO:0016348,GO:0007366,GO:0006355,GO:0006351,GO:0003676,GO:0048565,GO:0046872,GO:0005634	CG10016-PC				SM00355,SM00355		PF00096,PF00096	PS50157,PS50157		PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly747.6	Protein argonaute-3	GO:0005737,GO:0043186,GO:0035194,GO:0005829,GO:0005739,GO:0060213,GO:0003723,GO:0003676,GO:0034584,GO:0007275,GO:0010529	CG40300-PD				SM00949,SM00950		PF02170,PF02171	PS50822,PS50821			G3DSA:2.170.260.10,G3DSA:3.30.420.10,G3DSA:3.40.50.2300	SSF101690,SSF53098									
aly747.7	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	GO:0005737,GO:0008026,GO:0051536,GO:0005739,GO:0016226,GO:0003676,GO:0005506,GO:0005524	CG32857-PA				SM00932		PF01106,PF08712				G3DSA:3.30.1370.70	SSF110836,SSF117916									
aly747.8	Unknown	GO:0008063,GO:0005576,GO:0005121	CG7104-PA						PF16077					SSF57501									
aly747.9	Unknown		n/a																				
aly7472.1	Monocarboxylate transporter 9	GO:0015355,GO:0016021,GO:0055085,GO:0015293,GO:0005886	CG8389-PB						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	504~519								
aly7472.2	NADH dehydrogenase [ubiqui] iron-sulfur protein 3, mitochondrial	GO:2001243,GO:0072593,GO:0030308,GO:0043209,GO:0008137,GO:0005634,GO:0005739,GO:0031966,GO:0005743,GO:0021762,GO:0005747,GO:0003954,GO:0055114	CG12079-PA						PF00329,PF00329					SSF143243									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7472.3	Lachesin	GO:0004714,GO:0005515,GO:0005886,GO:0007155,GO:0007169,GO:0031225	CG32791-PA				SM00408,SM00408,SM00408,SM00409,SM00409,SM00409		PF07679,PF07679,PF07679	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726	402~422								
aly7480.1	Glycogen debranching enzyme	GO:0005737,GO:0007584,GO:0051384,GO:0005975,GO:0005980,GO:0005978,GO:0005634,GO:0030247,GO:0004134,GO:0004135,GO:0005654,GO:0016529,GO:0016234,GO:0004133,GO:0043033,GO:0006006,GO:0005829,GO:0044281	CG9485-PB					TIGR01531	PF14699,PF14702,PF06202,PF14701				G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.20.20.80	SSF51445,SSF51445,SSF48208,SSF48208	448~475	00500+2.4.1.25+3.2.1.33		PWY-6724,PWY-7238,PWY-6737,PWY-5941					
aly7480.2	Uncharacterized protein HI_1014	GO:0050662,GO:0003978,GO:0044237,GO:0003824	CG5955-PA						PF01370				G3DSA:3.40.50.720,G3DSA:3.90.25.10	SSF51735									
aly7480.3	Unknown		n/a						PF08208						561~581								
aly7480.4	40S ribosomal protein S4	GO:0005840,GO:0051297,GO:0005622,GO:0003735,GO:0007052,GO:0003723,GO:0000022,GO:0019843,GO:0022627,GO:0006412,GO:0051298	CG11276-PA	MF_00485		PIRSF002116	SM00739,SM00363		PF01479,PF00467,PF16121,PF08071,PF00900	PS50889		PS00528		SSF55174									
aly7483.1	Lipase 3	GO:0048812,GO:0004806,GO:0006629,GO:0016788,GO:0016042	CG31871-PA			PIRSF000862			PF04083				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly74900.1	Retinol dehydrogenase 13	GO:0042462,GO:0016614,GO:0010842,GO:0005743,GO:0008152,GO:0009644,GO:0016491	CG7675-PB						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735									
aly75044.1	Monoacylglycerol lipase ABHD12	GO:0046464,GO:0016021,GO:0047372	CG15111-PB										G3DSA:3.40.50.1820	SSF53474									
aly7527.1	Unknown		n/a												34~89								
aly7546.1	Zinc finger protein OZF	GO:0005737,GO:0005730,GO:0051726,GO:0003676,GO:0003677,GO:0046872	CG11247-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF12171,PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly7546.2	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0022857,GO:0005886,GO:0055085	CG4797-PB						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly755.1	Ubiquitin carboxyl-terminal hydrolase 8	GO:0019897,GO:0090263,GO:0071108,GO:0008587,GO:0045880,GO:0005737,GO:0043161,GO:0000281,GO:0036459,GO:0005654,GO:0006511,GO:0016579,GO:0070536,GO:0005794,GO:0061136,GO:0031313,GO:0007265,GO:0004843,GO:0007032,GO:0005829,GO:0030496,GO:0005622,GO:0004197,GO:0005769	CG5798-PA						PF00443	PS50235		PS00973		SSF54001									
aly755.10	Unknown		n/a																				
aly755.2	Unknown		n/a												31~51								
aly755.3	Unknown		n/a																				
aly755.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly755.5	Pyrazinamidase/nicotinamidase	GO:0008936,GO:0043524,GO:0005509,GO:0008152,GO:0008340,GO:0006979,GO:0019363	CG31216-PA				SM00054,SM00054		PF00857,PF13499	PS50222,PS50222		PS00018,PS00018	G3DSA:3.40.50.850,G3DSA:3.40.50.850,G3DSA:1.10.238.10	SSF47473,SSF52499										
aly755.6	Unknown		n/a																				
aly755.7	Plasma kallikrein	GO:0004252,GO:0042730,GO:0002542,GO:0070062,GO:0005615,GO:0007597,GO:0007596,GO:0097421,GO:0031638,GO:0051919,GO:0030198,GO:0005886,GO:0006508,GO:0008233,GO:0031639,GO:0022617,GO:0005576	CG15002-PB				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly755.8	Kinesin-like protein KLP2 (Fragment)	GO:0005783,GO:0051289,GO:0005871,GO:0007067,GO:0005873,GO:0005874,GO:0005875,GO:0051301,GO:0051298,GO:0005737,GO:0007100,GO:0005819,GO:0005813,GO:0031535,GO:0003774,GO:0005524,GO:0005794,GO:0051299,GO:0000278,GO:0009306,GO:0008017,GO:0008574,GO:0043148,GO:0007052,GO:0022008,GO:0007030,GO:0001578,GO:0007018,GO:0045169,GO:0003777	CG9191-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10	SSF52540	587~607,762~796,363~397,671~712,726~746,407~441								
aly755.9	NGFI-A-binding protein homolog	GO:0048666,GO:0007626,GO:0008283,GO:0005634,GO:0035222,GO:0003712,GO:0014019,GO:0045892,GO:0006351,GO:0008134	CG33545-PC						PF04905,PF04904														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly75523.1	Irregular chiasm C-roughest protein	GO:0048749,GO:0016202,GO:0045177,GO:0001745,GO:0007409,GO:0046667,GO:0016021,GO:0030165,GO:0046331,GO:0005913,GO:0005515,GO:0005886,GO:0007520,GO:0046666,GO:0007156,GO:0042802	CG4125-PA										G3DSA:2.60.40.10	SSF48726	56~57								
aly75554.1	Unknown		CG2909-PA						PF16062														
aly75842.1	DNA methyltransferase 1-associated protein 1	GO:0005737,GO:0000122,GO:0003714,GO:0006909,GO:0006338,GO:0043967,GO:0043968,GO:0005634,GO:0006281,GO:0040008,GO:0045471,GO:0005657,GO:0045892,GO:0035267,GO:0001103,GO:0003682,GO:0042993,GO:0006351	CG11132-PA																				
aly760.1	Unknown		n/a																				
aly760.2	Unknown	GO:0022008	CG31344-PA						PF09995														
aly760.3	Dynein intermediate chain 3, ciliary	GO:0005737,GO:0042623,GO:0007605,GO:0005929,GO:0007018,GO:0005875,GO:0005515,GO:0005868,GO:0030286,GO:0005874,GO:0003774	CG6053-PC				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320			PS50294			G3DSA:2.130.10.10	SSF50978										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly760.4	F-box/WD repeat-containing protein 7	GO:0035147,GO:0045926,GO:0030332,GO:0016567,GO:0060438,GO:0008054,GO:0031146,GO:0060253,GO:0030162,GO:0042023,GO:0042787,GO:0019005,GO:0005515,GO:0071456,GO:0007411,GO:0007096,GO:0007088,GO:0005634,GO:1903146,GO:1900038	CG9144-PA						PF12937				G3DSA:1.20.1280.50,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF81383										
aly760.5	Unknown		n/a																				
aly760.6	Unknown		n/a																				
aly760.7	Unknown		n/a																				
aly760.8	Unknown		n/a																				
aly760.9	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7600.1	Suppression of tumorigenicity 5 protein	GO:0070374,GO:0043547,GO:0017112	n/a				SM00800,SM00799,SM00801		PF03455,PF03456	PS50946,PS50947													
aly76088.1	Unknown		n/a																				
aly7615.1	Zinc finger protein 26	GO:0045931,GO:0031935,GO:0006357,GO:0003700,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF12874,PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly7615.2	DNA-directed RNA polymerase I subunit RPA49	GO:0005736,GO:0001179,GO:0001189,GO:0005730,GO:0005634,GO:0005654,GO:0006351,GO:0003677,GO:0003899,GO:0000183	CG18600-PA						PF06870						123~150								
aly7615.3	Zinc finger protein 271	GO:0045931,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF13912,PF13912,PF13912,PF13912,PF12874,PF12874,PF12874,PF12874,PF00096,PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:2.170.270.10,G3DSA:2.170.270.10,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly7615.4	Zinc finger protein 112	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13894,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667,SSF57667,SSF57667	139~159								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7615.5	Zinc finger protein 658	GO:0005737,GO:0005819,GO:0003700,GO:0005634,GO:0042254,GO:0071294,GO:0045892,GO:0008270,GO:0003676,GO:0000976,GO:0046872,GO:0005876,GO:0006351	CG8474-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly7615.6	Zinc finger protein 729	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG3032-PA				SM00692,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868,SM00868		PF05485,PF07776,PF12874	PS50157,PS50157,PS50157,PS50157,PS50950		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57716	643~651								
aly7615.7	Tubulin beta-1 chain	GO:0005737,GO:0051258,GO:0007017,GO:0051298,GO:0003924,GO:0005200,GO:0006184,GO:0005874,GO:0005525	CG4869-PB				SM00865,SM00864		PF00091,PF03953		PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01163,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161,PR01161	PS00227,PS00228	G3DSA:3.30.1330.20,G3DSA:3.40.50.1440,G3DSA:1.10.287.600	SSF55307,SSF52490			REACT_152						
aly7615.8	Transmembrane protein C5orf28 homolog	GO:0016021	CG10866-PA																				
aly7615.9	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly76171.1	Pre-rRNA-processing protein TSR1 homolog	GO:0022008,GO:0005730,GO:0042255,GO:0005634,GO:0042254	CG7338-PA						PF04950														
aly7622.1	Putative odorant receptor 85d	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG11742-PA						PF02949														
aly7622.2	Unknown		n/a																				
aly76312.1	Unknown		n/a																				
aly7645.1	ETS homologous factor	GO:0043565,GO:0030154,GO:0035071,GO:0005794,GO:0003700,GO:0005634,GO:0009987,GO:0005654,GO:0006355,GO:0001077,GO:0045944,GO:0006357,GO:0030855,GO:0000978,GO:0008219,GO:0048477,GO:0006914,GO:0000981,GO:0040034	CG32180-PB				SM00413		PF00178	PS50061	PR00454,PR00454,PR00454,PR00454		G3DSA:1.10.10.10	SSF46785									
aly7645.10	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0005737,GO:0007567,GO:0045786,GO:0003824,GO:0051287,GO:0097070,GO:0004022,GO:0016404,GO:0006693,GO:0048812,GO:0007179,GO:0070403,GO:0007565,GO:0004957,GO:0030728,GO:0070493,GO:0055114	CG4842-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7645.11	Unknown		n/a										G3DSA:1.10.150.50	SSF47769									
aly7645.2	Cytochrome P450 9e2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0035220,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG11466-PA						PF00067,PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086,PS00086	G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264,SSF48264,SSF48264			REACT_13433						
aly7645.3	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0005737,GO:0030728,GO:0070062,GO:0055114,GO:0004022,GO:0016323,GO:0003824,GO:0045786,GO:0007179,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly7645.4	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0016491,GO:0005737,GO:0030728,GO:0070062,GO:0007179,GO:0004022,GO:0016323,GO:0003824,GO:0008152,GO:0045786,GO:0055114,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7645.5	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0005737,GO:0030728,GO:0070062,GO:0055114,GO:0004022,GO:0016323,GO:0003824,GO:0045786,GO:0007179,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									
aly7645.6	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0016491,GO:0005737,GO:0030728,GO:0070062,GO:0007179,GO:0004022,GO:0016323,GO:0003824,GO:0008152,GO:0045786,GO:0055114,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									
aly7645.7	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0016491,GO:0005737,GO:0030728,GO:0070062,GO:0007179,GO:0004022,GO:0016323,GO:0003824,GO:0008152,GO:0045786,GO:0055114,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly7645.8	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0005737,GO:0030728,GO:0070062,GO:0055114,GO:0004022,GO:0016323,GO:0003824,GO:0045786,GO:0007179,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106		PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7645.9	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	GO:0006909,GO:0051287,GO:0004957,GO:0042572,GO:0042574,GO:0070493,GO:0005737,GO:0030728,GO:0070062,GO:0055114,GO:0004022,GO:0016323,GO:0003824,GO:0045786,GO:0007179,GO:0097070,GO:0007565,GO:0007567,GO:0016404,GO:0006693,GO:0070403,GO:0004745	CG4899-PA						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081,PR00081		G3DSA:3.40.50.720	SSF51735									
aly76655.1	Unknown		n/a																				
aly767.1	Unknown		n/a																				
aly767.10	Unknown		n/a																				
aly767.11	Protein shifted	GO:0008589,GO:0007224,GO:0016055,GO:0008039,GO:0050821,GO:0005576,GO:0045880,GO:0005515,GO:0005578	CG3135-PB				SM00181,SM00181,SM00181,SM00181,SM00181,SM00469		PF00008,PF02019,PF12661,PF12661	PS50814,PS50026,PS50026,PS50026	PR01901,PR01901,PR01901,PR01901	PS01186,PS00022,PS00022,PS00022,PS00022,PS00022,PS01186,PS01186,PS01186	G3DSA:2.10.25.10,G3DSA:2.170.300.10,G3DSA:2.10.25.10	SSF57196									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly767.12	Neuroglian	GO:0016319,GO:0048675,GO:0050808,GO:0045924,GO:0030175,GO:0008049,GO:0005923,GO:0016021,GO:0019991,GO:0048812,GO:0060857,GO:0005509,GO:0008366,GO:0035151,GO:0016328,GO:0072499,GO:0035011,GO:0008050,GO:0007173,GO:0048036,GO:0007409,GO:0005886,GO:0005919,GO:0005918,GO:0007560,GO:0048813,GO:0061343,GO:0021682,GO:0007158	CG1634-PG				SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00060,SM00060,SM00060,SM00060,SM00060,SM00408,SM00408,SM00408,SM00408,SM00408		PF00041,PF00041,PF00041,PF00041,PF13882,PF13927,PF07679,PF07679,PF07679,PF07679	PS50853,PS50835,PS50835,PS50853,PS50853,PS50835,PS50853,PS50853,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF49265,SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265									
aly767.13	Unknown		n/a																				
aly767.14	Scm-like with four MBT domains protein 2	GO:0042393,GO:0035064,GO:0007446,GO:0006342,GO:0005634,GO:0016235,GO:0005654,GO:0006355,GO:0010629,GO:0008270,GO:0005515,GO:0003682,GO:0048477,GO:0043231	CG16975-PC				SM00561,SM00561,SM00561,SM00561		PF02820,PF02820,PF02820,PF02820,PF12140	PS51079,PS51079,PS51079,PS51079			G3DSA:2.30.30.160,G3DSA:1.10.150.50,G3DSA:2.30.30.160,G3DSA:2.30.30.160,G3DSA:2.30.30.160	SSF63748,SSF47769,SSF63748,SSF63748,SSF63748									
aly767.15	CSC1-like protein 1	GO:0070062,GO:0006811,GO:0016020,GO:0000166,GO:0005765,GO:0016021	CG11210-PA						PF02714,PF13967						744~746								
aly767.16	Translocon-associated protein subunit beta	GO:0005786,GO:0044267,GO:0005783,GO:0006613,GO:0006412,GO:0016021,GO:0005811,GO:0006621,GO:0006614,GO:0010467,GO:0005789,GO:0005875,GO:0005048	CG5474-PA			PIRSF016400			PF05753														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly767.17	Centromere/kinetochore protein zw10 homolog	GO:0016020,GO:0005783,GO:0005789,GO:0070939,GO:0007059,GO:0007067,GO:0051301,GO:0034501,GO:0005737,GO:0007126,GO:0040020,GO:0005634,GO:0000940,GO:0000922,GO:0007080,GO:1990423,GO:0019237,GO:0000278,GO:0048193,GO:0006461,GO:0015031,GO:0007133,GO:0006888,GO:0022008,GO:0007264,GO:0000775,GO:0000776,GO:0000777,GO:0007030,GO:0000070,GO:0000132,GO:0005829,GO:0005828,GO:0007094,GO:0007096,GO:0007093	CG9900-PB						PF06248						657~677								
aly767.18	Williams-Beuren syndrome chromosomal region 16 protein homolog	GO:0044822,GO:0005739,GO:0005087,GO:0043547	CG3862-PA						PF13540,PF13540,PF00415,PF00415,PF00415	PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012	PR00633,PR00633,PR00633,PR00633	PS00626,PS00626,PS00626	G3DSA:2.130.10.30	SSF50985									
aly767.19	Mediator of RNA polymerase II transcription subunit 27	GO:0046425,GO:0005634,GO:0003712,GO:0001104,GO:0006355,GO:0006357,GO:0006351,GO:0006367,GO:0006366,GO:0016592	CG1245-PA						PF11571						48~68								
aly767.2	Zinc transporter 2	GO:0005737,GO:0005770,GO:0005765,GO:0016324,GO:0006812,GO:0016021,GO:0008324,GO:0005622,GO:0061090,GO:0016023,GO:0005385,GO:0010043,GO:0046873,GO:0055085	CG3994-PA					TIGR01297	PF01545				G3DSA:1.20.1510.10,G3DSA:1.20.1510.10	SSF161111,SSF161111									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly767.20	Neuronal acetylcholine receptor subunit alpha-7	GO:0000187,GO:0015643,GO:0007268,GO:0007613,GO:0046716,GO:0005892,GO:0007165,GO:0007271,GO:0001666,GO:0030054,GO:0001540,GO:0016021,GO:0045766,GO:0004889,GO:0006874,GO:0022848,GO:0042803,GO:0008284,GO:0006812,GO:0006811,GO:0042166,GO:0006816,GO:0034220,GO:0015464,GO:0005886,GO:0045211,GO:0050890,GO:0035094,GO:0017081,GO:0032720,GO:0017085,GO:0098655	CG4128-PE					TIGR00860	PF02932,PF02931		PR00254,PR00254,PR00254,PR00254,PR00252,PR00252,PR00252,PR00252	PS00236	G3DSA:1.20.120.370,G3DSA:1.20.120.370,G3DSA:2.70.170.10	SSF90112,SSF63712			REACT_13685						
aly767.21	Unknown		n/a																				
aly767.22	Unknown		n/a																				
aly767.23	Unknown		n/a																				
aly767.24	5-demethoxyubiquihydroxylase, mitochondrial	GO:0001306,GO:0070584,GO:0004497,GO:0001701,GO:0005743,GO:0005634,GO:0016709,GO:0005739,GO:0006979,GO:0042775,GO:0046872,GO:0031314,GO:0022904,GO:0001841,GO:0008340,GO:0034599,GO:0006744,GO:0022008,GO:0055114	CG14437-PA						PF03232				G3DSA:1.20.1260.10	SSF47240					UPA00232				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly767.3	Putative flavin containing monoamine oxidase AofH	GO:0005829,GO:0005886,GO:0016491	CG13611-PA						PF01593				G3DSA:3.90.660.10,G3DSA:3.50.50.60,G3DSA:1.10.405.10	SSF51905,SSF54373									
aly767.4	Transmembrane protein 205	GO:0016021,GO:0070062	CG32512-PA						PF13664														
aly767.5	Adenosine monophosphate-protein transferase FICD homolog	GO:0018117,GO:0070733,GO:0051608,GO:0007632,GO:0005886,GO:0050908,GO:0016021,GO:0005524	CG9523-PA						PF02661	PS51459,PS50293,PS50005			G3DSA:1.10.3290.10,G3DSA:1.25.40.120	SSF48452,SSF140931									
aly767.6	Kinesin-like protein Klp10A	GO:0005783,GO:0007057,GO:0090307,GO:0005871,GO:0005875,GO:0051301,GO:0072687,GO:0006983,GO:0005813,GO:0097431,GO:0000922,GO:0003774,GO:0005524,GO:0061673,GO:0051298,GO:0055028,GO:0000212,GO:0008017,GO:0051296,GO:0000091,GO:0007051,GO:0007052,GO:0090619,GO:0008152,GO:0007079,GO:0000775,GO:0008574,GO:0000070,GO:0030968,GO:0005828,GO:0007018,GO:0007019,GO:0003777	CG1453-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10	SSF52540	121~148								
aly767.7	Bifunctional arginine demethylase and lysyl-hydroxylase PSR	GO:0035212,GO:0018395,GO:0005634,GO:0070815,GO:0006355,GO:0043066,GO:0003674,GO:0006351,GO:0046329,GO:0046872,GO:0016568	CG5383-PB				SM00558		PF02373	PS51184			G3DSA:2.60.120.650	SSF51197									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly767.8	Cytochrome c oxidase subunit 5A, mitochondrial	GO:0004129,GO:0045787,GO:0005811,GO:0006123,GO:0005739,GO:0005751,GO:0005743,GO:0007406,GO:0046872	CG14724-PA						PF02284				G3DSA:1.25.40.40	SSF48479									
aly767.9	DNA-binding protein Ewg	GO:0007517,GO:0045886,GO:0003700,GO:0005634,GO:0007560,GO:0030177,GO:0006357,GO:0006351,GO:0003677,GO:0007417	CG3114-PK						PF10491														
aly7673.1	Retinol dehydrogenase 14	GO:0008106,GO:0016614,GO:0005783,GO:0005634,GO:0016020,GO:0005739,GO:0005789,GO:0005765,GO:0008152,GO:0042572,GO:0001649	CG7675-PB										G3DSA:3.40.50.720	SSF51735									
aly7673.2	Protein tyrosine phosphatase domain-containing protein 1	GO:0030030,GO:0004725,GO:0008138	n/a										G3DSA:3.90.190.10	SSF52799									
aly7673.3	Protein tyrosine phosphatase domain-containing protein 1	GO:0030030,GO:0004725,GO:0008138	n/a																				
aly768.1	Potassium channel subfamily K member 18	GO:0005267,GO:0071805,GO:0006813,GO:0016021,GO:0022841,GO:0071435,GO:0071467,GO:0005887,GO:0005886,GO:0015271,GO:0015269,GO:0030322	CG42594-PB						PF07885,PF07885		PR01333,PR01333		G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:1.10.287.70	SSF81324,SSF81324,SSF81324	311~331								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly768.2	Unknown		n/a																				
aly7682.1	Unknown	GO:0046983	n/a						PF05699,PF14291					SSF53098,SSF53098									
aly7682.2	Unknown	GO:0003676	n/a											SSF53098									
aly7682.3	Unknown		n/a																				
aly7682.4	Unknown		n/a																				
aly7682.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly76848.1	HEAT repeat-containing protein 5B	GO:0022008	CG2747-PF																				
aly7689.1	Zinc finger protein 1 homolog	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776,PF13912,PF13912,PF13912,PF05225,PF05225,PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF46689,SSF57667,SSF46689,SSF57667,SSF57667									
aly7689.2	PR domain zinc finger protein 10	GO:0051726,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0008168,GO:0046872	CG11247-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly7689.3	Zinc finger and BTB domain-containing protein 40	GO:0003700,GO:0005634,GO:0007476,GO:0006974,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872,GO:0030282	CG8367-PL				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60	SSF46689,SSF57667,SSF57667									
aly7689.4	PR domain zinc finger protein 14	GO:0031490,GO:0003676,GO:0044030,GO:0008168,GO:0000902,GO:0000122,GO:0060817,GO:0001708,GO:0040029,GO:0046872,GO:0010468,GO:0006351,GO:0019827,GO:0007281,GO:0040037,GO:0030718,GO:0048873,GO:0007566,GO:0009566,GO:0001827,GO:0048813,GO:0003723,GO:0034972,GO:0005634	CG2116-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF05225,PF07776	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60	SSF57667,SSF57667,SSF46689	248~268								
aly7689.5	Zinc finger protein 358	GO:0019827,GO:0021915,GO:0006355,GO:0005634,GO:0035115,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF00096,PF00096,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7689.6	Zinc finger protein 652-B	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG12299-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF13912,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly7690.1	Putative fatty acyl-CoA reductase CG5065	GO:0005737,GO:0045177,GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0035149,GO:0035002,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG1443-PA						PF07993,PF07993,PF03015				G3DSA:3.40.50.720	SSF51735,SSF51735	868~888		REACT_22258						
aly7690.2	PiggyBac transposable element-derived protein 3		n/a						PF13843														
aly7691.1	Neuromedin-B receptor	GO:0007218,GO:0016021,GO:0008261,GO:0031989,GO:0004946,GO:0005887,GO:0008188,GO:0005886,GO:0007186	CG30106-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly7691.2	Meiotic nuclear division protein 1 homolog	GO:0006310,GO:0005634,GO:0051321,GO:0003677	n/a			PIRSF026991			PF03962						127~147,179~106,152~172								
aly7691.3	Zinc finger HIT domain-containing protein 1	GO:0005737,GO:0043486,GO:0005634,GO:0005700,GO:0000812,GO:0031491,GO:0048812,GO:0031063,GO:0046872,GO:0042826	CG31917-PA						PF04438	PS51083													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7691.4	Protein atonal homolog 8	GO:0000122,GO:0003700,GO:0048797,GO:0005634,GO:0008586,GO:0007474,GO:0001947,GO:0006355,GO:2001014,GO:0046983,GO:0061074	CG11450-PB				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459									
aly770.1	Uncharacterized protein C15orf26	GO:0005575,GO:0003674,GO:0008150,GO:0004252,GO:0006508	CG5197-PA																				
aly770.10	Unknown		n/a																				
aly770.11	Unknown		n/a																				
aly770.12	Unknown		n/a																				
aly770.13	Serrate RNA effector molecule homolog	GO:0071011,GO:0035195,GO:0071013,GO:0045071,GO:0000398,GO:0005654,GO:0031053,GO:0033168,GO:0050829,GO:0022008,GO:0046685	CG7843-PD						PF04959,PF12066				G3DSA:3.30.70.330	SSF54928	201~221								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly770.14	Low-density lipoprotein receptor-related protein 1B	GO:0016319,GO:0006909,GO:0005887,GO:0030425,GO:0030424,GO:0021551,GO:0007419,GO:0008046,GO:0070593,GO:0007411,GO:0007413,GO:0032490,GO:0048846,GO:0016021,GO:0005509,GO:0043005,GO:0043025,GO:0042802,GO:0042803,GO:0048666,GO:0050976,GO:0003823,GO:0043235,GO:0050770,GO:0007422,GO:0006898,GO:0005041,GO:0048814,GO:0015031	CG33950-PAT				SM00192,SM00192,SM00192,SM00192		PF00057,PF00057,PF00057,PF00057	PS50068,PS50068,PS50068,PS50068	PR00261,PR00261,PR00261,PR00261	PS01209,PS01209,PS01209	G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10	SSF57424,SSF57424,SSF57424,SSF57424										
aly770.15	Sphingomyelin phosphodiesterase	GO:0043407,GO:0005615,GO:0005886,GO:0042493,GO:0016798,GO:0005764,GO:0023021,GO:0043065,GO:0004767,GO:0006685,GO:0042220,GO:0042599,GO:0005768,GO:0046513,GO:0035307,GO:0070062	CG3376-PC			PIRSF000948	SM00741		PF00149	PS50015			G3DSA:3.60.21.10,G3DSA:1.10.225.10	SSF47862,SSF56300										
aly770.16	F-box only protein 5	GO:0000082,GO:0000083,GO:0051439,GO:0051437,GO:0051436,GO:0051301,GO:0005737,GO:0007346,GO:0005819,GO:0005634,GO:0005654,GO:0046785,GO:0045835,GO:0046872,GO:0000278,GO:0031145,GO:0019901,GO:0007057,GO:0001556,GO:0005829,GO:0016050,GO:0007091	n/a						PF00646				G3DSA:1.20.1280.50	SSF81383	274~294									
aly770.17	Zinc finger protein 782	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003677,GO:0046872,GO:0006351	CG10366-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868,SM00868,SM00868		PF12874,PF12874,PF07776,PF13912,PF00096	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57716,SSF57667,SSF57667	160~180									
aly770.18	Delta and Notch-like epidermal growth factor-related receptor	GO:0007219,GO:0016021,GO:0048741,GO:0009986,GO:0030425,GO:0005769,GO:0007220,GO:0003015,GO:0010001,GO:0005886,GO:0007417,GO:0043025,GO:0005112,GO:0005509	CG31665-PB				SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00179,SM00179,SM00179,SM00179		PF00008,PF00008,PF00008,PF00008	PS50026,PS50026,PS50026,PS50026,PS50026,PS50026,PS50026	PR00010,PR00010,PR00010,PR00010	PS00010,PS00022,PS01187,PS01186,PS00022,PS00022,PS01186,PS01186,PS01186,PS00022,PS00022,PS01186,PS01186,PS00010,PS00022,PS01186,PS00022	G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57196,SSF57196,SSF57196,SSF57184,SSF57196									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly770.19	Protein grainyhead	GO:0042052,GO:0007464,GO:0061024,GO:0007009,GO:0003382,GO:0003677,GO:0043565,GO:0005634,GO:0042803,GO:0042127,GO:0035152,GO:0040003,GO:0035159,GO:0008362,GO:0008360,GO:0007402,GO:0007424,GO:0007426,GO:0007399,GO:0007419,GO:0003700,GO:0007428,GO:0061041,GO:0006357,GO:0045944,GO:0006351	CG42311-PJ						PF04516														
aly770.2	Band 4.1-like protein 4	GO:0003779,GO:0005856,GO:0005737,GO:0008092	CG34347-PB				SM00295		PF09379,PF09380,PF00373	PS50057	PR00935,PR00935,PR00935,PR00935	PS00660,PS00661	G3DSA:2.30.29.30,G3DSA:1.20.80.10,G3DSA:3.10.20.90	SSF54236,SSF47031,SSF50729									
aly770.20	Probable elongation factor 1-delta	GO:0003746,GO:0006414,GO:0005085,GO:0005853,GO:0005875	CG4912-PB				SM00888		PF00736,PF10587			PS00825	G3DSA:3.30.70.60	SSF54984	255~261,68~102		REACT_17015,REACT_71						
aly770.21	Cytoplasmic tRNA 2-thiolation protein 2	GO:0016779,GO:0000049,GO:0005829,GO:0032447,GO:0034227,GO:0002098	CG10189-PA	MF_03054					PF01171,PF10288				G3DSA:3.40.50.620	SSF52402					UPA00988				
aly770.22	Casein kinase II subunit alpha	GO:0007228,GO:0030177,GO:0045880,GO:0007411,GO:0007067,GO:0005737,GO:0005634,GO:0004674,GO:0016055,GO:0004672,GO:0031397,GO:0005524,GO:0048749,GO:0006468,GO:0007623,GO:0022416,GO:0045475,GO:0005956,GO:0005829,GO:0031647,GO:0046331,GO:0005515	CG17520-PF				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly770.23	Trafficking protein particle complex subunit 8	GO:0006888,GO:0000407,GO:0031410,GO:1990072,GO:0000045,GO:0034497,GO:0044804,GO:0003674,GO:0005515,GO:0030242,GO:0032258,GO:0030008	CG8793-PA						PF12739,PF08626				G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10										
aly770.24	Unknown	GO:0017022,GO:0001077,GO:0007165,GO:0004871,GO:0032869,GO:0007417,GO:0005737,GO:0043565,GO:0007517,GO:0000122,GO:0005634,GO:0071456,GO:0048477,GO:0000981,GO:0048666,GO:0043234,GO:0008347,GO:0007425,GO:0007424,GO:0007420,GO:0007422,GO:0003700,GO:0003705,GO:0045676,GO:0006355,GO:0048813,GO:0006357,GO:0045944,GO:0005667,GO:0046982	CG11987-PA																				
aly770.25	Aryl hydrocarbon receptor nuclear translocator homolog	GO:0017022,GO:0001077,GO:0007165,GO:0004871,GO:0032869,GO:0007417,GO:0005737,GO:0043565,GO:0007517,GO:0000122,GO:0005634,GO:0071456,GO:0048477,GO:0000981,GO:0048666,GO:0043234,GO:0006366,GO:0008347,GO:0007425,GO:0007424,GO:0007420,GO:0007422,GO:0003700,GO:0003705,GO:0045676,GO:0006355,GO:0048813,GO:0006357,GO:0045944,GO:0005667,GO:0046983,GO:0046982	CG11987-PA				SM00353,SM00086,SM00091,SM00091	TIGR00229	PF00989,PF14598,PF00010	PS50112,PS50888,PS50112	PR00785,PR00785,PR00785,PR00785,PR00785,PR00785,PR00785,PR00785		G3DSA:4.10.280.10,G3DSA:3.30.450.20,G3DSA:3.30.450.20	SSF47459,SSF55785,SSF55785,SSF55785									
aly770.26	Mono [ADP-ribose] polymerase PARP16	GO:0003950,GO:0016021,GO:0006986,GO:0005789	CG15925-PA						PF00644	PS51059			G3DSA:3.90.228.10	SSF56399									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly770.27	Acetylcholinesterase	GO:0016020,GO:0042136,GO:0016787,GO:0007268,GO:0031594,GO:0043083,GO:0006656,GO:0043236,GO:0001507,GO:0045202,GO:0030054,GO:0031225,GO:0007517,GO:0001540,GO:0005615,GO:0005634,GO:0004104,GO:0009611,GO:0051262,GO:0006260,GO:0007416,GO:0048471,GO:0042982,GO:0044281,GO:0042803,GO:0005794,GO:0006644,GO:0008283,GO:0006581,GO:0009986,GO:0042166,GO:0052689,GO:0045212,GO:0008150,GO:0005886,GO:0007155,GO:0017171,GO:0060041,GO:0005605,GO:0032223,GO:0031623,GO:0007399,GO:0050714,GO:0005575,GO:0005576,GO:0046474,GO:0001919,GO:0005518,GO:0003990,GO:0002076	CG12869-PA						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly770.28	Splicing factor 3B subunit 6	GO:0005689,GO:0071011,GO:0001825,GO:0071013,GO:0044822,GO:0005634,GO:0000398,GO:0000166,GO:0005654,GO:0007052,GO:0048812,GO:0003676,GO:0005686,GO:0022008,GO:0006397,GO:0008380,GO:0003729	CG13298-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928									
aly770.29	Tudor domain-containing protein 7A	GO:0005737,GO:0035770,GO:0010608,GO:0070306,GO:0007283,GO:0002089,GO:0003729	CG8920-PB				SM00333,SM00333		PF12872,PF00567,PF00567	PS51644,PS50304,PS51644			G3DSA:2.30.30.140,G3DSA:2.30.30.140	SSF63748,SSF63748									
aly770.3	PDZ domain-containing protein 2	GO:0048749,GO:0005737,GO:0005911,GO:0016324,GO:0005634,GO:0005576,GO:0003674,GO:0005912,GO:0005515,GO:0007155,GO:0005783	CG6741-PB				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly770.30	Polyadenylate-binding protein 4	GO:0008143,GO:0007596,GO:0030529,GO:0005875,GO:0007140,GO:0005737,GO:0005634,GO:0005811,GO:0000166,GO:0003730,GO:0006401,GO:0045727,GO:0048477,GO:0044822,GO:0048599,GO:0071011,GO:0071013,GO:0008266,GO:0007283,GO:0007268,GO:0007289,GO:0045314,GO:0022008,GO:1901215,GO:0010494,GO:0007112,GO:0009953,GO:0000398,GO:0003723,GO:0005515,GO:0006412,GO:0006396,GO:0003729	CG5119-PC				SM00517,SM00360,SM00360,SM00360,SM00360,SM00361,SM00361	TIGR01628	PF00076,PF00076,PF00076,PF00076,PF00658	PS50102,PS51309,PS50102,PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:1.10.1900.10,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF63570,SSF54928	265~288								
aly770.31	Glycylpeptide N-tetradecanoyltransferase 2	GO:0005737,GO:0005794,GO:0019068,GO:0016032,GO:0016056,GO:0004379,GO:0005829,GO:0005886,GO:0007603,GO:0006499,GO:0019898,GO:0007391,GO:0022400,GO:0018008,GO:0022008,GO:0075733,GO:0019082	CG7436-PA			PIRSF015892			PF01233,PF02799			PS00975,PS00976	G3DSA:3.40.630.30,G3DSA:3.40.630.30	SSF55729,SSF55729									
aly770.32	60S ribosomal protein L13	GO:0005840,GO:0022625,GO:0005622,GO:0003735,GO:0007052,GO:0000022,GO:0006412,GO:0051298	CG4651-PC						PF01294			PS01104											
aly770.33	Cip1-interacting zinc finger protein	GO:0005634,GO:0046427,GO:0003676,GO:0008270	CG8108-PB												463~501								
aly770.34	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly770.35	Unknown		CG15249-PD																				
aly770.36	Exostosin-1	GO:0030210,GO:0008589,GO:0050808,GO:0005783,GO:0008101,GO:0005789,GO:0007411,GO:0008375,GO:0031227,GO:0008354,GO:0006486,GO:0016021,GO:0048488,GO:0015020,GO:0046872,GO:0048312,GO:0005794,GO:0050508,GO:0050509,GO:0007224,GO:0016055,GO:0006044,GO:0000139,GO:0015012,GO:0005515,GO:0015014,GO:0006024	CG10117-PA						PF09258,PF03016				G3DSA:3.90.550.10	SSF53448									
aly770.37	Probable leucine--tRNA ligase, mitochondrial	GO:0004823,GO:0005739,GO:0006429,GO:0010467,GO:0002161,GO:0006418,GO:0005759,GO:0005524	CG7479-PA						PF09334,PF00133,PF08264		PR00985,PR00985,PR00985,PR00985,PR00985,PR00985,PR00985	PS00178	G3DSA:3.90.740.10,G3DSA:1.10.730.10,G3DSA:3.40.50.620,G3DSA:3.40.50.620,G3DSA:3.40.50.620	SSF50677,SSF52374,SSF52374,SSF47323		00970+6.1.1.4	REACT_71						
aly770.38	FUN14 domain-containing protein 1	GO:0031307,GO:0001666,GO:0000422	CG5676-PA						PF04930						122~142								
aly770.39	Unknown		n/a										G3DSA:1.10.30.10,G3DSA:1.10.30.10	SSF47095									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly770.4	Pro-interleukin 16	GO:0005737,GO:0030595,GO:0050930,GO:0005615,GO:0007444,GO:0005634,GO:0006955,GO:0006351,GO:0005515,GO:0005886,GO:0016032,GO:0007298	CG42230-PC				SM00228,SM00228,SM00228		PF00595,PF00595,PF00595	PS50106,PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156,SSF50156									
aly770.40	Nuclear speckle splicing regulatory protein 1	GO:0071011,GO:0071013,GO:0000398	CG15747-PA						PF09745						104~124,238~258,146~173								
aly770.41	Negative elongation factor D	GO:0006351,GO:0034244,GO:0032021,GO:0017053,GO:0005634,GO:0005705,GO:0005703,GO:0008023,GO:0045892,GO:0003723,GO:0022008,GO:0007070,GO:0003729	CG9984-PA						PF04858														
aly770.42	Potassium voltage-gated channel subfamily KQT member 5	GO:0001700,GO:0071805,GO:0006813,GO:0016021,GO:0006461,GO:0008076,GO:0005242,GO:0002027,GO:0007268,GO:0022843,GO:0005249,GO:0005886,GO:0005251,GO:0060048,GO:0055085	CG33135-PF						PF00520,PF03520		PR00169,PR00169,PR00169,PR00169,PR00169,PR01459,PR01459,PR01459		G3DSA:1.10.287.70	SSF81324	462~482								
aly770.43	Solute carrier family 12 member 8	GO:0006810,GO:0016021,GO:0015293,GO:0006813,GO:0003333,GO:0016020,GO:0008511,GO:0055085,GO:0015171	CG12773-PA						PF00324														
aly770.44	Survival of motor neuron-related-splicing factor 30	GO:0005737,GO:0016607,GO:0000381,GO:0000245,GO:0071011,GO:0005634,GO:0000398,GO:0003723,GO:0015030,GO:0005681,GO:0006397	CG17454-PA				SM00333		PF06003	PS50304			G3DSA:2.30.30.140	SSF63748	25~45,158~185								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly770.45	Lachesin	GO:0004714,GO:0005515,GO:0005886,GO:0007155,GO:0007169,GO:0031225	CG31708-PA				SM00408,SM00408,SM00408,SM00409,SM00409,SM00409		PF07679,PF07679,PF07679	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly770.46	General odorant-binding protein 83a	GO:0005549,GO:0007606,GO:0005576,GO:0008145,GO:0005550	CG11421-PC				SM00708		PF01395		PR00485,PR00485,PR00485,PR00485		G3DSA:1.10.238.20	SSF47565									
aly770.47	Gamma-interferon-inducible lysosomal thiol reductase	GO:0005737,GO:0050821,GO:0043202,GO:0019221,GO:0019886,GO:0048147,GO:0005764,GO:0060333,GO:0042590,GO:0005576,GO:0016667,GO:0005886,GO:0030054,GO:0043231	CG41378-PB						PF03227				G3DSA:3.40.30.10										
aly770.48	Splicing factor 45	GO:0000381,GO:0000380,GO:0006281,GO:0071011,GO:0000398,GO:0000166,GO:0005654,GO:0000375,GO:0003723,GO:0003676,GO:0001745,GO:0008380,GO:0005681,GO:0006397	CG17540-PA			PIRSF031066	SM00361,SM00443		PF00076,PF01585	PS50102,PS50174			G3DSA:3.30.70.330	SSF54928									
aly770.49	Serine/threonine-protein kinase greatwall	GO:0000086,GO:0030261,GO:0007067,GO:0007143,GO:0051301,GO:0005737,GO:0007346,GO:0040020,GO:0005813,GO:0005634,GO:0005635,GO:0034048,GO:0004674,GO:0071889,GO:0004672,GO:0007088,GO:0005524,GO:0006468,GO:0032154,GO:0006974,GO:0046602,GO:0051721,GO:0005515,GO:0007144	CG7719-PA				SM00220		PF00069,PF00069	PS51285,PS50011		PS00108	G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:1.10.510.10	SSF56112,SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly770.5	Neuronal acetylcholine receptor subunit alpha-7	GO:0007630,GO:0000187,GO:0007632,GO:0015643,GO:0005886,GO:0030425,GO:0030424,GO:0005892,GO:0007165,GO:0007271,GO:0001666,GO:0030054,GO:0005737,GO:0001540,GO:0043204,GO:0016021,GO:0045766,GO:0017081,GO:0006874,GO:0005216,GO:0032720,GO:0042803,GO:0008284,GO:0006812,GO:0006811,GO:0042166,GO:0006816,GO:0045211,GO:0014069,GO:0015464,GO:0007268,GO:0060079,GO:0043197,GO:0050890,GO:0035094,GO:0004889,GO:0098655	CG32538-PE					TIGR00860	PF02931,PF02932		PR00254,PR00254,PR00254,PR00254,PR00252,PR00252,PR00252,PR00252	PS00236	G3DSA:1.20.120.370,G3DSA:1.20.120.370,G3DSA:2.70.170.10	SSF63712,SSF90112			REACT_13685						
aly770.50	Serine proteinase stubble	GO:0004252,GO:0007010,GO:0016021,GO:0051017,GO:0035220,GO:0005886,GO:0006508	CG31728-PC				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly770.51	Unknown		n/a																				
aly770.6	Acetylcholine receptor subunit beta-like 1	GO:0006812,GO:0006811,GO:0016020,GO:0005892,GO:0045211,GO:0004889,GO:0005887,GO:0007271,GO:0098655,GO:0030054	CG11348-PA					TIGR00860	PF02931,PF02932		PR00252,PR00252,PR00252,PR00252,PR00254,PR00254,PR00254,PR00254	PS00236	G3DSA:2.70.170.10,G3DSA:1.20.120.370,G3DSA:1.20.120.370	SSF90112,SSF63712			REACT_13685						
aly770.7	Protein ariadne 2	GO:0005737,GO:0005634,GO:0008270,GO:0003676,GO:0004842,GO:0000209	CG5709-PA				SM00647,SM00647		PF01485,PF01485			PS00518	G3DSA:3.30.40.10	SSF57850,SSF57850,SSF57850	451~471,429~449,351~371								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly770.8	ATP-dependent 6-phosphofructokinase	GO:0005945,GO:0007525,GO:0046835,GO:0007520,GO:0005524,GO:0003872,GO:0046872,GO:0006096,GO:0006002	CG4001-PA	MF_03184		PIRSF000533		TIGR02478	PF00365,PF00365		PR00476,PR00476,PR00476,PR00476,PR00476,PR00476,PR00476,PR00476,PR00476	PS00433,PS00433	G3DSA:3.40.50.450,G3DSA:3.40.50.450	SSF53784,SSF53784		00010+2.7.1.11,00052+2.7.1.11,00051+2.7.1.11,00030+2.7.1.11,00680+2.7.1.11	REACT_474	PWY-1042,PWY-5484,PWY-1861,PWY-7385	UPA00109				
aly770.9	Translocating chain-associated membrane protein 1-like 1	GO:0006909,GO:0005783,GO:0016021,GO:0005811,GO:0006614,GO:0005789,GO:0015031	CG11642-PB				SM00724		PF08390,PF03798														
aly77194.1	Unknown		n/a																				
aly7733.1	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG4020-PA						PF07993				G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735,SSF51735			REACT_22258						
aly7754.1	Sodium- and chloride-dependent glycine transporter 1	GO:0005328,GO:0005283,GO:0016021,GO:0006836,GO:0005887,GO:0015375,GO:0005326	CG5549-PB						PF00209,PF00209	PS50267	PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176	PS00610		SSF161070,SSF161070										
aly77541.1	T-complex protein 11-like protein 1	GO:0005874	CG16721-PB						PF05794														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7758.1	Unknown	GO:0046872	n/a							PS50157		PS00028	G3DSA:3.30.160.60										
aly7758.10	Unknown		n/a										G3DSA:3.80.10.10										
aly7758.2	Unknown		n/a				SM00355,SM00355,SM00355,SM00355			PS50157		PS00028,PS00028	G3DSA:2.60.40.420	SSF57667,SSF57667									
aly7758.3	UPF0547 protein C16orf87 homolog		n/a																				
aly7758.4	Spermine oxidase	GO:0005737,GO:0006598,GO:0005829,GO:0006596,GO:0052894,GO:0052895,GO:0006805,GO:0034641,GO:0046592,GO:0044281,GO:0052901,GO:0046208,GO:0006595,GO:0005634,GO:0055114,GO:0016491	CG6034-PA						PF01593				G3DSA:3.90.660.10	SSF51905,SSF51905,SSF54373	474~477								
aly7758.5	Spermine oxidase	GO:0005737,GO:0006598,GO:0005829,GO:0006596,GO:0052894,GO:0052895,GO:0006805,GO:0034641,GO:0046592,GO:0044281,GO:0052901,GO:0046208,GO:0006595,GO:0005634,GO:0055114,GO:0016491	CG6034-PA						PF01593				G3DSA:3.90.660.10	SSF51905,SSF51905,SSF54373									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7758.6	Zinc finger protein 64 homolog, isoforms 1 and 2	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0022008,GO:0046872,GO:0048026,GO:0006351	CG7386-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13909,PF13909,PF13909	PS50157,PS50157			G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667									
aly7758.7	Unknown		n/a																				
aly7758.8	Protein LLP homolog		CG15019-PA						PF10169														
aly7758.9	Unknown	GO:0005515	CG5003-PA							PS50181			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF81383,SSF101967,SSF52047	141~161								
aly776.1	Glycine receptor subunit alpha-1	GO:0009897,GO:0060077,GO:2000344,GO:0002087,GO:0034707,GO:0006821,GO:0050905,GO:0001508,GO:0016934,GO:0030054,GO:0016594,GO:0007218,GO:0007340,GO:0050884,GO:0030977,GO:0016020,GO:0001964,GO:0060080,GO:0022824,GO:0051970,GO:0006811,GO:0060013,GO:0060012,GO:0006936,GO:0042391,GO:1902476,GO:0005230,GO:0006810,GO:0007601,GO:0007628,GO:0045211,GO:0005887,GO:0007268,GO:0043576,GO:0016935,GO:0043231,GO:0005622	CG12344-PA						PF02931,PF02932		PR00253,PR00253,PR00253,PR00253,PR00252,PR00252,PR00252,PR00252	PS00236	G3DSA:1.20.58.390,G3DSA:1.20.58.390,G3DSA:2.70.170.10	SSF63712,SSF90112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly776.2	Proton-coupled amino acid transporter 4	GO:0003333,GO:0006865,GO:0016021,GO:0015171,GO:0015293	CG8785-PB						PF01490														
aly776.3	Proton-coupled amino acid transporter 4	GO:0003333,GO:0006865,GO:0016021,GO:0015171,GO:0015293	CG8785-PB						PF01490														
aly776.4	Proton-coupled amino acid transporter 4	GO:0003333,GO:0006865,GO:0016021,GO:0015171,GO:0015293	CG8785-PB						PF01490														
aly776.5	Sensory neuron membrane protein 2	GO:0006952,GO:0050896,GO:0035073,GO:0005887,GO:0005044,GO:0016021,GO:0016020,GO:0030425,GO:0055088,GO:0007166,GO:0005886,GO:0007155,GO:0043025,GO:0019236,GO:0007608	CG7000-PA						PF01130		PR01609,PR01609,PR01609,PR01609,PR01609,PR01609												
aly777.1	Zinc finger protein Gfi-1	GO:0071222,GO:0009996,GO:0007638,GO:0000083,GO:0042660,GO:0008270,GO:0003676,GO:0001078,GO:0016604,GO:0000122,GO:0005634,GO:0016363,GO:0070105,GO:0006351,GO:0017053,GO:0034121,GO:0042472,GO:0010977,GO:0010957,GO:0010956,GO:0044212,GO:0045165,GO:0042491,GO:0032088,GO:0000977,GO:0016032,GO:0030099,GO:0045892	CG31632-PA							PS50157		PS00028	G3DSA:3.30.160.60	SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly777.2	Unknown		n/a																				
aly777.3	Zinc finger protein Gfi-1b	GO:0050767,GO:0016363,GO:0051569,GO:0006351,GO:0000122,GO:0005634,GO:0005667,GO:0008270,GO:0003676,GO:0030099,GO:0046872,GO:0016568,GO:0000977	CG31632-PA				SM00355,SM00355		PF00096,PF13912	PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667									
aly777.4	Unknown		n/a																				
aly77756.1	Lipoma-preferred partner homolog	GO:0005856,GO:0001725,GO:0045572,GO:0005925,GO:0005515,GO:0007430,GO:0005634,GO:0007593,GO:0005737,GO:0035002,GO:0035003,GO:0007155,GO:0008270,GO:0005911,GO:0045805,GO:0035329,GO:0048526	CG32018-PB						PF00412	PS50023			G3DSA:2.10.110.10	SSF57716									
aly77925.1	Unknown		n/a												149~169								
aly78.1	Zinc finger protein 1 homolog	GO:0005737,GO:0005819,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0005876,GO:0006351	CG8474-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly78.2	Mothers against decapentaplegic homolog 3	GO:0030878,GO:0001102,GO:0048589,GO:0008586,GO:0048100,GO:0008270,GO:0001745,GO:0050728,GO:2000134,GO:0032332,GO:0045668,GO:0045705,GO:0016202,GO:0000790,GO:0001756,GO:0042993,GO:0007179,GO:0043235,GO:0030618,GO:0060395,GO:0005667,GO:0048340,GO:0002076,GO:0090263,GO:0050821,GO:0010629,GO:0035413,GO:0003677,GO:0005654,GO:0000988,GO:0000987,GO:0007183,GO:0000983,GO:0000980,GO:0048701,GO:0009880,GO:0006810,GO:0017015,GO:0007050,GO:0006955,GO:0035019,GO:0002520,GO:0007424,GO:0038092,GO:0010718,GO:0000122,GO:0006357,GO:0006351,GO:0000978,GO:0007492,GO:0042078,GO:0030308,GO:0031490,GO:0042177,GO:0001666,GO:1901203,GO:0005737,GO:0043565,GO:0001707,GO:0033689,GO:0005637,GO:0005634,GO:0030707,GO:0001947,GO:0003690,GO:0007480,GO:0070306,GO:0097191,GO:0001105,GO:0045595,GO:0045216,GO:0001657,GO:0030718,GO:0050776,GO:0050678,GO:0051098,GO:0045944,GO:0005515,GO:0048617,GO:0032909,GO:0019049,GO:0042110,GO:0045887,GO:0001889,GO:0061045,GO:0007476,GO:0061353,GO:0045930,GO:0060039,GO:0006919,GO:0005886,GO:0007488,GO:0035290,GO:0007507,GO:0003700,GO:0003705,GO:0007391,GO:0001933,GO:0071144,GO:0071141	CG12399-PB				SM00523,SM00524		PF03166,PF03165	PS51076,PS51075			G3DSA:2.60.200.10,G3DSA:3.90.520.10	SSF56366,SSF49879									
aly78.3	Guanine nucleotide-binding protein G(f) subunit alpha	GO:0051489,GO:0031683,GO:0008152,GO:0005834,GO:0007606,GO:0003924,GO:0019001,GO:0035208,GO:0004871,GO:0007191,GO:0001664,GO:0046872,GO:0007186,GO:0031234,GO:0007498,GO:0005525	CG12232-PA				SM00275		PF00503		PR00318,PR00318,PR00318,PR00318,PR00318		G3DSA:1.10.400.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF47895			REACT_14797						
aly78.4	Histone H2B.1	GO:0005634,GO:0003677,GO:0006333,GO:0000786,GO:0046982,GO:0006334	CG33910-PA				SM00427		PF00125		PR00621,PR00621,PR00621,PR00621		G3DSA:1.10.20.10	SSF47113									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly78.5	Histone H4	GO:0005634,GO:0000786,GO:0006333,GO:0003677,GO:0046982,GO:0006334	CG33909-PA				SM00417,SM00803		PF15511		PR00623,PR00623,PR00623,PR00623,PR00623,PR00623,PR00623	PS00047	G3DSA:1.10.20.10	SSF47113									
aly78.6	Unknown		n/a																				
aly78.7	Histone H2A	GO:0005634,GO:0003677,GO:0006333,GO:0000786,GO:0046982,GO:0006334	CG33859-PA				SM00414		PF16211,PF00125		PR00620,PR00620,PR00620,PR00620,PR00620,PR00620	PS00046	G3DSA:1.10.20.10	SSF47113									
aly78.8	Histone H3	GO:0005634,GO:0003677,GO:0006333,GO:0000786,GO:0046982,GO:0006334	CG33866-PA				SM00428		PF00125		PR00622,PR00622,PR00622,PR00622,PR00622,PR00622,PR00622	PS00959,PS00322	G3DSA:1.10.20.10	SSF47113									
aly78.9	MLN64 N-terminal domain homolog	GO:0043231,GO:0016021,GO:0016020,GO:0017127,GO:0005765,GO:0006694,GO:0031902,GO:0015485	CG3522-PA						PF10457	PS51439													
aly78235.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly78255.1	Unknown		n/a																				
aly78257.1	Kynurenine formamidase	GO:0019441,GO:0016272,GO:0034354,GO:0005829,GO:0004061,GO:0005634	CG9542-PA						PF12695				G3DSA:3.40.50.1820	SSF53474									
aly7840.1	Heart- and neural crest derivatives-expressed protein 2	GO:0003700,GO:0005634,GO:0035050,GO:0007508,GO:0006355,GO:0048813,GO:0001077,GO:0006351,GO:0003677,GO:0043066,GO:0030097,GO:0046983,GO:0032968,GO:0007275	CG18144-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459									
aly785.1	Zinc finger protein 891	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG7987-PA				SM00355,SM00355			PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667									
aly78547.1	Protein bric-a-brac 2	GO:0007478,GO:0003700,GO:0007455,GO:0005634,GO:0005700,GO:0006355,GO:0061040,GO:0006351,GO:0003677,GO:0003680	CG8924-PB				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695									
aly78691.1	Unknown	GO:0005319,GO:0005615,GO:0015918,GO:0008289,GO:0045178,GO:0034196,GO:0005875	CG15828-PC																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly788.1	Very-long-chain 3-oxoacyl-CoA reductase	GO:0016229,GO:0006703,GO:0010811,GO:0016021,GO:0005578,GO:0005789,GO:0019432,GO:0004303,GO:0030198,GO:0035338,GO:0044281,GO:0008152,GO:0044255,GO:0008201,GO:0006633	CG1444-PA			PIRSF000126			PF00106		PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080		G3DSA:3.40.50.720	SSF51735									
aly78882.1	Coiled-coil domain-containing protein 130 homolog	GO:0005575,GO:0008150,GO:0003674	CG15084-PA						PF04502						235~255								
aly7895.1	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6467-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly7895.2	Unknown		n/a																				
aly7915.1	Protein embryonic gonad	GO:0043565,GO:0006351,GO:0030522,GO:0003700,GO:0005634,GO:0030154,GO:0003707,GO:0006355,GO:0008270,GO:0043401,GO:0004879,GO:0007417	CG7383-PB				SM00399		PF00105	PS51030	PR00047,PR00047,PR00047,PR00047	PS00031	G3DSA:1.10.565.10,G3DSA:3.30.50.10	SSF57716			REACT_71						
aly7915.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7915.3	Unknown		n/a																				
aly7917.1	BMP and activin membrane-bound inhibitor homolog	GO:0005737,GO:0008284,GO:0032092,GO:0010718,GO:0090263,GO:0016021,GO:0016020,GO:0005109,GO:0008360,GO:0045893,GO:0035413,GO:0005886,GO:0016477,GO:0030512,GO:0007179	n/a						PF06211				G3DSA:2.10.60.10	SSF57302									
aly7917.2	4-hydroxyphenylpyruvate dioxygenase	GO:0006572,GO:0006559,GO:0003868,GO:0055114,GO:0046872,GO:0009072	CG11796-PA					TIGR01263	PF00903,PF00903				G3DSA:3.10.180.10,G3DSA:3.10.180.10,G3DSA:3.10.180.10,G3DSA:3.10.180.10,G3DSA:3.10.180.10	SSF54593,SSF54593	151~171								
aly7917.3	Translocation protein SEC62	GO:0008565,GO:0005784,GO:0005791,GO:0045111,GO:0016021,GO:0006620,GO:0006614,GO:0016235,GO:0015031,GO:0005789	CG4758-PB						PF03839														
aly7917.4	Probable serine hydrolase	GO:0017171,GO:0007586,GO:0009636,GO:0052689,GO:0005575,GO:0008152,GO:0007275	CG3943-PA						PF00561		PR00111,PR00111,PR00111		G3DSA:3.40.50.1820	SSF53474									
aly7917.5	Helicase required for RNAi-mediated heterochromatin assembly 1	GO:0030702,GO:0005829,GO:0005634,GO:0005524,GO:0003723,GO:0007059,GO:0031048,GO:0004386,GO:0031380,GO:0007049,GO:0031379	CG6204-PA						PF13087,PF13086				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	602~622								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly793.1	Unknown	GO:0005319,GO:0005615,GO:0006869,GO:0015026,GO:0036122,GO:0043395,GO:0007474,GO:0030513	CG31150-PA						PF09172,PF01347	PS51211			G3DSA:1.25.10.20,G3DSA:1.25.10.20,G3DSA:2.30.230.10	SSF48431,SSF56968			REACT_22258						
aly793.2	Glutamate receptor ionotropic, kainate 2	GO:0060025,GO:0019228,GO:0050806,GO:0030425,GO:0050804,GO:0043524,GO:0043525,GO:0060080,GO:0046328,GO:0048169,GO:0035249,GO:0030054,GO:0001662,GO:0032983,GO:0006886,GO:0015277,GO:0007215,GO:0007268,GO:0032839,GO:0035235,GO:0006874,GO:0006811,GO:0006810,GO:0005234,GO:0034220,GO:0051402,GO:0014069,GO:0005887,GO:0005886,GO:0060079,GO:0043204,GO:0043195,GO:0042734,GO:0045211,GO:0048812,GO:0051967,GO:0048172,GO:0043113	CG11155-PA				SM00918,SM00079		PF01094,PF10613,PF00060		PR00177,PR00177		G3DSA:3.40.190.10,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:1.10.287.70	SSF53822,SSF53822,SSF53850,SSF53850									
aly793.3	Unknown	GO:0006811,GO:0060025,GO:0015277,GO:0005234,GO:0048812,GO:0005886	CG11155-PA						PF01094				G3DSA:3.40.50.2300	SSF53822									
aly79371.1	Ferrochelatase, mitochondrial	GO:0006783,GO:0006782,GO:0051537,GO:0004325,GO:0005743,GO:0046872,GO:0005875	CG2098-PA						PF00762			PS00534	G3DSA:3.40.50.1400	SSF53800		00860+4.99.1.1			UPA00252				
aly794.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7953.1	Limbic system associated membrane protein	GO:0050767,GO:0016337,GO:0043005,GO:0009986,GO:0007606,GO:0005575,GO:0035641,GO:0003674,GO:0005911,GO:0005886,GO:0043025,GO:0031225	CG33996-PB				SM00409,SM00409,SM00408,SM00408		PF07686,PF13895	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726									
aly7956.1	Unknown	GO:0003677	n/a						PF13518,PF01498				G3DSA:1.10.10.10	SSF46689									
aly7956.2	Unknown		n/a						PF13843,PF13843														
aly7956.3	Unknown		n/a																				
aly7956.4	Unknown		n/a																				
aly7956.5	Unknown		n/a																				
aly7956.6	Unknown		n/a																				
aly798.1	Unknown		n/a																				
aly798.10	COMM domain-containing protein 10	GO:0005737,GO:0006355,GO:0005634,GO:0006351	CG2371-PB						PF07258														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly798.11	E3 ubiquitin-protein ligase arih1l	GO:0005737,GO:0016874,GO:0005634,GO:0016567,GO:0042787,GO:0008270,GO:0004842	CG5659-PA				SM00647,SM00647		PF01485,PF01485	PS50089			G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57850,SSF57850,SSF57850	437~457								
aly798.12	Sodium channel protein para	GO:0007638,GO:0005886,GO:0019228,GO:0016591,GO:0001666,GO:0005634,GO:0043967,GO:0009612,GO:0000166,GO:0035725,GO:0005671,GO:0005509,GO:0006366,GO:0046684,GO:0046680,GO:0005272,GO:0043966,GO:0008283,GO:0035079,GO:0006814,GO:0007268,GO:0005887,GO:0003899,GO:0022008,GO:0086010,GO:0001518,GO:0045433,GO:0005705,GO:0042493,GO:0005700,GO:0005701,GO:0005665,GO:0005515,GO:0005248,GO:0007095,GO:0003682	CG9907-PBF						PF11933,PF06512,PF00520,PF00520,PF00520,PF00520	PS50222	PR00170,PR00170		G3DSA:1.20.5.150,G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350	SSF81324,SSF81324,SSF81324,SSF81324,SSF81324,SSF81324	24~58,422~478		REACT_18266						
aly798.13	Unknown		n/a																				
aly798.14	Cytochrome P450 6B5 (Fragment)	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG13977-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly798.15	Cytochrome P450 6B2	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0070330,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264	267~287		REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly798.16	Phosphomevalonate kinase	GO:0005737,GO:0005777,GO:0008299,GO:0006695,GO:0004631,GO:0019287,GO:0005524	CG10268-PA					TIGR01223	PF04275				G3DSA:3.40.50.300			00900+2.7.4.2		PWY-922,PWY-7391	UPA00057				
aly798.17	Protein groucho-2	GO:0043234,GO:0007015,GO:0003714,GO:0007399,GO:0000122,GO:0071837,GO:0008134,GO:0007541,GO:0045879,GO:0090090,GO:0006355,GO:0048813,GO:0046331,GO:0045892,GO:0005515,GO:0003677,GO:0005634,GO:0001106,GO:0030178,GO:0070491	CG8384-PE				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF03920,PF00400	PS50082,PS50294,PS50082,PS50294,PS50082	PR01850,PR01850,PR01850,PR01850,PR01850	PS00678,PS00678	G3DSA:2.130.10.10	SSF50978	22~49								
aly798.18	Krueppel-like factor 15	GO:0043565,GO:0072112,GO:0006351,GO:0044212,GO:0003700,GO:0005634,GO:2000757,GO:0015758,GO:0045944,GO:1901653,GO:0010001,GO:0003677,GO:0046872,GO:0014898,GO:0010468,GO:0045893	CG2932-PA				SM00355,SM00355,SM00355		PF00096	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly798.19	Unconventional myosin-IXa	GO:0032027,GO:0008586,GO:0005902,GO:0031477,GO:0035556,GO:0035317,GO:0005737,GO:0042623,GO:0016021,GO:0045179,GO:0008407,GO:0003779,GO:0048800,GO:0016459,GO:0046872,GO:0003774,GO:0005524,GO:0007605,GO:0005096,GO:0030898,GO:0030048,GO:0035293,GO:0007469,GO:0007015,GO:0007423,GO:0016461	CG7595-PA				SM00242,SM00015,SM00015,SM00015,SM00314		PF00612,PF00612,PF00612,PF00063,PF00063,PF00788	PS50096,PS51456,PS50096,PS50096,PS50200	PR00193,PR00193,PR00193,PR00193,PR00193,PR00193			SSF52540,SSF52540,SSF54236	1102~1122									
aly798.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly798.20	Unconventional myosin-IXa	GO:0048749,GO:0030675,GO:0016337,GO:0005622,GO:0007480,GO:0019992,GO:0016021,GO:0005096,GO:0032314,GO:0005575,GO:0032855,GO:0016459,GO:0046872,GO:0007165,GO:0035556,GO:0034334,GO:0003774,GO:0005524,GO:0043408	CG3208-PA				SM00324,SM00109,SM00109		PF00130,PF00130,PF00620	PS50081,PS50081,PS50238		PS00479	G3DSA:1.10.555.10,G3DSA:3.30.60.20,G3DSA:3.30.60.20	SSF57889,SSF57889,SSF48350			REACT_11044						
aly798.21	Protein LAS1	GO:0005737,GO:0005730,GO:0005634,GO:0030687,GO:0005739,GO:0000460,GO:0000448,GO:0000470,GO:0022008	CG32075-PA						PF04031														
aly798.22	Probable phospholipid-transporting ATPase IM	GO:0005794,GO:0007030,GO:0000287,GO:0006812,GO:0015914,GO:0004012,GO:0019829,GO:0045332,GO:0005886,GO:0015662,GO:0016021,GO:0005524	CG42321-PH					TIGR01494,TIGR01652	PF12710,PF16212,PF16209,PF00122		PR00119,PR00119,PR00119	PS00154	G3DSA:2.70.150.10,G3DSA:2.70.150.10,G3DSA:3.40.50.1000,G3DSA:3.40.50.1000,G3DSA:3.40.1110.10,G3DSA:3.40.1110.10	SSF81665,SSF81665,SSF81665,SSF81660,SSF81660,SSF81653,SSF81653,SSF56784,SSF56784,SSF56784									
aly798.23	Unknown		n/a																				
aly798.24	Methyl-CpG-binding domain protein 3	GO:0003714,GO:0048568,GO:0044030,GO:0003677,GO:0007275,GO:0005737,GO:0032355,GO:0001701,GO:0000122,GO:0006325,GO:0005634,GO:0043044,GO:0006346,GO:0005654,GO:0016573,GO:0042826,GO:0042803,GO:0008327,GO:0009888,GO:0000792,GO:0000790,GO:0045892,GO:0007420,GO:0043234,GO:0007507,GO:0007568,GO:0016581,GO:0031667,GO:0005700,GO:0006351,GO:0005515,GO:0003682	CG8208-PC				SM00391		PF16564,PF14048,PF01429	PS50982			G3DSA:3.30.890.10	SSF54171	225~248								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly798.25	GPI mannosyltransferase 2	GO:0051205,GO:0045052,GO:0016021,GO:0005789,GO:0006506,GO:0042996,GO:0016758,GO:0004584,GO:0070863,GO:0045313,GO:0000030	CG44239-PA						PF04188										UPA00196				
aly798.26	Ubiquilin-1	GO:2000785,GO:0005783,GO:0005886,GO:0016235,GO:1901340,GO:0031593,GO:0042982,GO:0005737,GO:0070628,GO:0031410,GO:0005776,GO:0005654,GO:0035973,GO:0031398,GO:0071456,GO:0031396,GO:0048471,GO:0042802,GO:1902175,GO:1903071,GO:0019900,GO:0034140,GO:1902453,GO:0030433,GO:0000502,GO:0043234,GO:0016241,GO:0034976	CG14224-PA				SM00165,SM00727,SM00727,SM00727,SM00727,SM00213		PF00240,PF00627	PS50030,PS50053			G3DSA:1.10.8.10,G3DSA:3.10.20.90	SSF54236,SSF46934									
aly798.27	Tubulin polyglutamylase ttll6	GO:0005737,GO:0036064,GO:0015631,GO:0018095,GO:0030030,GO:0006464,GO:0016874,GO:0004835	CG5987-PA						PF03133	PS51221				SSF56059,SSF56059									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly798.28	Cyclin-dependent kinase 7	GO:0032806,GO:0008022,GO:0000086,GO:0001111,GO:0000082,GO:0004672,GO:0004693,GO:0008353,GO:0007067,GO:0050434,GO:0051301,GO:0006283,GO:0005737,GO:0006361,GO:0030521,GO:0005634,GO:0008283,GO:0003713,GO:0040029,GO:0005739,GO:0005654,GO:0004674,GO:0010467,GO:0006362,GO:0005509,GO:0006367,GO:0005675,GO:0006368,GO:0045814,GO:0005524,GO:0006468,GO:0000278,GO:0006281,GO:0050681,GO:0006366,GO:0006289,GO:0007050,GO:0012501,GO:0045893,GO:0006360,GO:0048471,GO:0008094,GO:0000718,GO:0000079,GO:0006370,GO:0045944,GO:0016032,GO:0006363,GO:0000990	CG3319-PA				SM00220		PF00069	PS50011		PS00107,PS00108	G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112									
aly798.29	DET1 homolog	GO:0005634,GO:0003682,GO:0048477,GO:0005700,GO:0000122	CG6093-PA						PF09737					SSF82171,SSF82171									
aly798.3	Unknown		n/a																				
aly798.30	Tyrosine-protein kinase CSK	GO:0005737,GO:0008285,GO:0006468,GO:0045926,GO:0005524,GO:0045197,GO:0018108,GO:0034334,GO:0002376,GO:0007293,GO:0004715,GO:0004713,GO:0004672,GO:0043068,GO:0010669,GO:0007165	CG42317-PG				SM00219,SM00252		PF07714,PF00017	PS50001,PS50011	PR00401,PR00401,PR00401,PR00401,PR00401,PR00109,PR00109,PR00109,PR00109,PR00109	PS00107,PS00109	G3DSA:3.30.505.10,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF55550,SSF55550,SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly798.31	Cytochrome c oxidase assembly protein COX16 homolog, mitochondrial	GO:0016021,GO:0031966	CG14865-PB						PF14138														
aly798.32	ADAM 17-like protease	GO:0006509,GO:0006508,GO:0016021,GO:0004222,GO:0008270	CG7908-PA				SM00050		PF16698,PF01562,PF00200,PF13574	PS50215,PS50214			G3DSA:4.10.70.10,G3DSA:3.40.390.10	SSF57552,SSF55486									
aly798.33	Dynein heavy chain, cytoplasmic	GO:0016319,GO:0045198,GO:0034501,GO:0045197,GO:0007301,GO:0008088,GO:0007294,GO:0005524,GO:0030286,GO:0007067,GO:0030723,GO:0005874,GO:0005875,GO:0005737,GO:0040003,GO:0005938,GO:0040001,GO:0042623,GO:0006886,GO:0047497,GO:0007349,GO:0005739,GO:0030529,GO:0048134,GO:0007098,GO:0048477,GO:0003774,GO:0003777,GO:0005794,GO:0007298,GO:0048311,GO:0034063,GO:0035011,GO:0007051,GO:0046604,GO:0007282,GO:0007312,GO:0005868,GO:0051237,GO:0007405,GO:0051642,GO:0000776,GO:0050658,GO:0007279,GO:0045172,GO:0007018,GO:0007052,GO:0045169,GO:0030071,GO:0048813,GO:0008298,GO:0045478,GO:0043148,GO:0051683,GO:2001019	CG7507-PI				SM00382,SM00382,SM00382,SM00382		PF12781,PF12774,PF08385,PF07728,PF12777,PF03028,PF12775,PF12780,PF08393				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540	1273~1300,1166~1186,597~617,3170~3190,3764~3784,867~887,3201~3246,4655~4656,3250~3270,538~565,3424~3465,3396~3416							
aly798.34	Unknown	GO:0005549,GO:0016020,GO:0007608,GO:0004984	n/a						PF02949														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly798.35	Unknown		n/a																				
aly798.4	Phorbol ester/diacylglycerol-binding protein unc-13	GO:0019992,GO:0043051,GO:0048786,GO:0005622,GO:0045202,GO:0005515,GO:0007268,GO:0035556,GO:0046872,GO:0046662	n/a						PF00168				G3DSA:2.60.40.150	SSF49562	840~912,614~650								
aly798.5	Protein prenyltransferase alpha subunit repeat-containing protein 1	GO:0018342,GO:0005968,GO:0008318,GO:0004663	CG3073-PA						PF01239	PS51147,PS51147,PS51147,PS51147,PS51147			G3DSA:1.25.40.120,G3DSA:1.25.40.120	SSF48439,SSF48439									
aly798.6	Ras GTPase-activating protein 1	GO:0016319,GO:0048149,GO:0030539,GO:0005161,GO:0030036,GO:0000281,GO:0009790,GO:0007162,GO:0043524,GO:0007165,GO:0046326,GO:0001953,GO:0044325,GO:0043087,GO:0005737,GO:0030833,GO:0043547,GO:0040008,GO:0016020,GO:0036120,GO:0044344,GO:0048146,GO:0032403,GO:0005099,GO:0031965,GO:0008134,GO:0005096,GO:0019901,GO:0019900,GO:0030971,GO:0046580,GO:0005886,GO:0007155,GO:0042493,GO:0031235,GO:0001570,GO:0071364,GO:0050731,GO:0005829,GO:0090630,GO:0032868,GO:0032320,GO:0001934	CG9209-PD				SM00323,SM00252,SM00252,SM00326,SM00233		PF00168,PF00017,PF00017,PF00018,PF00169,PF00616	PS50018,PS50001,PS50004,PS50001,PS50002,PS50003	PR00401,PR00401,PR00401,PR00401,PR00401		G3DSA:3.30.505.10,G3DSA:3.30.505.10,G3DSA:2.30.30.40,G3DSA:2.30.29.30,G3DSA:1.10.506.10,G3DSA:2.60.40.150	SSF50729,SSF48350,SSF50044,SSF49562,SSF55550,SSF55550									
aly798.7	Endophilin-A	GO:0005737,GO:0005543,GO:0007269,GO:0050803,GO:0005829,GO:0016020,GO:0008152,GO:0097320,GO:0042171,GO:0005515,GO:0048488	CG14296-PA				SM00326,SM00721		PF14604,PF03114	PS51021,PS50002	PR00452,PR00452,PR00452,PR00452		G3DSA:1.20.1270.60,G3DSA:2.30.30.40	SSF50044,SSF103657									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly798.8	DmX-like protein 2	GO:0007424,GO:0030672,GO:0005615,GO:0007035,GO:0008021,GO:0017137,GO:0005515,GO:0008593,GO:0030054	CG3585-PB				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF12234,PF12234	PS50082,PS50082,PS50294			G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978,SSF50978,SSF50978									
aly798.9	Isoleucine--tRNA ligase, cytoplasmic	GO:0005737,GO:0004812,GO:0070062,GO:0004822,GO:0005829,GO:0016020,GO:0006428,GO:0000166,GO:0005654,GO:0051020,GO:0001649,GO:0002161,GO:0006418,GO:0005524	CG11471-PD	MF_02003				TIGR00392	PF08264,PF00133		PR00984,PR00984,PR00984,PR00984,PR00984	PS00178	G3DSA:3.90.740.10,G3DSA:1.10.730.10,G3DSA:3.40.50.620,G3DSA:3.40.50.620	SSF47323,SSF52374,SSF52374,SSF50677		00970+6.1.1.5	REACT_71						
aly7985.1	Unknown	GO:0009987	CG42700-PD																				
aly7985.10	Unknown		n/a																				
aly7985.11	Unknown		n/a																				
aly7985.2	Cytochrome c oxidase assembly factor 5		CG13018-PA						PF10203														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7985.3	Cysteine--tRNA ligase, mitochondrial	GO:0006423,GO:0004817,GO:0005829,GO:0005759,GO:0046872,GO:0005524	CG8257-PA	MF_00041				TIGR00435	PF01406		PR00983,PR00983,PR00983,PR00983		G3DSA:3.40.50.620	SSF47323,SSF52374	372~392	00970+6.1.1.16	REACT_71						
aly7985.4	Transmembrane protein 39A	GO:0016021,GO:1903146	CG13016-PA						PF10271,PF10271														
aly7985.5	Membrane-bound transcription factor site-2 protease	GO:0005737,GO:1990440,GO:0051091,GO:0034976,GO:0004222,GO:0035103,GO:0016021,GO:0031293,GO:0006508,GO:0046872,GO:0008237,GO:0008203	CG8988-PA						PF02163		PR01000,PR01000,PR01000,PR01000		G3DSA:2.30.42.10	SSF50156									
aly7985.6	LYR motif-containing protein 2		CG34229-PA						PF13232														
aly7985.7	Sine oculis-binding protein homolog	GO:0048749,GO:0007626,GO:0042472,GO:0007605,GO:0008134,GO:0046872,GO:0032184	CG8991-PA						PF15279														
aly7985.8	Guanine nucleotide-binding protein subunit beta-like protein 1	GO:0005737,GO:0035176,GO:0009898,GO:0005515,GO:0035556,GO:0007186	CG13192-PA				SM00320,SM00320,SM00320,SM00320		PF00400	PS50294,PS50082		PS00678	G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly7985.9	Exostosin-2	GO:0030206,GO:0005783,GO:0008101,GO:0005789,GO:0008375,GO:0031227,GO:0005615,GO:0006486,GO:0016021,GO:0015020,GO:0046872,GO:0030210,GO:0005794,GO:0050508,GO:0050509,GO:0007224,GO:0016055,GO:0006044,GO:0000139,GO:0015012,GO:0005515,GO:0015014,GO:0006024	CG8433-PB						PF09258,PF03016				G3DSA:3.90.550.10	SSF53448										
aly7999.1	Probable inactive tRNA-specific adenosine deaminase-like protein 3	GO:0016787,GO:0008033,GO:0008270	CG10927-PA						PF00383				G3DSA:3.40.140.10,G3DSA:3.40.140.10	SSF53927,SSF53927	368~369								
aly7999.2	FMRFamide-related neuropeptides	GO:0005179,GO:0007218,GO:0005184,GO:0005615,GO:0007621,GO:0048018,GO:0048047,GO:0005576,GO:0071855	CG33527-PB																				
aly7999.3	FMRFamide-related neuropeptides	GO:0005179,GO:0007218,GO:0005184,GO:0005615,GO:0007621,GO:0048018,GO:0048047,GO:0005576,GO:0071855	CG33527-PB																				
aly7999.4	Unconventional myosin-Va	GO:0060001,GO:0032027,GO:0042052,GO:0007291,GO:0032869,GO:0031475,GO:0032593,GO:0016028,GO:0000146,GO:0042623,GO:0006886,GO:0047497,GO:0003779,GO:0016459,GO:0048477,GO:0003774,GO:0005524,GO:0031941,GO:0045856,GO:0030898,GO:0008595,GO:0051015,GO:0008152,GO:0072659,GO:0016192,GO:0030048,GO:0043025,GO:0000139,GO:0005516	CG2146-PC				SM00015,SM00015,SM00015,SM00015,SM00015,SM00242		PF00063,PF00612,PF00612,PF00612,PF01843	PS51456,PS50096,PS50096,PS50096,PS50096,PS50096,PS51126,PS50096,PS50096	PR00193,PR00193,PR00193,PR00193,PR00193,PR00193		G3DSA:1.20.5.190,G3DSA:1.20.5.190	SSF52540,SSF52540,SSF50084	974~1040,1305~1332,919~946,1200~1220,1161~1181									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8.1	Unknown		n/a																				
aly8.10	Unknown		CG13868-PA																				
aly8.11	Probable G-protein coupled receptor 52	GO:0001588,GO:0007626,GO:0009744,GO:0042594,GO:0010579,GO:0004930,GO:0016021,GO:0035100,GO:0035075,GO:0043410,GO:0008306,GO:0009267,GO:0046959,GO:0005887,GO:0005886,GO:0007186,GO:0008227,GO:0071329	CG18314-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly8.12	Unknown		n/a																				
aly8.13	Unknown		n/a																				
aly8.2	Unknown		n/a								PR01217,PR01217,PR01217,PR01217												

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8.3	Unknown		n/a																				
aly8.4	Unknown		n/a																				
aly8.5	Unknown		n/a																				
aly8.6	Probable RNA directed DNA polymerase from transposon X-element	GO:0003964,GO:0006278,GO:0006313	n/a										G3DSA:3.60.10.10	SSF56219									
aly8.7	Unknown		n/a						PF14529				G3DSA:3.60.10.10										
aly8.8	Unknown		CG13868-PA												25~45								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8.9	Unknown		CG13868-PA																				
aly80.1	Unknown	GO:0030176,GO:0004168,GO:0043048	CG8311-PA																				
aly80.10	Tropomyosin-1, isoforms 9A/A/B	GO:0010591,GO:0031941,GO:0006936,GO:0005829,GO:0007315,GO:0051015,GO:0003779,GO:0030017,GO:0048813,GO:0016529,GO:0070865,GO:0048477,GO:0005862,GO:0045451	CG4898-PE												232~259								
aly80.11	Tropomyosin	GO:0010591,GO:0031941,GO:0006936,GO:0007315,GO:0051015,GO:0003779,GO:0030017,GO:0048813,GO:0016529,GO:0070865,GO:0048477,GO:0005862,GO:0045451	CG4898-PE						PF00261				G3DSA:1.20.5.340	SSF57997	4~52,78~134		REACT_17044						
aly80.12	Tropomyosin-1	GO:0003779,GO:0007507,GO:0005862	CG4843-PA						PF00261		PR00194,PR00194,PR00194,PR00194		G3DSA:1.20.5.340,G3DSA:1.20.5.340,G3DSA:1.20.5.340	SSF57997	1~196		REACT_17044						
aly80.2	NAD-dependent protein deacetylase Sirt6	GO:0008340,GO:0046872,GO:0031937,GO:0070403,GO:0016787	CG6284-PB						PF02146,PF02146	PS50305			G3DSA:3.40.50.1220,G3DSA:3.40.50.1220	SSF52467									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly80.3	Nuclear cap-binding protein subunit 1	GO:0005846,GO:0071013,GO:0071011,GO:0030422,GO:0005634,GO:0045071,GO:0000398,GO:0006370,GO:0031047,GO:0000339,GO:0045292,GO:0022008,GO:0035195,GO:0051028	CG7035-PA				SM00543		PF09088,PF02854,PF09090				G3DSA:1.25.40.180,G3DSA:1.25.40.180,G3DSA:1.25.40.180,G3DSA:1.25.40.180	SSF48371,SSF48371,SSF48371	612~639								
aly80.4	Fructose-1,6-bisphosphatase 1	GO:0005737,GO:0042132,GO:0005975,GO:0030308,GO:0071286,GO:0051289,GO:0016311,GO:0005829,GO:0016208,GO:0042578,GO:0035690,GO:0048029,GO:0046580,GO:0045820,GO:0046872,GO:0006111,GO:0006002,GO:0006094	CG31692-PE	MF_01855		PIRSF000904,PIRSF500210			PF00316		PR00115,PR00115,PR00115,PR00115,PR00115,PR00115	PS00124	G3DSA:3.40.190.80,G3DSA:3.30.540.10	SSF56655		00051+3.1.3.11,00030+3.1.3.11,00010+3.1.3.11,00680+3.1.3.11,00710+3.1.3.11	REACT_474	PWY-5484	UPA00138				
aly80.5	Mortality factor 4-like protein 1	GO:0035064,GO:0000123,GO:0008283,GO:0043968,GO:0043486,GO:0005634,GO:0000724,GO:0006355,GO:0016575,GO:0043967,GO:0035267,GO:0016573,GO:0006342,GO:0016580,GO:0003682,GO:0040008,GO:0006351	CG6363-PB			PIRSF038133	SM00298		PF05712,PF11717	PS51640			G3DSA:2.30.30.270,G3DSA:2.30.30.270	SSF54160,SSF54160									
aly80.6	Tropomyosin-2	GO:0003779,GO:0007507,GO:0005862	CG4843-PA						PF00261		PR00194,PR00194,PR00194,PR00194	PS00326	G3DSA:1.20.5.340,G3DSA:1.20.5.340	SSF57997	1~251		REACT_17044						
aly80.7	Synaptotagmin 4	GO:0008021,GO:0031045,GO:0031594,GO:0048167,GO:0031340,GO:0030054,GO:0031982,GO:0016021,GO:0016020,GO:0005544,GO:0045955,GO:0043005,GO:0048471,GO:0046872,GO:0001786,GO:0017156,GO:0031339,GO:0005215,GO:0045211,GO:0046928,GO:0030276,GO:0007269,GO:0005886,GO:0016192,GO:0030672,GO:0007420,GO:0016079,GO:0048791,GO:0000149	CG10047-PA				SM00239,SM00239		PF00168,PF00168	PS50004,PS50004	PR00399,PR00399,PR00399,PR00399,PR00360,PR00360		G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly80.8	Tumor necrosis factor, alpha-induced protein 8-like protein 2 A	GO:0005737,GO:0050728,GO:0050868,GO:0035071,GO:0045087,GO:0048102,GO:0043027	CG4091-PC						PF05527														
aly80.9	Unknown		n/a												973~995								
aly800.1	Exonuclease 3' 5' domain-containing protein 2	GO:0005737,GO:0008408,GO:0005634,GO:0090305,GO:0003676,GO:0016444	CG6744-PA				SM00474		PF01612	PS51257			G3DSA:3.30.420.10	SSF53098									
aly800.10	PAX3- and PAX7-binding protein 1	GO:0007517,GO:2000288,GO:0006355,GO:0071011,GO:0071013,GO:0000398,GO:0014842,GO:0003700,GO:0045944,GO:0006351,GO:0031062,GO:0003677,GO:0000978,GO:0005634,GO:0005829	CG1965-PA																				
aly800.11	60S acidic ribosomal protein P0	GO:0005737,GO:0003735,GO:0005840,GO:0022625,GO:0005634,GO:0006281,GO:0042254,GO:0003906,GO:0006414,GO:0006412	CG7490-PB			PIRSF039087			PF00466					SSF160369									
aly800.12	E3 ubiquitin-protein ligase RNF13	GO:0061630,GO:0016021,GO:0031902,GO:0051865,GO:0004842,GO:0008270,GO:0005515,GO:0016874,GO:0005634	CG10277-PA				SM00184		PF02225,PF13639	PS50089			G3DSA:3.30.40.10,G3DSA:3.50.30.30	SSF52025,SSF57850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly800.2	Probable ATP-dependent RNA helicase DDX23	GO:0003676,GO:0070062,GO:0005730,GO:0005634,GO:0005739,GO:0005654,GO:0010467,GO:0010501,GO:0044822,GO:0005524,GO:0071011,GO:0071013,GO:0004004,GO:0000375,GO:0000354,GO:0005886,GO:0022008,GO:0030532,GO:0000398,GO:0008380,GO:0005682,GO:0005681	CG10333-PA				SM00487,SM00490		PF00270,PF00271	PS51195,PS51194,PS51192		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	142~162,180~215,315~345,221~241								
aly800.3	Unknown		CG5903-PA						PF09769														
aly800.4	Unknown	GO:0004862,GO:0006469	n/a						PF02827														
aly800.5	Wiskott-Aldrich syndrome protein	GO:0035017,GO:0019901,GO:0008582,GO:0012506,GO:0007596,GO:0006900,GO:0042110,GO:0030041,GO:0005902,GO:0045886,GO:0034314,GO:0003383,GO:0008544,GO:0007413,GO:0008356,GO:0006955,GO:0015629,GO:0005737,GO:0016028,GO:0070062,GO:0006886,GO:0008407,GO:0050790,GO:0003779,GO:0016476,GO:0042802,GO:0016203,GO:0038096,GO:0050852,GO:2000601,GO:0035212,GO:0045087,GO:0006461,GO:0072583,GO:0008154,GO:0030695,GO:0030833,GO:0043274,GO:0007409,GO:0007286,GO:0007520,GO:0007264,GO:0043234,GO:0006952,GO:0045165,GO:0005911,GO:0007423,GO:0030048,GO:0009913,GO:0001578,GO:0005829,GO:0016197,GO:0017124,GO:0005515,GO:2000146,GO:0005634,GO:0002625	CG1520-PA				SM00285,SM00461		PF00786,PF00568	PS50229,PS50108,PS51082			G3DSA:2.30.29.30,G3DSA:3.90.810.10	SSF50729,SSF47912									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly800.6	Zinc finger protein Xfin	GO:0045931,GO:0005737,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0003723,GO:0003676,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00868,SM00868		PF13912,PF13912,PF13894,PF12874,PF12874,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57716	1635~1637								
aly800.7	RCC1 domain-containing protein 1		CG6678-PA						PF00415,PF00415	PS50012,PS50012	PR00633,PR00633,PR00633		G3DSA:2.130.10.30	SSF50985									
aly800.8	Putative protein arginine N-methyltransferase 9	GO:0005737,GO:0006479,GO:0016274,GO:0005575,GO:0008168,GO:0019919	CG9882-PB						PF06325	PS50293			G3DSA:3.40.50.150,G3DSA:2.70.160.11,G3DSA:1.25.40.10	SSF48452,SSF53335									
aly800.9	PAX3- and PAX7-binding protein 1	GO:0007517,GO:0005829,GO:2000288,GO:0071011,GO:0005634,GO:0008134,GO:0000398,GO:0014842,GO:0006355,GO:0045944,GO:0003700,GO:0031062,GO:0003677,GO:0000978,GO:0071013,GO:0006351	CG1965-PA						PF07842														
aly8000.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8009.1	Unknown		n/a																				
aly80248.1	Unconventional myosin-Va	GO:0060001,GO:0031941,GO:0000146,GO:0000139,GO:0016459,GO:0005516,GO:0008152,GO:0032869,GO:0032593,GO:0072659,GO:0005524,GO:0016192	n/a																				
aly804.1	Sodium-independent sulfate anion transporter	GO:0045434,GO:0005794,GO:0005783,GO:0015301,GO:0016021,GO:0005886,GO:0005765,GO:0008271,GO:0008272,GO:0098656,GO:0008509,GO:0070062	CG7005-PA						PF01740,PF00916														
aly8044.1	Unknown		n/a																				
aly8044.10	Unknown		n/a																				
aly8044.11	Chitinase A	GO:0005975,GO:0000272,GO:0005575,GO:0004568,GO:0006032,GO:0006036	CG2054-PA				SM00089,SM00636		PF00704,PF08329			PS01095	G3DSA:2.60.40.10,G3DSA:3.20.20.80,G3DSA:3.20.20.80,G3DSA:3.10.50.10	SSF54556,SSF51445,SSF51445,SSF81296		00520+3.2.1.14		PWY-6902					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8044.12	Cell adhesion molecule 1	GO:0008021,GO:0016338,GO:0030425,GO:0030424,GO:0001889,GO:0045202,GO:0007416,GO:0009826,GO:0042271,GO:0070062,GO:0016021,GO:0045954,GO:0042803,GO:0008037,GO:0030154,GO:0006915,GO:0016323,GO:0007283,GO:0030165,GO:0005911,GO:0005886,GO:0007155,GO:0051606,GO:0007157,GO:0007156,GO:0070852,GO:0007420,GO:0050715,GO:0043196,GO:0060348,GO:0002376,GO:0005515,GO:0005102	CG34113-PO				SM00408,SM00408,SM00408,SM00409,SM00409		PF08205,PF07679,PF13927	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly8044.13	Unknown		n/a																				
aly8044.2	Unknown		n/a																				
aly8044.3	Unknown		n/a																				
aly8044.4	tRNA pseudouridine synthase A, mitochondrial	GO:0005730,GO:0004730,GO:0031119,GO:0044822,GO:0009982,GO:0030374,GO:0000790,GO:0005739,GO:0045944,GO:0003723,GO:0005667,GO:0009451,GO:0001522	CG4159-PB					TIGR00071	PF01416,PF01416				G3DSA:3.30.70.660,G3DSA:3.30.70.580	SSF55120									
aly8044.5	Protein tipE	GO:0045433,GO:0016021,GO:0005248,GO:0035725,GO:0006814,GO:0017080,GO:0005887,GO:0005886,GO:0034605,GO:0002028	CG12806-PB						PF16972,PF16972														
aly8044.6	Cyclin-J	GO:0016538,GO:0007067,GO:0005634,GO:0045448	CG10308-PA				SM00385		PF00134				G3DSA:1.10.472.10,G3DSA:1.10.472.10	SSF47954									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8044.7	Actin-interacting protein 1	GO:0005737,GO:0003779,GO:0030833,GO:0006909,GO:0005856,GO:0001736,GO:0008154,GO:0045214,GO:0034316,GO:0030834,GO:0007298,GO:0030042,GO:0035317	CG10724-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50082,PS50082,PS50082,PS50294		PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50998,SSF50998,SSF50978									
aly8044.8	Longitudinals lacking protein, isoform G	GO:0007409,GO:0019730,GO:0035167,GO:0045467,GO:0003677,GO:0007411,GO:0002121,GO:0031987,GO:0005634,GO:0044719,GO:0008406,GO:0005654,GO:0001964,GO:0046872,GO:0045893,GO:0045476,GO:0022008,GO:0007526,GO:0003700,GO:0048854,GO:0007464,GO:0016199,GO:0006355,GO:0048813,GO:0006351	CG32121-PB				SM00355,SM00355,SM00225		PF00651	PS50157,PS50097		PS00028	G3DSA:3.30.710.10,G3DSA:3.30.160.60	SSF57667,SSF54695									
aly8044.9	Unknown		n/a												21~44								
aly8046.1	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly8046.2	Zinc finger protein OZF	GO:0005737,GO:0043565,GO:0005730,GO:0005634,GO:0006355,GO:0001077,GO:0003677,GO:0046872,GO:0032968,GO:0007527	CG11924-PA				SM00355,SM00355,SM00355,SM00355,SM00355		PF12874,PF13912,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8048.1	Mitochondrial intermembrane space import and assembly protein 40	GO:0051084,GO:0005575,GO:0045041,GO:0022417,GO:0003674,GO:0008150,GO:0005758,GO:0015035	CG7950-PA						PF06747														
aly8048.10	Phytanoyl-CoA dioxygenase, peroxisomal	GO:0031418,GO:0006631,GO:0001561,GO:0005777,GO:0048244,GO:0046872	CG14688-PB						PF05721				G3DSA:2.60.120.620	SSF51197	31~51								
aly8048.11	Unknown		n/a																				
aly8048.2	Unknown		CG15601-PA				SM00980,SM00595		PF10545,PF05485	PS51029,PS50950				SSF57716									
aly8048.3	Unknown		CG15601-PA				SM00595		PF10545	PS51029					138~158								
aly8048.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8048.5	Unknown		n/a																				
aly8048.6	Unknown		CG5910-PA																				
aly8048.7	Nuclear pore complex protein Nup133	GO:0016020,GO:0031080,GO:0005643,GO:0000940,GO:0031965,GO:0048339,GO:0006999,GO:0006406,GO:0005515,GO:0015031,GO:0005487,GO:0007184	CG6958-PA						PF08801				G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF117289			REACT_6185,REACT_474,REACT_15518						
aly8048.8	Structural maintenance of chromosomes protein 2	GO:0005737,GO:0051276,GO:0007067,GO:0005829,GO:0008278,GO:0007052,GO:0000796,GO:0051301,GO:0005515,GO:0003677,GO:0007076,GO:0000785,GO:0022008,GO:0005634,GO:0005694,GO:0005875,GO:0005524,GO:0007062	CG10212-PA				SM00968		PF06470,PF02463				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF75553,SSF52540,SSF52540	464~484,239~294,359~379,391~460,210~230,178~198,296~316,671~705								
aly8048.9	Structural maintenance of chromosomes protein 2	GO:0005737,GO:0007067,GO:0005829,GO:0008278,GO:0007052,GO:0000796,GO:0051301,GO:0003677,GO:0007076,GO:0000785,GO:0022008,GO:0005634,GO:0005875,GO:0005524,GO:0007062	CG10212-PA						PF02463				G3DSA:3.40.50.300	SSF52540,SSF52540	217~237,45~121								
aly80531.1	POC1 centriolar protein homolog A	GO:0007017,GO:0051013,GO:0008017,GO:0030030,GO:0005515,GO:0008352,GO:0046843	CG13956-PB				SM00320,SM00320,SM00320,SM00320		PF00400	PS50082,PS50294,PS50082			G3DSA:2.130.10.10	SSF50978									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly806.1	Alpha-soluble NSF attachment protein	GO:0006909,GO:0019898,GO:0034214,GO:0001745,GO:0007274,GO:0031201,GO:0005483,GO:0005737,GO:0006888,GO:0043679,GO:0016023,GO:0031410,GO:0006886,GO:0016020,GO:0051260,GO:0000281,GO:0005774,GO:0032781,GO:0016082,GO:0035540,GO:0019905,GO:0007269,GO:0007268,GO:0001671,GO:0006891,GO:0043195,GO:0031629,GO:0048812,GO:0035494,GO:0048526,GO:0000149	CG6625-PA						PF14938		PR00448,PR00448,PR00448,PR00448,PR00448,PR00448,PR00448		G3DSA:1.25.40.10	SSF48452	239~259,126~146								
aly806.10	Unknown		n/a																				
aly806.11	Uncharacterized protein CG43427	GO:0005575,GO:0003674,GO:0007476,GO:0008270	CG43427-PO				SM00132		PF00412,PF15949	PS50023		PS00478	G3DSA:2.10.110.10		417~437,950~995								
aly806.12	Transient receptor potential channel pyrexia	GO:0005261,GO:0005262,GO:0007605,GO:0006812,GO:0016021,GO:0070588,GO:0006816,GO:0051290,GO:0048060,GO:0009270,GO:0034703,GO:0009408,GO:0098655,GO:0055085	CG31284-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796,PF00520,PF13637	PS50088,PS50088,PS50088,PS50088,PS50088,PS50297,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20	SSF48403	921~955								
aly806.13	Protein unc-79 homolog	GO:0030534,GO:0072347,GO:0048149,GO:0016021,GO:0005575,GO:0003674,GO:0045475,GO:0035264	CG5237-PC						PF14776														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly806.14	Unknown	GO:0006030,GO:0005576,GO:0008061	CG14608-PC				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625									
aly806.15	Uncharacterized protein CG1785	GO:0005575,GO:0022008,GO:0003674	CG1785-PA			PIRSF017302			PF07767						349~369,310~340								
aly806.16	Unknown	GO:0005575,GO:0008150,GO:0003674	CG11693-PB						PF05335						160~187,244~271								
aly806.17	Alpha-taxilin	GO:0005737,GO:0006887,GO:0016020,GO:0042113,GO:0098779,GO:0019905	CG5886-PA						PF09728						438~461,213~249,283~310,94~192								
aly806.18	Unknown		n/a												113~143								
aly806.19	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly806.2	Phosphatidylinositol-binding clathrin assembly protein LAP	GO:0008021,GO:0005543,GO:0030136,GO:0042331,GO:0005794,GO:0006898,GO:0005545,GO:0030131,GO:0048268,GO:0016183,GO:0030276,GO:0005905,GO:0007269,GO:0007268,GO:0007270,GO:0030118,GO:2000370,GO:0048488,GO:0048489	CG2520-PD				SM00273		PF07651	PS50942			G3DSA:1.20.58.150,G3DSA:1.25.40.90	SSF48464,SSF89009										
aly806.20	Protein jagunal	GO:0007029,GO:0048477,GO:0016021,GO:0006887,GO:0007018,GO:0008407,GO:0005789,GO:0007303,GO:0003674,GO:0007296,GO:0051686,GO:0001555,GO:0022416	CG10978-PB						PF07086														
aly806.21	Hematopoietically-expressed homeobox protein hhex	GO:0000122,GO:0043565,GO:0009744,GO:0001570,GO:0009952,GO:0007507,GO:0003700,GO:0005634,GO:0016055,GO:0030177,GO:0035162,GO:0006355,GO:0048813,GO:0001889,GO:0006351,GO:0003677,GO:0045892,GO:0022008,GO:0006006	CG7056-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689										
aly806.22	Homeobox protein ceh-9	GO:0043565,GO:0003700,GO:0005634,GO:0006355,GO:0003677,GO:0007275	CG8524-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689										
aly806.23	Homeobox protein Nkx-6.1	GO:0032024,GO:0035094,GO:0010629,GO:0003677,GO:0001078,GO:0045686,GO:0007417,GO:0043565,GO:0070062,GO:0000122,GO:0045687,GO:0005634,GO:0005654,GO:0045666,GO:0006366,GO:0045944,GO:0070491,GO:0021913,GO:0021912,GO:0030182,GO:0008283,GO:0048709,GO:2001222,GO:0030516,GO:0022008,GO:0071375,GO:0007399,GO:0007224,GO:0003700,GO:0042493,GO:0003705,GO:0006355,GO:0000976,GO:0003323,GO:0000978,GO:0003682,GO:0071345	CG13475-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024,PR00031,PR00031	PS00027	G3DSA:1.10.10.60	SSF46689	63~83									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly806.24	Unknown	GO:0030182,GO:0007399,GO:0000122,GO:0003700,GO:0005634,GO:0003705,GO:0006355,GO:0010629,GO:0000976,GO:0045944,GO:0007417,GO:0070491	CG13475-PA																				
aly806.25	Transketolase-like protein 2	GO:0004802,GO:0005737,GO:0031935,GO:0005811,GO:0031122,GO:0046872,GO:0005875	CG8036-PC				SM00861		PF02780,PF02779,PF00456			PS00802	G3DSA:3.40.50.970,G3DSA:3.40.50.920,G3DSA:3.40.50.970	SSF52518,SSF52922,SSF52518		00900+2.2.1.7,00730+2.2.1.7		PWY-6891,PWY-6892,PWY-7560	UPA00064				
aly806.26	Unknown		CG10710-PA												571~591								
aly806.27	B1 protein (Fragment)	GO:0005549,GO:0005576	n/a				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly806.28	Adenosine 3'-phospho 5'-phosphosulfate transporter 1	GO:0005794,GO:1902559,GO:0016021,GO:0000139,GO:0015012,GO:0046964,GO:0046963,GO:0007310,GO:0005459,GO:0055085	CG7623-PA						PF08449					SSF103481									
aly806.29	Prostaglandin E2 receptor EP3 subtype	GO:0007015,GO:0006468,GO:0016021,GO:0004957,GO:0004930,GO:0004674,GO:0008360,GO:0005886,GO:0007186	CG7497-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly806.3	Unknown	GO:0003700,GO:0005634,GO:0046872,GO:0008270,GO:0006351	CG1647-PA				SM00355,SM00868		PF07776	PS50157		PS00028	G3DSA:3.30.160.60	SSF57667,SSF57716									
aly806.30	Arfaptin-1	GO:0034452,GO:0005737,GO:0050708,GO:0070273,GO:0048149,GO:0005829,GO:0005802,GO:0032588,GO:0000139,GO:0045887,GO:0034315,GO:0019904,GO:0006886	CG17184-PA				SM01015		PF06456	PS50870			G3DSA:1.20.1270.60	SSF103657									
aly806.31	DPH3 homolog	GO:0005737,GO:0005654,GO:0050709,GO:0017183,GO:0051099,GO:0005575,GO:0008150,GO:0003674,GO:0046872	CG14701-PA						PF05207	PS51074				SSF144217					UPA00559				
aly806.32	EH domain-containing protein 1	GO:1990090,GO:1901741,GO:0055038,GO:0008587,GO:0030139,GO:0007291,GO:2001137,GO:0031175,GO:0010008,GO:0031095,GO:0043209,GO:0006886,GO:0005811,GO:0007474,GO:0005509,GO:0048471,GO:0048477,GO:0031901,GO:0005525,GO:0003924,GO:0005886,GO:0042632,GO:0006897,GO:0034383,GO:0010886,GO:0005524,GO:0032456	CG6148-PA				SM00027		PF00350,PF16880,PF12763	PS50031,PS50222,PS51718	PR00195,PR00195,PR00195	PS00018	G3DSA:1.10.238.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF47473									
aly806.33	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	GO:0005575,GO:0003674,GO:0007274,GO:0005515,GO:0005737	CG5094-PA				SM00028,SM00028,SM00028		PF13414,PF16546,PF07719	PS50005,PS50005,PS50293,PS50005			G3DSA:1.25.40.10	SSF48452	61~88,169~189								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly806.34	Actin-related protein 10	GO:0005737,GO:0005200,GO:0007010,GO:0007018,GO:0003779,GO:0005884,GO:0005869	CG12235-PA				SM00268		PF00022,PF00022				G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.30.420.40	SSF53067,SSF53067									
aly806.35	Unknown	GO:0005811	CG32694-PB																				
aly806.36	Unknown	GO:0005575,GO:0003674,GO:0008150	CG43386-PC																				
aly806.37	Unknown		n/a																				
aly806.38	Protein unc-79 homolog	GO:0030534,GO:0072347,GO:0048149,GO:0016021,GO:0005575,GO:0003674,GO:0045475,GO:0035264	CG5237-PC																				
aly806.39	Protein unc-79 homolog	GO:0030534,GO:0072347,GO:0048149,GO:0016021,GO:0005575,GO:0003674,GO:0045475,GO:0035264	CG5237-PC																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly806.4	Prohormone-4	GO:0005576,GO:0030228,GO:0005515	CG31221-PC				SM00192		PF00057	PS50068		PS01209	G3DSA:4.10.400.10	SSF57424									
aly806.40	Unknown		n/a																				
aly806.5	Unknown		CG14312-PA												29~56								
aly806.6	Trypsin, alkaline B	GO:0004252,GO:0005615,GO:0006508	CG13430-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly806.7	Trypsin, alkaline C	GO:0004252,GO:0005615,GO:0006508	CG18735-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly806.8	Trypsin, alkaline C	GO:0004252,GO:0005615,GO:0006508	CG9564-PC				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly806.9	Transient receptor potential channel pyrexia	GO:0005261,GO:0005262,GO:0007605,GO:0006812,GO:0016021,GO:0070588,GO:0006816,GO:0051290,GO:0048060,GO:0009270,GO:0034703,GO:0009408,GO:0098655,GO:0055085	CG31284-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF12796,PF12796,PF00520,PF00023	PS50297,PS50088,PS50088,PS50088,PS50088,PS50088			G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403									
aly8073.1	Tankyrase	GO:0007016,GO:0005200,GO:0006471,GO:0090364,GO:0035220,GO:0022416,GO:0097110,GO:0005515,GO:0003950	CG4719-PB				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF00023,PF13637,PF12796,PF12796,PF13857	PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50088,PS50297,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403									
aly8073.2	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0060179,GO:0009744,GO:0016021,GO:0070328,GO:0005783,GO:0017105,GO:0019216,GO:0046872,GO:0031410,GO:0016717,GO:0005811,GO:0006631,GO:0042593,GO:0042811,GO:0048047,GO:0004768,GO:0010506,GO:0006723,GO:0055114	CG5887-PA								PR00075,PR00075,PR00075,PR00075												
aly8073.3	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0060179,GO:0009744,GO:0016021,GO:0070328,GO:0005783,GO:0017105,GO:0019216,GO:0046872,GO:0031410,GO:0016717,GO:0005811,GO:0006631,GO:0042593,GO:0042811,GO:0048047,GO:0004768,GO:0010506,GO:0006723,GO:0055114	CG5887-PA						PF00487		PR00075,PR00075,PR00075,PR00075,PR00075,PR00075,PR00075												
aly8073.4	Unknown		n/a																				
aly8073.5	Acyl-CoA Delta(11) desaturase	GO:0006633,GO:0060179,GO:0009744,GO:0016021,GO:0070328,GO:0005783,GO:0017105,GO:0019216,GO:0046872,GO:0031410,GO:0016717,GO:0005811,GO:0006631,GO:0042593,GO:0042811,GO:0048047,GO:0004768,GO:0010506,GO:0006723,GO:0055114	CG5887-PA						PF00487		PR00075,PR00075,PR00075,PR00075,PR00075,PR00075,PR00075												

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly808.1	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG5065-PA						PF07993,PF07993,PF03015				G3DSA:3.40.50.720	SSF51735,SSF51735			REACT_22258						
aly808.2	Unknown		n/a																				
aly808.3	Ropporin-1-like protein		n/a										G3DSA:1.20.890.10	SSF47391									
aly808.4	Myelin regulatory factor	GO:0043565,GO:0032286,GO:0022010,GO:0003700,GO:0016021,GO:0048709,GO:0005789,GO:0006355,GO:0045893,GO:0003677,GO:0014003,GO:0008233,GO:0031643,GO:0005634,GO:0006351	CG3328-PA						PF13887,PF05224,PF13888,PF13884	PS51517,PS51688			G3DSA:2.60.40.1390	SSF49417									
aly8084.1	Probable G-protein coupled receptor No9	GO:0008227,GO:0030728,GO:0004935,GO:0006874,GO:0016021,GO:0007211,GO:0007612,GO:0060278,GO:0007188,GO:0005887,GO:0005886,GO:0004989,GO:0008049,GO:0051482	CG3856-PD						PF00001	PS50262	PR01103,PR01103,PR01103,PR01103,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly8084.2	N-acetyl-D-glucosamine kinase	GO:0005332,GO:0009384,GO:0005328,GO:0070062,GO:0016021,GO:0005886,GO:0006044,GO:0045127,GO:0046835,GO:0019262,GO:0006836,GO:0005524	CG6218-PA						PF01869					SSF53067,SSF53067,SSF53067									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8084.3	Serine protease HTRA2, mitochondrial	GO:0004252,GO:0035234,GO:0016021,GO:0006915,GO:0005739,GO:0031966,GO:0007283,GO:0016006,GO:0005758,GO:0008233,GO:0042981,GO:0006508,GO:0007005	CG8464-PA				SM00228		PF13180,PF13365	PS50106	PR00834,PR00834,PR00834,PR00834,PR00834		G3DSA:2.40.10.10,G3DSA:2.30.42.10,G3DSA:2.40.10.10	SSF50156,SSF50494									
aly8084.4	Unknown		CG8861-PC										G3DSA:2.10.60.10										
aly80977.1	Unknown		n/a						PF04500														
aly81071.1	Unknown	GO:0035011,GO:0008286,GO:0008103,GO:0005158,GO:0033588,GO:0005575	CG9829-PA						PF09807														
aly81163.1	GTP-binding protein 128up	GO:0005525	CG8340-PA					TIGR00231	PF16897,PF01926	PS51710	PR00326,PR00326,PR00326,PR00326	PS00905	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									
aly813.1	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	GO:0004252,GO:0042645,GO:0006457,GO:0051603,GO:0017111,GO:0005739,GO:0051082,GO:0005759,GO:0006508,GO:0046872,GO:0009368,GO:0005524	CG4538-PC				SM01086		PF10431,PF07724				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.8.60	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly813.2	Sorting nexin-27	GO:0016197,GO:0005737,GO:1990126,GO:0006886,GO:0008333,GO:0042493,GO:0032266,GO:0005769,GO:0005654,GO:0007165,GO:0005515,GO:0030904,GO:0071203,GO:0005768,GO:0005829,GO:0031901,GO:0001772	CG32758-PA				SM00228,SM00312		PF00595,PF00788,PF00787	PS50200,PS50106,PS50195			G3DSA:2.30.42.10,G3DSA:3.30.1520.10	SSF54236,SSF50156,SSF64268									
aly813.3	Uncharacterized family 31 glucosidase KIAA1161	GO:0017177,GO:0005975,GO:0048741,GO:0043568,GO:0016021,GO:0031965,GO:0004553,GO:0004558,GO:0051897	CG33080-PA						PF01055					SSF51445									
aly813.4	Microtubule-associated protein futsch	GO:0008582,GO:0030425,GO:0030424,GO:0000226,GO:0005874,GO:0005875,GO:0008355,GO:0005737,GO:0008088,GO:0043025,GO:0048749,GO:0016787,GO:0015630,GO:0060052,GO:0008017,GO:0007528,GO:0019900,GO:0007409,GO:1901215,GO:0007017,GO:0007399,GO:0048813,GO:0005515,GO:0043524	CG34387-PC																				
aly813.5	S-antigen protein	GO:0020003	n/a																				
aly81353.1	U4/U6 small nuclear ribonucleoprotein Prp4	GO:0016607,GO:0046540,GO:0030532,GO:0071011,GO:0071013,GO:0071001,GO:0000398,GO:0030621,GO:0005688,GO:0005687,GO:0015030,GO:0008380,GO:0005681,GO:0017070	CG6322-PA				SM00500		PF08799					SSF158230									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly814.1	Follistatin	GO:0005737,GO:0043616,GO:0045596,GO:0042475,GO:0032926,GO:0032927,GO:0001501,GO:0090099,GO:0005634,GO:0000122,GO:0008585,GO:0030509,GO:0002244,GO:0005576,GO:0051798,GO:0007276,GO:0005515,GO:0007389,GO:0031069,GO:0048185	CG33466-PA				SM00274,SM00274,SM00274,SM00280,SM00280,SM00280		PF07648,PF07648,PF07648	PS51465,PS51364,PS51465,PS51465			G3DSA:3.30.60.30,G3DSA:3.30.60.30,G3DSA:3.30.60.30	SSF100895,SSF100895,SSF100895										
aly814.10	Unknown		n/a																				
aly814.11	Unknown		n/a																				
aly814.12	Dynein intermediate chain 2, ciliary	GO:0005737,GO:0042623,GO:0007605,GO:0005929,GO:0007018,GO:0003774,GO:0005515,GO:0005868,GO:0030286,GO:0005874,GO:0005875	CG9313-PB				SM00320,SM00320,SM00320,SM00320,SM00320						G3DSA:2.130.10.10	SSF50978										
aly814.13	Fukutin-related protein	GO:0005794,GO:0005791,GO:0005615,GO:0016021,GO:0000139,GO:0016740,GO:0016485,GO:0042383,GO:0035269,GO:0009101	CG15651-PA																				
aly814.14	ATPase ASNA1 homolog	GO:0045048,GO:0005783,GO:0015446,GO:0006810,GO:0016887,GO:0046872,GO:0005524	CG1598-PA	MF_03112				TIGR00345	PF02374				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly814.15	GPI ethanolamine phosphate transferase 3	GO:0044267,GO:0016021,GO:0016020,GO:0051377,GO:0005789,GO:0006501,GO:0003824,GO:0008152,GO:0006506,GO:0016254,GO:0043687	CG12263-PA						PF01663				G3DSA:3.40.720.10	SSF53649	397~424								
aly814.16	Unknown		n/a																				
aly814.17	Unknown		CG3907-PB											SSF57997	248~268,119~160								
aly814.18	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GO:0019518,GO:0006520,GO:0008890,GO:0005739,GO:0005654,GO:0009058,GO:0030170	CG10361-PA					TIGR01822	PF00155			PS00599	G3DSA:3.40.640.10,G3DSA:3.90.1150.10	SSF53383	119~122	00260+2.3.1.29			UPA00046				
aly814.19	Alpha-amylase 2	GO:0043169,GO:0005975,GO:0003824,GO:0004556,GO:0005509,GO:0046872	CG17876-PA				SM00632,SM00642		PF00128,PF02806		PR00110,PR00110,PR00110,PR00110,PR00110		G3DSA:2.60.40.1180,G3DSA:3.20.20.80	SSF51011,SSF51445		00500+3.2.1.1,00500+2.4.1.18	REACT_474	PWY-622,PWY-5067					
aly814.2	Mitotic spindle assembly checkpoint protein MAD1	GO:0005737,GO:0031577,GO:0072686,GO:0090235,GO:0005634,GO:0005635,GO:0005815,GO:0005654,GO:0003674,GO:0051301,GO:0007094,GO:0007067,GO:0051315,GO:0000776,GO:0000777	CG2072-PA						PF05557					SSF75704	595~615,90~110,391~460,562~582,276~313,252~272,175~241,472~532,341~361,136~163								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly814.20	Protein twisted gastrulation	GO:0007630,GO:0007362,GO:0017015,GO:0048636,GO:0010629,GO:0005576,GO:0008293,GO:0007354,GO:0008201,GO:0030510	CG12410-PA						PF04668	PS51257													
aly814.21	Transcription factor HNF-4 homolog	GO:0043565,GO:0007492,GO:0006351,GO:0030522,GO:0004879,GO:0034440,GO:0003700,GO:0005634,GO:0003707,GO:0006355,GO:0008270,GO:0043401,GO:0016042,GO:0007498,GO:0008610	CG9310-PB				SM00430,SM00399		PF00105,PF00104	PS51030	PR00398,PR00398,PR00398,PR00398,PR00398,PR00047,PR00047,PR00047,PR00047,PR00545,PR00545,PR00545	PS00031	G3DSA:3.30.50.10,G3DSA:1.10.565.10	SSF48508,SSF57716	211~217,197~197		REACT_71							
aly814.22	Fanconi-associated nuclease 1	GO:0005737,GO:0008409,GO:0045171,GO:0070336,GO:0006281,GO:0005634,GO:0017108,GO:0036297,GO:0016788,GO:0006289,GO:0005654,GO:0000724,GO:0043130,GO:0033683,GO:0000737,GO:0046872,GO:0004528	n/a				SM00990		PF08774														
aly814.23	Tctex1 domain containing protein 1	GO:0030286,GO:0007018,GO:0005875,GO:0042623	CG14763-PA						PF03645														
aly814.24	Synaptic vesicle membrane protein VAT-1 homolog-like	GO:0016491,GO:0005811,GO:0016295,GO:0004320,GO:0016296,GO:0004312,GO:0004313,GO:0009058,GO:0004316,GO:0004317,GO:0004314,GO:0004315,GO:0004319,GO:0055114,GO:0008270	CG3523-PC				SM00829		PF08240,PF13602			PS01162	G3DSA:3.40.50.720,G3DSA:3.90.180.10	SSF50129,SSF51735										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly814.25	Putative ribosome-binding factor A, mitochondrial	GO:0006364,GO:0005739	CG15916-PA						PF02033				G3DSA:3.30.300.20	SSF89919									
aly814.26	Retinoblastoma-like protein 1	GO:0007307,GO:0001012,GO:0010629,GO:0000785,GO:0003677,GO:0007049,GO:2000134,GO:0000122,GO:0035189,GO:0005654,GO:0043066,GO:0042127,GO:0008285,GO:0005667,GO:0043550,GO:0051101,GO:0008134,GO:0042023,GO:0008156,GO:0044212,GO:0007113,GO:0008630,GO:0051726,GO:0031523,GO:0006351,G	CG7413-PA				SM00385		PF11934,PF01857,PF01858				G3DSA:1.10.472.10,G3DSA:1.10.472.10	SSF47954,SSF47954									
aly814.27	SAGA-associated factor 29 homolog	GO:0000124,GO:0035064,GO:0043966,GO:0006338,GO:0005634,GO:0004402,GO:0006355,GO:0070461,GO:0005671,GO:0006351,GO:0016573	CG30390-PA						PF07039	PS51518													
aly814.28	Polyadenylate-binding protein 2	GO:0005737,GO:0000289,GO:0008143,GO:0005634,GO:0000398,GO:0000166,GO:0071011,GO:0003723,GO:0022008,GO:0071013,GO:0006378,GO:0003729	CG2163-PA				SM00360		PF00076	PS50102			G3DSA:3.30.70.330	SSF54928	44~74								
aly814.29	Ubiquitin-conjugating enzyme E2 4	GO:0005737,GO:0000070,GO:1901694,GO:0043161,GO:0005829,GO:0006915,GO:0031146,GO:0045842,GO:0000209,GO:0016874,GO:0043130,GO:0046668,GO:0019005,GO:0016485,GO:0042787,GO:0061631,GO:0004842,GO:0005634,GO:0005524,GO:0043224	CG15437-PA				SM00256,SM00212		PF12937,PF00179	PS50181,PS50127			G3DSA:3.10.110.10,G3DSA:1.20.1280.50	SSF54495,SSF81383									
aly814.3	Probable protein arginine N-methyltransferase 6.1	GO:0006479,GO:0070611,GO:0016274,GO:0005634,GO:0034970,GO:0008168	CG16840-PA						PF05185	PS51678			G3DSA:2.70.160.11,G3DSA:3.40.50.150	SSF53335									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly814.30	Unknown		n/a																				
aly814.31	Unknown		n/a																				
aly814.32	WW domain-containing adapter protein with coiled-coil	GO:0016607,GO:0006974,GO:0003682,GO:0032435,GO:0005634,GO:0010390,GO:0005575,GO:0016239,GO:0003674,GO:0045893,GO:0005515,GO:0008150,GO:0044783,GO:0000993,GO:0005654,GO:0071894,GO:0005681,GO:0006351	CG8949-PF				SM00456		PF00397	PS50020		PS01159	G3DSA:2.20.70.10	SSF51045									
aly814.4	Transcription factor TFIIIB component B" homolog	GO:0005737,GO:0001026,GO:0000126,GO:0003700,GO:0005634,GO:0005654,GO:0006355,GO:0048812,GO:0006351,GO:0003677,GO:0022008,GO:0003682	CG9305-PA						PF15963						391~427,555~593,350~370								
aly814.5	tRNA selenocysteine 1-associated protein 1	GO:0005737,GO:0000049,GO:0005634,GO:0000398,GO:0000166,GO:0001514,GO:0003676	CG15440-PA				SM00360,SM00360		PF00076,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									
aly814.6	Lipoma-preferred partner homolog	GO:0005856,GO:0001725,GO:0045572,GO:0005925,GO:0005515,GO:0007430,GO:0005634,GO:0007593,GO:0005737,GO:0035002,GO:0035003,GO:0007155,GO:0008270,GO:0005911,GO:0045805,GO:0035329,GO:0048526	CG32018-PB				SM00132,SM00132,SM00132		PF00412,PF00412,PF00412	PS50023,PS50023,PS50023		PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716,SSF57716									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly814.7	XK-related protein 6	GO:0016021	n/a						PF09815														
aly814.8	Gamma-tubulin complex component 4	GO:0005200,GO:0000086,GO:0055037,GO:0008274,GO:0000226,GO:0007067,GO:0005815,GO:0005874,GO:0000278,GO:0007020,GO:0005813,GO:0016020,GO:0000922,GO:0015631,GO:0015630,GO:0051298,GO:0051297,GO:0006461,GO:0007052,GO:0007058,GO:0045450,GO:0007112,GO:0005829	CG6176-PA						PF04130								REACT_152						
aly814.9	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2	GO:0042391,GO:0007637,GO:0005221,GO:0050802,GO:0005222,GO:0014059,GO:0071805,GO:0016020,GO:0035725,GO:0042802,GO:0006813,GO:0045938,GO:0045475,GO:0005887,GO:0005886,GO:0008340,GO:0055085,GO:0030552,GO:0071321,GO:0071320,GO:0005249,GO:0005248,GO:0005244	CG8585-PE				SM00100		PF08412,PF00027,PF00520	PS50042	PR01463,PR01463,PR01463,PR01463,PR01463	PS00888	G3DSA:1.10.287.630,G3DSA:1.10.287.70,G3DSA:1.10.287.70,G3DSA:2.60.120.10	SSF51206,SSF81324,SSF81324									
aly81432.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly819.1	Protein extra-macrochaetae	GO:0046552,GO:0007541,GO:0007494,GO:0008258,GO:0008586,GO:0045466,GO:0002121,GO:0007530,GO:0005737,GO:0001191,GO:0007458,GO:0000122,GO:0005634,GO:0003714,GO:0007476,GO:0008407,GO:0005654,GO:0001964,GO:0031987,GO:0008283,GO:0042675,GO:0048056,GO:0045892,GO:0043392,GO:0007286,GO:0007422,GO:0007460,GO:0030381,GO:0007391,GO:0046331,GO:0006351,GO:0048854,GO:0046983,GO:0046982,GO:0046843	CG1007-PA						PF00010				G3DSA:4.10.280.10	SSF47459										
aly819.2	Unknown		n/a																				
aly819.3	Splicing factor 3B subunit 3	GO:0005689,GO:0030532,GO:0071011,GO:0071013,GO:0000398,GO:0007052,GO:0042177,GO:0003723,GO:0005515,GO:0005686,GO:0022008,GO:0003684	CG13900-PA						PF10433,PF03178					SSF50978,SSF50978										
aly819.4	Unknown		n/a																				
aly819.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly82.1	Glycine receptor subunit beta	GO:0042391,GO:0007268,GO:0008144,GO:0034707,GO:0016934,GO:0008068,GO:0016933,GO:0016594,GO:0007218,GO:0007340,GO:0016021,GO:0016020,GO:0001964,GO:0030054,GO:0060013,GO:0060012,GO:1902476,GO:0006811,GO:0051291,GO:0007628,GO:0007601,GO:0034220,GO:0005887,GO:0005886,GO:0055085,GO:0007399,GO:0045211,GO:0048812,GO:0097112	CG7535-PN						PF02932,PF02931		PR00253,PR00253,PR00253,PR00253,PR00252,PR00252,PR00252,PR00252	PS00236	G3DSA:2.70.170.10,G3DSA:1.20.58.390,G3DSA:1.20.58.390	SSF90112,SSF63712									
aly82.10	Unknown		n/a																				
aly82.11	Unknown		n/a																				
aly82.12	Alpha-scruin	GO:0005575,GO:0008150,GO:0003674,GO:0005515	CG30357-PA				SM00875,SM00225,SM00612,SM00612,SM00612,SM00612,SM00612,SM00612		PF01344,PF01344,PF07707,PF13415,PF00651	PS50097			G3DSA:2.120.10.80,G3DSA:3.30.710.10	SSF117281,SSF54695									
aly82.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly82.14	Unknown		n/a												152~172,187~207								
aly82.15	Unknown		n/a																				
aly82.16	Venom peptide SjAPI	GO:0005576,GO:0004867	n/a						PF01826				G3DSA:2.10.25.10	SSF57567									
aly82.17	Unknown		n/a																				
aly82.18	Pescadillo homolog	GO:0005730,GO:0030687,GO:0042254,GO:0005654,GO:0000463,GO:0000466,GO:0043021,GO:0022008	CG4364-PA	MF_03028			SM00292		PF16589,PF06732	PS50172			G3DSA:3.40.50.10190	SSF52113	577~606								
aly82.19	Protein pelota	GO:0071025,GO:0008315,GO:0007067,GO:0001745,GO:0007140,GO:0007141,GO:0005737,GO:0007126,GO:0005634,GO:0046872,GO:0048749,GO:0051078,GO:0000212,GO:0007283,GO:0007054,GO:0048132,GO:0070481,GO:0048137,GO:0030718,GO:0070966,GO:0004519,GO:0006412	CG3959-PA					TIGR00111	PF03464,PF03463,PF03465				G3DSA:3.30.1330.30	SSF55315,SSF159065,SSF53137									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly82.2	Mitochondrial inner membrane protease ATP23 homolog	GO:0046872,GO:0004222	CG5131-PA						PF09768														
aly82.20	Restin homolog	GO:0005794,GO:0007017,GO:0035371,GO:0008017,GO:0051010,GO:0007349,GO:0045169,GO:0003779,GO:0005876,GO:0005938,GO:0005515,GO:0005875,GO:0000776	CG5020-PA				SM01052,SM01052		PF16641,PF16641,PF01302,PF01302	PS50245,PS50245		PS00845,PS00845	G3DSA:2.30.30.190,G3DSA:2.30.30.190	SSF74924,SSF74924,SSF90257	1311~1415,1720~1740,1047~1134,743~816,435~525,583~617,864~905,533~553,665~685,1638~1672,1139~1198,91								
aly82.21	DNA-directed RNA polymerase II subunit RPB11	GO:0005634,GO:0003677,GO:0005665,GO:0006351,GO:0006366,GO:0003899,GO:0046983	CG6840-PA						PF13656			PS01154	G3DSA:3.30.1360.10	SSF55257	91~111	00240+2.7.7.6,00230+2.7.7.6							
aly82.22	Syntaxin-1A	GO:0008021,GO:0016020,GO:0006906,GO:0007349,GO:0005484,GO:0007274,GO:0031201,GO:0042335,GO:0016021,GO:0006887,GO:0000281,GO:0005886,GO:0017157,GO:0007482,GO:0006936,GO:0016081,GO:0000149,GO:0007317,GO:0048278,GO:0012505,GO:0007269,GO:0007268,GO:0043195,GO:0016192,GO:0031629,GO:0005515,GO:0006886	CG31136-PB				SM00397,SM00503		PF05739,PF00804	PS50192		PS00914	G3DSA:1.20.58.70,G3DSA:1.20.5.110	SSF47661	25~52,74~101		REACT_11184						
aly82.23	Elongation factor Tu, mitochondrial	GO:0007030,GO:0042645,GO:0000278,GO:0008283,GO:0043209,GO:0070062,GO:0006886,GO:0016020,GO:0003924,GO:0006913,GO:0005739,GO:0005743,GO:0007165,GO:0003746,GO:0006414,GO:0044822,GO:0005525	CG6050-PB				SM00174,SM00175,SM00176,SM00173	TIGR00485,TIGR00231,TIGR00231	PF00071,PF03143,PF03144,PF00009	PS51722,PS51418	PR00627,PR00627,PR00627,PR00627,PR00627	PS00301	G3DSA:3.40.50.300,G3DSA:2.40.30.10,G3DSA:3.40.50.300,G3DSA:2.40.30.10	SSF50447,SSF52540,SSF50465,SSF52540			REACT_11044						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly82.24	Zinc finger CW-type PWWP domain protein 1	GO:0008270	n/a				SM00293		PF00855	PS50812			G3DSA:2.30.30.160	SSF63748	126~146								
aly82.25	RING finger protein 10	GO:0005737,GO:0044212,GO:0005634,GO:0031643,GO:0045944,GO:0008270,GO:0010626,GO:0006351	CG12099-PB				SM00184		PF13920	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850	337~360,307~334								
aly82.26	Kelch domain-containing protein 10 homolog	GO:0031462,GO:0003674,GO:0032874,GO:0005515	CG5186-PA						PF01344,PF13418				G3DSA:2.120.10.80	SSF117281									
aly82.27	Adenosine receptor A2b	GO:0031284,GO:0004930,GO:0090281,GO:0030819,GO:0006109,GO:0016021,GO:0005886,GO:0031668,GO:0043306,GO:0032722,GO:0001609,GO:0008306,GO:0007189,GO:0001973,GO:0007268,GO:0010575,GO:0022008,GO:0007186,GO:0002882,GO:0032755,GO:0060087	CG9753-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00424,PR00424,PR00424,PR00424,PR00424	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797							
aly82.28	Odorant receptor 67a	GO:0005549,GO:0007608,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984,GO:0032590	CG12526-PA						PF02949,PF02949														
aly82.29	Laccase-1	GO:0040003,GO:0052716,GO:0046274,GO:0005576,GO:0005507,GO:0055114	CG42345-PA						PF00394,PF07732,PF07731				G3DSA:2.60.40.420,G3DSA:2.60.40.420,G3DSA:2.60.40.420	SSF49503,SSF49503,SSF49503									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly82.3	Protein-lysine N-methyltransferase EEF2KMT	GO:0005737,GO:0018023,GO:0016279	CG7889-PA						PF10294				G3DSA:3.40.50.150	SSF53335									
aly82.30	Transmembrane protease serine 11A	GO:0004252,GO:0005576,GO:0005887,GO:0007049,GO:0006508	CG7142-PA						PF00089,PF00089	PS50240		PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494,SSF50494									
aly82.31	Laccase-7	GO:0040003,GO:0052716,GO:0048046,GO:0046274,GO:0005507,GO:0055114	CG42345-PA						PF07731			PS00080,PS00079	G3DSA:2.60.40.420	SSF49503									
aly82.32	Laccase-1	GO:0040003,GO:0052716,GO:0046274,GO:0005576,GO:0005507,GO:0055114	CG42345-PA						PF07732,PF00394,PF02949,PF07731			PS00079,PS00080	G3DSA:2.60.40.420,G3DSA:2.60.40.420,G3DSA:2.60.40.420	SSF49503,SSF49503,SSF49503,SSF49503									
aly82.33	Troponin C, isoform 1	GO:0005509	CG2981-PA				SM00054,SM00054,SM00054,SM00054		PF13499,PF13499	PS50222,PS50222,PS50222,PS50222		PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									
aly82.34	Troponin C, isoform 1	GO:0005509	CG2981-PA				SM00054,SM00054,SM00054		PF00036,PF13499	PS50222,PS50222,PS50222,PS50222		PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly82.35	Unknown		n/a																				
aly82.36	Leucine-rich repeats and immunoglobulin-like domains protein 2	GO:0005737,GO:0060384,GO:0007605,GO:0016021,GO:0048812,GO:0005886,GO:0010640	CG14762-PB				SM00365,SM00365,SM00365,SM00365,SM00365,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369		PF00560,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									
aly82.37	Unknown		n/a																				
aly82.38	Unknown		n/a																				
aly82.39	Unknown		n/a																				
aly82.4	S1 RNA-binding domain-containing protein 1	GO:0006139,GO:0003723,GO:0016788	CG31156-PA				SM00316,SM00732		PF00575,PF16921,PF09371,PF12836	PS50126			G3DSA:2.40.50.140,G3DSA:1.10.10.650,G3DSA:3.30.420.140,G3DSA:1.10.3500.10,G3DSA:1.10.3500.10,G3DSA:1.10.150.310	SSF47781,SSF53098,SSF158832,SSF47781,SSF50249			REACT_216							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly82.40	Unknown		n/a																				
aly82.41	Unknown		n/a																				
aly82.5	Coiled-coil domain-containing protein 108	GO:0016021,GO:0044822	n/a										G3DSA:2.60.40.360										
aly82.6	Activated CDC42 kinase 1	GO:2000369,GO:0016020,GO:0016310,GO:0030154,GO:0006468,GO:0018108,GO:0030424,GO:0071944,GO:0005905,GO:0007169,GO:0030425,GO:0030136,GO:0005737,GO:0038083,GO:0005634,GO:0005154,GO:0070436,GO:0004674,GO:0004715,GO:0004712,GO:0004713,GO:0005886,GO:0016477,GO:0043025,GO:0005524,GO:0042127,GO:0042169,GO:0050699,GO:0045087,GO:0034613,GO:0043066,GO:0030426,GO:0030659,GO:0005912,GO:0007286,GO:0051427,GO:0031234,GO:0046872,GO:0006897,GO:0050731,GO:0007391,GO:0042802,GO:0005768	CG14992-PA				SM00219,SM00326		PF07714,PF00018	PS50002,PS50011	PR00109,PR00109,PR00109,PR00109,PR00109	PS00109,PS00107	G3DSA:2.30.30.40,G3DSA:1.10.510.10,G3DSA:3.30.200.20	SSF56112,SSF50044									
aly82.7	Receptor-type tyrosine-protein phosphatase N2	GO:0030658,GO:0048565,GO:0051046,GO:0006470,GO:0004725,GO:0005001,GO:0008270,GO:0005886,GO:0016021	CG31795-PC				SM00194		PF00102,PF11548	PS50055	PR00700,PR00700,PR00700		G3DSA:3.90.190.10	SSF52799									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly82.8	Glyoxalase domain-containing protein 4	GO:0022008,GO:0070062,GO:0005739	CG1532-PA										G3DSA:3.10.180.10,G3DSA:3.10.180.10	SSF54593									
aly82.9	Regulator of G protein signaling 9	GO:0038032,GO:0005834,GO:0007601,GO:0008277,GO:0004871,GO:0035556,GO:0007186	CG42450-PB				SM00049,SM00315,SM00224		PF00615,PF00610,PF00631	PS50186,PS50132	PR01301,PR01301,PR01301,PR01301		G3DSA:1.10.167.10,G3DSA:1.10.196.10,G3DSA:1.10.10.10,G3DSA:4.10.260.10	SSF48670,SSF46785,SSF48097	296~316								
aly82038.1	Unknown		n/a												19~53								
aly8204.1	Unknown	GO:0016021,GO:0050909	n/a						PF08395														
aly8205.1	Unknown		n/a																				
aly8211.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8211.10	GTP-binding protein 10 homolog	GO:0005730,GO:0000287,GO:0003924,GO:0042254,GO:0005575,GO:0008150,GO:0003674,GO:0005525	CG10628-PA						PF01018,PF01926	PS51710	PR00326,PR00326,PR00326,PR00326		G3DSA:2.70.210.12,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF82051,SSF52540									
aly8211.11	Myeloid differentiation primary response protein MyD88-A	GO:0005737,GO:0006952,GO:0002755,GO:0002804,GO:0006954,GO:0005121,GO:0009620,GO:0045087,GO:0008063,GO:0006965,GO:0050832,GO:0050830,GO:0007165,GO:0005515,GO:0006955,GO:0009953,GO:0005886,GO:0002781,GO:0005546,GO:0019732,GO:0043123	CG2078-PA				SM00255		PF00531,PF13676	PS50017,PS50104			G3DSA:1.10.533.10,G3DSA:3.40.50.10140	SSF52200,SSF47986									
aly8211.12	Probable elongator complex protein 2	GO:0005737,GO:0010950,GO:0005634,GO:0061133,GO:0006355,GO:0043248,GO:0005515,GO:0000502,GO:0006368	CG11887-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50294,PS50082,PS50294			G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50998,SSF50998,SSF50998									
aly8211.13	Regulator of telomere elongation helicase 1 homolog	GO:0006310,GO:0010569,GO:0051539,GO:0006281,GO:0004003,GO:0032508,GO:0006289,GO:0006260,GO:0003677,GO:0046872,GO:0005634,GO:0005524,GO:0000723	CG4078-PA	MF_03065			SM00487,SM00488,SM00491	TIGR00604	PF06733,PF13307	PS51193			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540									
aly8211.14	39S ribosomal protein L21, mitochondrial	GO:0005840,GO:0032543,GO:0003735,GO:0005743,GO:0003723,GO:0005762,GO:0006412	CG9730-PA						PF00829					SSF141091									
aly8211.15	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8211.2	BTB/POZ domain-containing protein 9	GO:0005737,GO:0032225,GO:0042428,GO:0007616,GO:0045938,GO:1900242,GO:0030674,GO:0060586,GO:0050951,GO:0005515,GO:0031463,GO:0008344,GO:0042748	CG1826-PA				SM00875,SM00225		PF00651,PF07707,PF00754	PS50097			G3DSA:2.60.120.260,G3DSA:2.60.120.260,G3DSA:3.30.710.10	SSF54695,SSF49785,SSF49785									
aly8211.3	D-glucuronyl C5-epimerase	GO:0030210,GO:0016857,GO:0005794,GO:0047464,GO:0016021,GO:0000139,GO:0050379,GO:0015012,GO:0006024	CG3194-PA						PF06662					SSF81853		00534+5.1.3.17		PWY-6558	UPA00756,UPA00862				
aly8211.4	Unknown		n/a																				
aly8211.5	Unknown		n/a																				
aly8211.6	Unknown		n/a																				
aly8211.7	Cell death activator CIDE-3	GO:0005811,GO:0005783,GO:0097194,GO:0005829,GO:0006915,GO:0005622,GO:0006355,GO:0034389,GO:0006351,GO:0022008,GO:1901215,GO:0042981,GO:0005634	CG1975-PB				SM00266		PF02017	PS51135			G3DSA:3.10.20.10	SSF54277									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8211.8	Unknown	GO:0046872	n/a							PS50103													
aly8211.9	Post-GPI attachment to proteins factor 3	GO:0016021,GO:0016788,GO:0000139,GO:0006505,GO:0006506,GO:0031227	CG3271-PB						PF04080														
aly822.1	Homeotic protein deformed	GO:0043565,GO:0006351,GO:0007420,GO:0033613,GO:0000122,GO:0007380,GO:0005634,GO:0003705,GO:0001158,GO:0035289,GO:1902339,GO:0060322,GO:0045944,GO:0003700,GO:0003677,GO:0009790,GO:0010468,GO:1990403,GO:0000977	CG2189-PA				SM00389		PF00046	PS50071	PR00025,PR00025	PS00032	G3DSA:1.10.10.60	SSF46689									
aly822.10	Homeobox protein abdominal-A homolog	GO:0007494,GO:0035224,GO:0035225,GO:0007385,GO:0010002,GO:0007275,GO:0008354,GO:0043565,GO:0005634,GO:0008406,GO:0014019,GO:0007438,GO:0048806,GO:0006915,GO:0009987,GO:0035053,GO:0007280,GO:0048636,GO:0007400,GO:0007506,GO:0007507,GO:0009952,GO:0007399,GO:0007422,GO:0003700,GO:0007501,GO:0003705,GO:0048738,GO:0006355,GO:0045944,GO:0005667,GO:0042694	CG10325-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly822.11	Homeobox protein abdominal-B	GO:0045843,GO:0007494,GO:0048087,GO:0060439,GO:0030540,GO:0035224,GO:0035225,GO:0048066,GO:0008584,GO:0035263,GO:0035261,GO:0003677,GO:0009997,GO:0008354,GO:0007431,GO:0005634,GO:0008406,GO:0007385,GO:0045944,GO:1902339,GO:0045705,GO:0007486,GO:0035215,GO:0007484,GO:0048094,GO:0007621,GO:0007507,GO:0048071,GO:0008595,GO:0035277,GO:0007506,GO:0007424,GO:0007548,GO:0007280,GO:0007379,GO:0030539,GO:0003700,GO:0000976,GO:0061101,GO:0000980,GO:0046693	CG11648-PB				SM00389		PF00046	PS50071	PR00031,PR00031,PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689	119~146									
aly822.12	Unknown		n/a																				
aly822.13	Unknown		n/a																				
aly822.14	Protein wings apart-like	GO:0006325,GO:0005634,GO:0016321,GO:0005700,GO:0003674,GO:0007062	CG3707-PA						PF07814	PS51271,PS51271					463~483								
aly822.15	IQ and ubiquitin-like domain-containing protein	GO:0031514,GO:0001669,GO:0060271,GO:0007224	CG13855-PA											SSF54236	416~436								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly822.16	Sex determination protein fruitless	GO:0060179,GO:0007618,GO:0007617,GO:0048065,GO:0048047,GO:0003676,GO:0003677,GO:0008049,GO:0007275,GO:0007530,GO:0007417,GO:0007517,GO:0005634,GO:0044719,GO:0021954,GO:0046872,GO:0007620,GO:0046661,GO:0045433,GO:0003700,GO:0002118,GO:0016543,GO:0016544,GO:0016545,GO:0016199,GO:0048813,GO:0006351	CG14307-PN				SM00225,SM00614		PF00651	PS50097		PS00028	G3DSA:3.30.710.10	SSF54695										
aly822.17	Unknown	GO:0006030,GO:0005576,GO:0008061	CG14304-PA				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625										
aly822.18	Unknown	GO:0006030,GO:0005576,GO:0008061	CG14301-PB				SM00494		PF01607	PS50940			G3DSA:2.170.140.10	SSF57625										
aly822.19	E3 ubiquitin-protein ligase arc-1	GO:0043186,GO:0035194,GO:0005634,GO:0005622,GO:0016567,GO:0008270,GO:0007264,GO:0016874,GO:0005525	CG43726-PB				SM00336,SM00336		PF00567,PF00643	PS50304,PS50119			G3DSA:4.10.45.10,G3DSA:2.30.30.140	SSF57845,SSF63748	244~267								
aly822.2	Unknown		n/a												62~65								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly822.20	RING finger protein 17	GO:0005737,GO:0043186,GO:0035194,GO:0005634,GO:0008270,GO:0007286,GO:0007275,GO:0042803	CG43726-PB				SM00333,SM00333,SM00333,SM00333		PF00567,PF00567,PF00567,PF00567	PS50304,PS50304,PS50304			G3DSA:2.30.30.140,G3DSA:2.30.30.140,G3DSA:2.30.30.140,G3DSA:2.30.30.140	SSF63748,SSF63748,SSF63748,SSF63748	904~924								
aly822.21	Kynurenine formamidase	GO:0004061,GO:0004328,GO:0043420,GO:0019441	n/a						PF04199				G3DSA:3.50.30.50	SSF102198		00630+3.5.1.9,00380+3.5.1.9		PWY-5651,PWY-6309	UPA00333				
aly822.22	DNA polymerase delta subunit 3	GO:0005654,GO:0006297,GO:0005634,GO:0005739,GO:0003887,GO:0006260	n/a						PF09507														
aly822.23	TAF5-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 5L	GO:0000124,GO:0043966,GO:0043970,GO:0006325,GO:0005634,GO:0003713,GO:0033276,GO:0030914,GO:0005654,GO:0003700,GO:0005515,GO:0006366	CG4448-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF04494,PF04494,PF00400,PF00400,PF00400,PF00400	PS50294,PS50082,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320		G3DSA:2.130.10.10	SSF50978,SSF50978,SSF160897,SSF160897	286~306								
aly822.24	LIM and senescent cell antigen-like-containing domain protein 2	GO:0016337,GO:0009880,GO:0008258,GO:2001046,GO:0031252,GO:0007391,GO:0007475,GO:0043066,GO:0008270,GO:0045216,GO:0005886,GO:0046329,GO:0005925,GO:2000178,GO:2000346	CG7954-PC			PIRSF038003	SM00132,SM00132,SM00132,SM00132		PF00412,PF00412,PF00412,PF00412	PS50023,PS50023,PS50023,PS50023		PS00478,PS00478,PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716,SSF57716,SSF57716,SSF57716			REACT_20676						
aly822.25	Renin receptor	GO:0016197,GO:0045177,GO:0015991,GO:0001737,GO:0016021,GO:0016055,GO:0035317,GO:0005622,GO:0060071,GO:0005109,GO:0090251,GO:0004872,GO:0005886,GO:0048104,GO:0009986,GO:0016471,GO:0005110	CG8444-PA						PF07850														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly822.26	Protein-lysine methyltransferase METTL21D	GO:0005737,GO:0018023,GO:0016279	CG5013-PA						PF10294				G3DSA:3.40.50.150	SSF53335									
aly822.27	Unknown		n/a																				
aly822.28	Unknown		n/a																				
aly822.29	E3 ubiquitin-protein ligase RNF181	GO:0004842,GO:0005575,GO:0051865,GO:0008150,GO:0008270,GO:0005515,GO:0016874	CG7694-PA				SM00184		PF13639	PS50089			G3DSA:3.30.40.10	SSF57850									
aly822.3	Unknown		n/a																				
aly822.30	Unknown		CG32436-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly822.31	Uncharacterized protein CG16817	GO:0003674,GO:0007030,GO:0031965,GO:0005634,GO:0005783	CG16817-PA						PF04969	PS51203			G3DSA:2.60.40.790	SSF49764									
aly822.32	Programmed cell death protein 2-like	GO:0005737,GO:0016020,GO:0007049	CG5333-PA						PF04194														
aly822.33	Retinoid-inducible serine carboxypeptidase	GO:0070062,GO:0045776,GO:0005829,GO:0045909,GO:0004185,GO:0006508,GO:0042573	CG3344-PA						PF00450		PR00724,PR00724,PR00724		G3DSA:3.40.50.1820	SSF53474									
aly822.34	RUN and FYVE domain containing protein 2	GO:0005634,GO:0046872,GO:0006909	CG31064-PG				SM00064,SM00593		PF02759,PF01363	PS50826,PS50178			G3DSA:3.30.40.10	SSF57903,SSF140741	391~418,276~324,461~495,433~453								
aly822.35	Unknown	GO:0003824,GO:0005975,GO:0016616,GO:0055114	n/a										G3DSA:3.90.110.10										
aly822.36	Lachesin	GO:0007155,GO:0007169,GO:0004714,GO:0005886,GO:0031225	CG31814-PA				SM00408,SM00408,SM00408,SM00409,SM00409,SM00409		PF07679,PF07679,PF07679	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly822.37	Unknown		n/a																				
aly822.38	Lachesin	GO:0004714,GO:0005515,GO:0005886,GO:0007155,GO:0007169,GO:0031225	CG31814-PA				SM00409,SM00409,SM00409,SM00408,SM00408,SM00408		PF07679,PF07679,PF07686	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726										
aly822.39	Luciferin 4-monooxygenase	GO:0046872,GO:0006637,GO:0045289,GO:0004321,GO:0005777,GO:0004467,GO:0046949,GO:0001676,GO:0008218,GO:0047077,GO:0005524	CG6178-PA						PF13193,PF00501			PS00455	G3DSA:2.30.38.10,G3DSA:3.40.50.980,G3DSA:3.30.300.30,G3DSA:3.40.50.980	SSF56801										
aly822.4	Homeotic protein Sex combs reduced	GO:0043565,GO:0007548,GO:0007494,GO:0003700,GO:0007381,GO:0005634,GO:0006355,GO:0045498,GO:0006357,GO:0045944,GO:0000977,GO:0003677,GO:0007379,GO:0007432,GO:0042803	CG1030-PA									PS00032											
aly822.40	Unknown		n/a																				
aly822.41	Autophagy-related protein 16-1	GO:0039689,GO:0000421,GO:0005776,GO:0000045,GO:0005575,GO:0003674,GO:0034045,GO:0015031,GO:0010506,GO:0005930,GO:0042802	CG31033-PF				SM00320,SM00320		PF08614,PF00400	PS50082,PS50082,PS50294		PS00678	G3DSA:2.130.10.10	SSF50978	203~223,75~95,145~193								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly822.42	Unknown	GO:0016476,GO:0016021,GO:0003383	CG7802-PA				SM00241,SM00473,SM00473,SM00473		PF00024,PF00024,PF00024,PF00100	PS51034,PS50948,PS50948,PS50948			G3DSA:3.50.4.10,G3DSA:3.50.4.10	SSF57414,SSF57414									
aly822.43	Homeobox protein Hox-D3	GO:0007160,GO:0035289,GO:0001077,GO:0010628,GO:0003677,GO:0035282,GO:0008354,GO:0007417,GO:0043565,GO:0007219,GO:0007366,GO:0000122,GO:0005634,GO:0005654,GO:0045666,GO:0030878,GO:0000980,GO:0048704,GO:0021615,GO:0007350,GO:0035290,GO:0007506,GO:0051216,GO:0009952,GO:0003700,GO:0003705,GO:0006355,GO:0006357,GO:0045944,GO:0006351,GO:0001708	CG2047-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly822.44	Homeobox protein vab-7	GO:0009997,GO:0008045,GO:0035289,GO:0003677,GO:0007275,GO:0007417,GO:0043565,GO:0007517,GO:0007366,GO:0000122,GO:0005634,GO:0001709,GO:0000980,GO:0003007,GO:0008595,GO:1901739,GO:0007350,GO:0035290,GO:0007507,GO:0045165,GO:0050770,GO:0007377,GO:0007376,GO:0003700,GO:0007512,GO:0003705,GO:0006355,GO:0045944,GO:0006351,GO:0007399	CG2328-PA				SM00389		PF00046	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689	398~398								
aly822.45	Homeobox protein Hox-A1	GO:0007389,GO:0009953,GO:0007420,GO:0000122,GO:0003700,GO:0006355,GO:0005634,GO:0007398,GO:0043565,GO:0007275,GO:0007419,GO:0010629,GO:0006357,GO:0006351,GO:0003677,GO:0007417,GO:0008134,GO:0007400	CG11551-PB				SM00389		PF00046	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689									
aly822.46	Ventral anterior homeobox 2	GO:0043565,GO:0090259,GO:0006351,GO:0003700,GO:0005634,GO:0016055,GO:0006355,GO:0030900,GO:0021554,GO:0060042,GO:0003677,GO:0061386,GO:1902254,GO:0060041	CG18599-PA				SM00389		PF00046	PS50071			G3DSA:1.10.10.60	SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly822.47	Homeobox protein Hox-B3	GO:0033613,GO:0001158,GO:0035289,GO:0060322,GO:0060324,GO:0003677,GO:0001525,GO:0043565,GO:0000122,GO:0007380,GO:0005634,GO:0002244,GO:0030878,GO:0010468,GO:0006351,GO:0048704,GO:0050767,GO:0021615,GO:0021546,GO:0060216,GO:0009952,GO:0051216,GO:0007420,GO:0009790,GO:0003700,GO:0003705,GO:1902339,GO:0045944,GO:0000977,GO:0000979	CG2189-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly822.48	Zinc finger protein 862	GO:0006355,GO:0005634,GO:0046872,GO:0006351,GO:0003676	n/a				SM00597																
aly822.49	Sex determination protein fruitless	GO:0060179,GO:0007618,GO:0007617,GO:0048065,GO:0048047,GO:0003676,GO:0003677,GO:0008049,GO:0007275,GO:0007530,GO:0007417,GO:0007517,GO:0005634,GO:0044719,GO:0021954,GO:0046872,GO:0007620,GO:0046661,GO:0045433,GO:0003700,GO:0002118,GO:0016543,GO:0016544,GO:0016545,GO:0016199,GO:0048813,GO:0006351	CG14307-PN				SM00355,SM00355			PS50157		PS00028	G3DSA:3.30.160.60	SSF57667									
aly822.5	Homeobox protein HB1	GO:0005737,GO:0007507,GO:0007494,GO:0043565,GO:0009948,GO:0006355,GO:0005634,GO:0007383,GO:0007384,GO:0003705,GO:0014019,GO:0003700,GO:0006357,GO:0045944,GO:0003677,GO:0007275,GO:0007379,GO:0042694,GO:0048542	CG1028-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024,PR00031,PR00031	PS00027	G3DSA:1.10.10.60	SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly822.50	Unknown		n/a																				
aly822.51	Unknown		n/a																				
aly822.6	Homeotic protein antennapedia	GO:0005737,GO:0007507,GO:0007494,GO:0043565,GO:0009948,GO:0005634,GO:0007383,GO:0007384,GO:0003705,GO:0014019,GO:0003700,GO:0006357,GO:0045944,GO:0003677,GO:0007379,GO:0042694,GO:0048542	CG1028-PA				SM00389		PF00046	PS50071	PR00025,PR00025,PR00024,PR00024,PR00024	PS00032,PS00027	G3DSA:1.10.10.60	SSF46689									
aly822.7	Unknown		n/a																				
aly822.8	Homeotic protein ultrabithorax	GO:0007494,GO:0061327,GO:0048636,GO:0003677,GO:0007275,GO:0043565,GO:0001706,GO:0000122,GO:0005634,GO:0001709,GO:0007384,GO:0007385,GO:0000980,GO:0007482,GO:0007507,GO:0035052,GO:0042659,GO:0019904,GO:0007525,GO:0060969,GO:0007424,GO:0007501,GO:0003700,GO:0010092,GO:0006355,GO:0007480,GO:0006357,GO:0006351,GO:0005515,GO:0045570,GO:0042694	CG10388-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00032,PS00027	G3DSA:1.10.10.60	SSF46689	211~244								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly822.9	Homeobox protein abdominal-A homolog (Fragment)	GO:0007494,GO:0035224,GO:0035225,GO:0007385,GO:0010002,GO:0003677,GO:0007275,GO:0008354,GO:0043565,GO:0005634,GO:0008406,GO:0014019,GO:0007438,GO:0048806,GO:0006915,GO:0009987,GO:0035053,GO:0007280,GO:0048636,GO:0007400,GO:0007506,GO:0007507,GO:0009952,GO:0007399,GO:0007422,GO:0003700,GO:0007501,GO:0003705,GO:0048738,GO:0006355,GO:0045944,GO:0005667,GO:0042694	CG10325-PB				SM00389		PF00046,PF12407	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689	65~106								
aly82294.1	Unknown		n/a																				
aly8230.1	Gustatory receptor for sugar taste 64a	GO:0009731,GO:0001582,GO:0033041,GO:0007637,GO:0016021,GO:0005886,GO:0008527,GO:0050912,GO:0051594,GO:0050916,GO:0050909,GO:0034289	CG32261-PA			PIRSF038981			PF06151														
aly8230.10	Probable uridine nucleosidase 2	GO:0005737,GO:0045437	CG11158-PA						PF01156				G3DSA:3.90.245.10	SSF53590									
aly8230.11	Uncharacterized protein in bps2 5'region (Fragment)	GO:0016799	CG11158-PA						PF01156				G3DSA:3.90.245.10	SSF53590									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8230.2	Gustatory receptor for sugar taste 64f	GO:0033041,GO:0016021,GO:0005886,GO:0008527,GO:0050912,GO:0050916,GO:0050909,GO:0001582	CG32255-PA						PF06151														
aly8230.3	Gustatory receptor for sugar taste 64f	GO:0033041,GO:0016021,GO:0005886,GO:0008527,GO:0050912,GO:0050916,GO:0050909,GO:0001582	CG32255-PA						PF06151														
aly8230.4	Gustatory receptor for sugar taste 64f	GO:0033041,GO:0016021,GO:0005886,GO:0008527,GO:0050912,GO:0050916,GO:0050909,GO:0001582	CG32255-PA						PF06151														
aly8230.5	Unknown		n/a																				
aly8230.6	Gustatory receptor for sugar taste 64f	GO:0033041,GO:0016021,GO:0005886,GO:0008527,GO:0050912,GO:0050916,GO:0050909,GO:0001582	CG32255-PA						PF06151,PF06151														
aly8230.7	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8230.8	Unknown	GO:0004930,GO:0033041,GO:0007637,GO:0016021,GO:0008527,GO:0050912,GO:0050916,GO:0050909,GO:0010353	CG15779-PA						PF06151														
aly8230.9	Inosine-uridine preferring nucleoside hydrolase	GO:0045437,GO:0047724,GO:0009117,GO:0005509,GO:0008477,GO:0043101	CG11158-PA						PF01156				G3DSA:3.90.245.10	SSF53590									
aly8233.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0022857,GO:0005886,GO:0055085	CG8234-PA						PF00083				G3DSA:1.20.1250.20	SSF103473									
aly824.1	Unknown	GO:0016772	CG1561-PB				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly824.10	Unknown		n/a																				
aly824.11	Sperm-associated antigen 7	GO:0005634,GO:0003676	CG2608-PA			PIRSF037943			PF01424	PS51061			G3DSA:3.30.1370.50	SSF82708	18~56,218~238,126~150								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly824.12	Sodium-dependent neutral amino acid transporter B(0)AT3	GO:0006810,GO:0005328,GO:0005215,GO:0016021,GO:0016020,GO:0031526,GO:0005887,GO:0006836,GO:0003333,GO:0005886,GO:0005326	CG10804-PC						PF00209	PS50267	PR01206,PR01206,PR01206,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176,PR00176	PS00610		SSF161070,SSF161070			REACT_13,REACT_20679,REACT_19419,REACT_15518							
aly824.13	40S ribosomal protein S28	GO:0005840,GO:0003735,GO:0002181,GO:0006407,GO:0006412,GO:0022627	CG2998-PA	MF_00292					PF01200			PS00961	G3DSA:2.40.50.140	SSF50249										
aly824.14	Translocon-associated protein subunit alpha	GO:0005785,GO:0005048,GO:0016021,GO:0005811,GO:0045169,GO:0005789	CG32701-PA						PF03896														
aly824.15	Alanine--glyoxylate aminotransferase 2, mitochondrial	GO:0047305,GO:0008453,GO:0006206,GO:0016223,GO:0019481,GO:0009436,GO:0044281,GO:0034641,GO:0005739,GO:0030170,GO:0005759,GO:0046135,GO:0046487,GO:0045429,GO:0055086,GO:0019265	CG11241-PB						PF00202			PS00600	G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383										
aly824.16	Alanyl-tRNA editing protein Aarsd1	GO:0005737,GO:0004813,GO:0006419,GO:0005634,GO:0043039,GO:0016876,GO:0003676,GO:0046872,GO:0005524	CG10802-PA				SM00863		PF07973,PF01411	PS50860				SSF50447,SSF55186	274~301	00970+6.1.1.7								
aly824.17	ER membrane protein complex subunit 8/9 homolog	GO:0008150,GO:0003674,GO:0005875,GO:0012505	CG3501-PA						PF03665														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly824.18	1-phosphatidylinositol 3-phosphate 5-kinase	GO:0034504,GO:0012506,GO:0016310,GO:0008333,GO:0032288,GO:0008270,GO:0035556,GO:0010008,GO:0044267,GO:0031410,GO:0000046,GO:0052810,GO:0046854,GO:0048471,GO:0031902,GO:0031901,GO:0016308,GO:0042147,GO:0030659,GO:0005911,GO:0005829,GO:0045121,GO:0000139,GO:0005524,GO:0000285,GO:0005768	CG6355-PB				SM00064		PF00118,PF01363	PS50178			G3DSA:3.30.260.10,G3DSA:3.30.260.10,G3DSA:3.50.7.10,G3DSA:3.30.40.10	SSF52029,SSF57903										
aly824.19	1-phosphatidylinositol 3-phosphate 5-kinase	GO:0034504,GO:0012506,GO:0016310,GO:0008333,GO:0032288,GO:0008270,GO:0043813,GO:0035556,GO:0010008,GO:0044267,GO:0031410,GO:0000046,GO:0046854,GO:0006661,GO:0048471,GO:0046872,GO:0031902,GO:0031901,GO:0016308,GO:0036092,GO:0016307,GO:0042147,GO:0046488,GO:0005911,GO:0005829,GO:0045121,GO:0006644,GO:0000139,GO:0005524,GO:0000285,GO:0005768,GO:0044281	CG6355-PB				SM00330		PF01504	PS51455			G3DSA:3.30.810.10,G3DSA:3.30.810.10	SSF56104										
aly824.2	Unknown	GO:0016772	CG1561-PB				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly824.20	Unknown		n/a												349~369,373~393								
aly824.21	Transmembrane protein 64	GO:0004177,GO:0045780,GO:0043462,GO:0005783,GO:0051480,GO:0005829,GO:0030145,GO:0005575,GO:0045672,GO:0003674,GO:0006508,GO:0008150,GO:0008235,GO:0016021	CG11367-PA						PF09335														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly824.22	Zinc finger CCCH domain containing protein 15 homolog	GO:0005575,GO:0008150,GO:0046872,GO:0003674	CG8635-PA				SM00356,SM00356		PF16543,PF00642	PS50103,PS50103			G3DSA:4.10.1000.10	SSF90229	235~255,376~396,44~64								
aly824.23	Phosphotriesterase-related protein	GO:0016787,GO:0016788,GO:0005575,GO:0008270,GO:0004063,GO:0009056	CG18473-PA						PF02126	PS51347		PS01322	G3DSA:3.20.20.140	SSF51556,SSF51556									
aly824.24	Dyslexia susceptibility 1 candidate gene 1 protein homolog	GO:0005737,GO:0033146,GO:0030331,GO:0061136,GO:0007368,GO:0036159,GO:0036158,GO:0005575,GO:0001764,GO:0003674,GO:0005886,GO:0003341,GO:0007274,GO:0005634	CG5094-PA				SM00028,SM00028		PF13414				G3DSA:2.60.40.790,G3DSA:1.25.40.10	SSF49764,SSF48452									
aly824.25	Probable cytosolic oligopeptidase A	GO:0004222,GO:0005829,GO:0048046,GO:0046686,GO:0006508,GO:0046872,GO:0008237,GO:0009507	CG11771-PA						PF01432				G3DSA:3.40.390.10,G3DSA:1.10.1370.10,G3DSA:1.10.1370.10	SSF55486	151~171,188~208								
aly824.26	Organic cation transporter 1	GO:0015226,GO:0016021,GO:0015695,GO:0008340,GO:0015101,GO:0055085	CG3790-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly824.27	Lysophosphatidylcholine acyltransferase 2B	GO:0008654,GO:0016021,GO:0005575,GO:0016746,GO:0005509,GO:0008152	CG32699-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly824.3	Unknown	GO:0016772	CG31975-PB						PF02958				G3DSA:3.90.1200.10	SSF56112									
aly824.4	Unknown	GO:0016772	CG31975-PB						PF02958				G3DSA:3.90.1200.10	SSF56112									
aly824.5	Unknown	GO:0016772	CG1561-PB				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly824.6	Unknown	GO:0016772	CG13813-PA				SM00587		PF02958				G3DSA:3.90.1200.10	SSF56112									
aly824.7	Unknown		n/a																				
aly824.8	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly824.9	1-acylglycerophosphocholine O acyltransferase 1	GO:0005794,GO:0005783,GO:0008654,GO:0016021,GO:0000139,GO:0005575,GO:0016746,GO:0005509,GO:0008152,GO:0047184,GO:0005789	CG32699-PB				SM00563,SM00054,SM00054		PF13499,PF01553	PS50222,PS50222			G3DSA:3.40.1130.10,G3DSA:1.10.238.10	SSF69593,SSF47473									
aly8254.1	DCN1-like protein 4	GO:0005634	CG6597-PA						PF03556	PS51229													
aly8254.2	Protein FRG1 homolog	GO:0031936,GO:0007517,GO:0005730,GO:0005575,GO:0070511,GO:0003674,GO:0006364,GO:0015030,GO:0030018	CG6480-PA						PF06229				G3DSA:2.80.10.50	SSF50405									
aly8254.3	Eukaryotic translation initiation factor 3 subunit A	GO:0005852,GO:0016282,GO:0006446,GO:0033290,GO:0001732,GO:0001731,GO:0003743	n/a																				
aly8269.1	Unknown	GO:0003677	n/a						PF02944,PF10545	PS51031													
aly827.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly827.10	Carboxypeptidase D	GO:0040003,GO:0006909,GO:0007616,GO:0004181,GO:0004180,GO:0007476,GO:0004185,GO:0042302,GO:0005576,GO:0008270,GO:0006508,GO:0048471,GO:0016021,GO:0012505	CG4122-PG				SM00631,SM00631		PF00246,PF00246,PF13620,PF13620		PR00765,PR00765,PR00765,PR00765	PS00132,PS00133,PS00132	G3DSA:3.40.630.10,G3DSA:3.40.630.10,G3DSA:3.40.630.10,G3DSA:2.60.40.1120,G3DSA:3.40.630.10,G3DSA:2.60.40.1120	SSF53187,SSF53187,SSF53187,SSF49464,SSF49464										
aly827.11	Uncharacterized protein KIAA2013 homolog	GO:0016021	CG7289-PA						PF10222														
aly827.12	Moesin/ezrin/radixin homolog 2	GO:0008101,GO:0019898,GO:0046669,GO:0007291,GO:0051307,GO:0009798,GO:0001745,GO:0042981,GO:0005737,GO:0009966,GO:0035330,GO:0016020,GO:0007476,GO:0003779,GO:0016324,GO:0016006,GO:0042802,GO:0042127,GO:0008285,GO:0005515,GO:0042048,GO:0046621,GO:0019094,GO:0060253,GO:0007050,GO:0045595,GO:0001558,GO:0005938,GO:0005886,GO:0007267,GO:0035329,GO:0072659,GO:0001751,GO:0042327,GO:0007112,GO:0006897,GO:0008092,GO:0005856,GO:0036375,GO:0007283,GO:0045169,GO:0006355,GO:0006351,GO:0032456,GO:0001934,GO:0005912	CG14228-PA				SM00295		PF09379,PF09380,PF00373,PF00769	PS50057	PR00935,PR00935,PR00935,PR00935,PR00661,PR00661,PR00661,PR00661,PR00661,PR00661	PS00661	G3DSA:3.10.20.90,G3DSA:2.30.29.30,G3DSA:1.20.5.450,G3DSA:1.20.80.10	SSF47031,SSF50729,SSF54236	309~462									
aly827.13	RRP12-like protein	GO:0005575,GO:0005634,GO:0048812,GO:0003674,GO:0005488	CG2691-PA						PF08161				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371	1127~1154								
aly827.14	Ataxin-7-like protein 1		n/a						PF08313	PS51505													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly827.15	Mitochondrial inner membrane protease subunit 2	GO:0030728,GO:0042720,GO:0006627,GO:0061300,GO:0007420,GO:0033108,GO:0008015,GO:0016021,GO:0016020,GO:0006974,GO:0005743,GO:0007283,GO:0001541,GO:0022904,GO:0006508,GO:0008233,GO:0006801,GO:0008236	CG11110-PA						PF00717		PR00727,PR00727,PR00727		G3DSA:2.10.109.10	SSF51306									
aly827.16	YrdC domain-containing protein, mitochondrial	GO:0016020,GO:0003725,GO:0051051,GO:0005739	n/a					TIGR00057	PF01300	PS51163			G3DSA:3.90.870.10	SSF55821									
aly827.17	DNA-directed RNA polymerase III subunit RPC10	GO:0006386,GO:0051607,GO:0005730,GO:0045087,GO:0003677,GO:0006359,GO:0003725,GO:0006351,GO:0045182,GO:0005666,GO:0003899,GO:0006412,GO:0008270	CG33005-PB			PIRSF005586	SM00440,SM00661		PF02150,PF01096	PS51133		PS00466	G3DSA:2.20.25.10,G3DSA:2.20.25.10,G3DSA:2.20.28.10	SSF57783,SSF57783									
aly827.18	Ceramide synthase 6	GO:0030148,GO:0043565,GO:0016020,GO:0032933,GO:0006641,GO:0003700,GO:0031965,GO:0016021,GO:0005886,GO:0050995,GO:0005789,GO:0006665,GO:0044281,GO:0003677,GO:0046889,GO:0050291,GO:0046513	CG3576-PA			PIRSF005225	SM00724		PF03798,PF00046	PS50071,PS50922			G3DSA:1.10.10.60	SSF46689			REACT_22258						
aly827.19	Ceramide synthase 6	GO:0030148,GO:0043565,GO:0016020,GO:0032933,GO:0006641,GO:0003700,GO:0031965,GO:0016021,GO:0005886,GO:0050995,GO:0005789,GO:0006665,GO:0044281,GO:0003677,GO:0046889,GO:0050291,GO:0046513	CG3576-PA			PIRSF005225	SM00724		PF03798	PS50922			G3DSA:1.10.10.60	SSF46689			REACT_22258						
aly827.2	Unknown	GO:0005575,GO:0003674,GO:0008150	CG17162-PG																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly827.20	RNA-binding protein 12	GO:0000381,GO:0005634,GO:0000166,GO:0003723,GO:0003676,GO:0003729	CG7879-PA				SM00360,SM00360,SM00360,SM00360,SM00360		PF00076,PF14259,PF14259	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928,SSF54928,SSF54928,SSF54928									
aly827.21	Sex-lethal homolog	GO:0009994,GO:0048024,GO:0003676,GO:0008187,GO:0048025,GO:0048027,GO:0007530,GO:0005737,GO:0000381,GO:0000380,GO:0000900,GO:0005634,GO:0000166,GO:0003730,GO:0048477,GO:0019099,GO:0019101,GO:0030237,GO:0008266,GO:0007131,GO:0008083,GO:0043234,GO:0007281,GO:0007548,GO:0007549,GO:0007446,GO:0018993,GO:0007224,GO:0007541,GO:0000398,GO:0003723,GO:0005515,GO:0017148,GO:0003729	CG43770-PX				SM00360,SM00360		PF00076,PF00076	PS50102,PS50102	PR00961,PR00961,PR00961,PR00961,PR00961		G3DSA:3.30.70.330	SSF54928,SSF54928									
aly827.22	Serine protease gd	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG31326-PA				SM00020		PF16030,PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494	572~572								
aly827.23	Serine protease gd	GO:0004252,GO:0004175,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0022008,GO:0008233,GO:0008236	CG9649-PA				SM00020		PF16030,PF00089	PS50240	PR00722,PR00722,PR00722		G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly827.24	Fatty acid synthase	GO:0006633,GO:0047451,GO:0006631,GO:0004320,GO:0015939,GO:0031325,GO:0008144,GO:0035338,GO:0008270,GO:0001649,GO:0016491,GO:0005737,GO:0070062,GO:0016295,GO:0005835,GO:0016020,GO:0071353,GO:0005739,GO:0006112,GO:0030879,GO:0005794,GO:0006767,GO:0006766,GO:0044822,GO:0004315,GO:0016788,GO:0047117,GO:0042587,GO:0005886,GO:0044255,GO:0055114,GO:0006084,GO:0042470,GO:0005829,GO:0004312,GO:0004313,GO:0016296,GO:0019432,GO:0004316,GO:0004317,GO:0004314,GO:0070402,GO:0004319,GO:0044281	CG17374-PC				SM00825		PF16197,PF02801				G3DSA:3.40.47.10	SSF53901										
aly827.25	Unknown		n/a																				
aly827.26	Unknown		n/a																				
aly827.27	Unknown		n/a																				
aly827.3	Rho GTPase-activating protein 15	GO:0005737,GO:0016020,GO:0005096,GO:0005622,GO:0005575,GO:0008360,GO:0007165,GO:0005100,GO:0007266,GO:0031290	CG10538-PA				SM00233,SM00324		PF00620,PF00169	PS50238,PS50003			G3DSA:1.10.555.10,G3DSA:2.30.29.30	SSF48350,SSF50729			REACT_11044						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly827.4	Unknown		n/a																				
aly827.5	Probable beta-hexosaminidase fdl	GO:0005794,GO:0016231,GO:0016063,GO:0007420,GO:0006491,GO:0032428,GO:0005770,GO:0004563,GO:0006517,GO:0005886,GO:0006032,GO:0005783	CG8824-PB			PIRSF001093			PF14845,PF00728		PR00738,PR00738,PR00738,PR00738,PR00738,PR00738,PR00738,PR00738		G3DSA:3.20.20.80,G3DSA:3.30.379.10	SSF51445,SSF55545		00604+3.2.1.52,00520+3.2.1.52,00511+3.2.1.52,00603+3.2.1.52,00513+3.2.1.52,00531+3.2.1.52		PWY-6902					
aly827.6	Unknown		n/a												63~83,198~218								
aly827.7	Meckel syndrome type 1 protein	GO:0061009,GO:0048754,GO:0060322,GO:0010669,GO:0005737,GO:0036064,GO:2000095,GO:0005813,GO:0007368,GO:0016020,GO:0005814,GO:1901620,GO:0001843,GO:0044458,GO:1990403,GO:0042384,GO:0035058,GO:0060271,GO:0060122,GO:0006996,GO:0042733,GO:0036038,GO:0090175,GO:0005829,GO:0048706,GO:0060828	CG15730-PA						PF07162														
aly827.8	Rhomboid-related protein 3	GO:0004252,GO:0016021,GO:0005509,GO:0005886,GO:0016485,GO:0006508,GO:0008236	CG1697-PA			PIRSF037470	SM00054,SM00054		PF01694,PF13499	PS50222,PS50222		PS00018	G3DSA:1.10.238.10,G3DSA:1.20.1540.10	SSF144091,SSF47473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly827.9	Carboxypeptidase D	GO:0040003,GO:0006909,GO:0007616,GO:0004181,GO:0004180,GO:0007476,GO:0004185,GO:0042302,GO:0005576,GO:0008270,GO:0006508,GO:0048471,GO:0016021,GO:0012505	CG4122-PG										G3DSA:2.60.40.1120	SSF49464									
aly82866.1	Unknown		n/a												10~51								
aly83.1	Unknown		n/a																				
aly83.10	Transcriptional repressor p66 alpha	GO:0060912,GO:0016607,GO:0030674,GO:0001701,GO:0016581,GO:0000122,GO:0021506,GO:0005634,GO:0005654,GO:0012501,GO:0045887,GO:0045892,GO:0006351,GO:0005515,GO:0046959,GO:0010172,GO:0046872,GO:0001568,GO:0001842	CG32067-PE						PF16563						136~163								
aly83.11	Unknown		n/a																				
aly83.12	S-methyl-5'-thioadenosine phosphorylase	GO:0005737,GO:0019509,GO:0016310,GO:0005634,GO:0004645,GO:0005575,GO:0009116,GO:0016763,GO:0017061,GO:0043101,GO:0006166	CG4802-PB	MF_01963					PF01048			PS01240	G3DSA:3.40.50.1580	SSF53167									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly83.13	Cytochrome c oxidase assembly factor 7 homolog	GO:0005575,GO:0008150,GO:0003674	CG13865-PA				SM00671,SM00671,SM00671,SM00671		PF08238,PF08238,PF08238,PF08238,PF08238				G3DSA:1.25.40.10	SSF81901										
aly83.14	Heme oxygenase 1	GO:1902042,GO:0005783,GO:0004392,GO:0034395,GO:0034605,GO:0045909,GO:0019899,GO:0071243,GO:0032764,GO:0005901,GO:0055072,GO:0043524,GO:0044281,GO:0004871,GO:0048662,GO:0008219,GO:0001525,GO:0035556,GO:0006778,GO:0002246,GO:0006788,GO:0020037,GO:0005730,GO:0045765,GO:0031670,G	CG14716-PA			PIRSF000343			PF01126		PR00088,PR00088,PR00088,PR00088		G3DSA:1.20.910.10	SSF48613	104~124	00860+1.14.99.3	REACT_9431	PWY-7170,PWY-5915,PWY-5917,PWY-7580,PWY-7578,PWY-7579,PWY-5874					
aly83.15	Apolipophorins	GO:0005319,GO:0005615,GO:0015918,GO:0006869,GO:0016055,GO:0008289,GO:0045178,GO:0005576,GO:0034196,GO:0005875	CG15828-PC				SM00638		PF09172,PF01347,PF01347,PF06448	PS51211,PS51233			G3DSA:2.30.230.10,G3DSA:2.20.80.10,G3DSA:2.20.50.20,G3DSA:2.20.50.20,G3DSA:1.25.10.20	SSF48431,SSF56968,SSF56968			REACT_22258						
aly83.16	Unknown		n/a																				
aly83.17	Lysozyme c-1	GO:0019835,GO:0035071,GO:0019730,GO:0048102,GO:0003796,GO:0042742	CG11159-PA				SM00263		PF00062	PS51348	PR00135,PR00135,PR00135,PR00135,PR00135,PR00135,PR00135	PS00128	G3DSA:1.10.530.10	SSF53955									
aly83.18	Leucine-rich repeats and immunoglobulin-like domains protein 3	GO:0043234,GO:0005615,GO:0016021,GO:0030659,GO:0005515,GO:0005886,GO:0005927,GO:2001283,GO:2001282,GO:0032474	CG11136-PC				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00082,SM00365,SM00365,SM00365,SM00365,SM00365		PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly83.19	Lysozyme	GO:0019835,GO:0035071,GO:0019730,GO:0048102,GO:0003796,GO:0042742	CG11159-PA				SM00263		PF00062	PS51348	PR00135,PR00135,PR00135,PR00135,PR00135	PS00128	G3DSA:1.10.530.10	SSF53955									
aly83.2	Neurofilament heavy polypeptide	GO:0005200,GO:0015643,GO:0021510,GO:0030424,GO:0021766,GO:0031175,GO:0021987,GO:0005737,GO:0045110,GO:0043204,GO:0005634,GO:0031103,GO:0071392,GO:0005882,GO:0042220,GO:0001552,GO:0034599,GO:0030674,GO:1903935,GO:0007420,GO:1903937,GO:0046982	CG30101-PA																				
aly83.20	Apolipophorins	GO:0005319,GO:0005615,GO:0015918,GO:0006869,GO:0016055,GO:0008289,GO:0045178,GO:0005576,GO:0034196,GO:0005875	CG15828-PC						PF01347				G3DSA:1.25.10.20	SSF48431			REACT_22258						
aly83.21	Unknown		n/a																				
aly83.3	Juvenile hormone epoxide hydrolase	GO:0008096,GO:0006719,GO:0033961,GO:0016021,GO:0005789,GO:0004301,GO:0055114,GO:0019439,GO:0006979,GO:0004602	CG15101-PA						PF00255,PF06441	PS51355	PR01011,PR01011,PR01011	PS00763,PS00460	G3DSA:3.40.50.1820,G3DSA:3.40.30.10	SSF52833,SSF53474		00980+3.3.2.9							
aly83.4	Proteasome subunit alpha type-5	GO:0005737,GO:0004175,GO:0005839,GO:0000502,GO:0043161,GO:0005829,GO:0009987,GO:0010499,GO:0004298,GO:0005654,GO:0006511,GO:0019773,GO:0006508,GO:0005634,GO:0070062	CG10938-PB				SM00948		PF10584,PF00227	PS51475		PS00388	G3DSA:3.60.20.10	SSF56235			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_110						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly83.5	Alpha-xylosidase	GO:0017177,GO:0005975,GO:0030246,GO:0005576,GO:0061634,GO:0004558,GO:0005875	CG14476-PB						PF00754,PF13802,PF01055	PS50022,PS50853			G3DSA:2.60.120.260,G3DSA:2.60.40.10	SSF49265,SSF51011,SSF49785,SSF51445,SSF51445,SSF74650									
aly83.6	Unknown		CG12822-PA						PF01980	PS51668			G3DSA:2.40.30.70	SSF118196,SSF118196									
aly83.7	Cleavage and polyadenylation specificity factor subunit 1	GO:0005847,GO:0005634,GO:0017022,GO:0003730,GO:0003676,GO:0006378,GO:0006379,GO:0022008,GO:0003729	CG10110-PA						PF03178,PF10433														
aly83.8	Maternal protein exuperantia-1	GO:0005737,GO:0007300,GO:0001700,GO:0008359,GO:0071011,GO:0000932,GO:0000398,GO:0007317,GO:0008595,GO:0007283,GO:0046331,GO:0003723,GO:0003676,GO:0007275,GO:0045450,GO:0045451	CG8994-PA											SSF53098									
aly83.9	Exosome complex component RRP41	GO:0071044,GO:0071028,GO:0030307,GO:0005737,GO:0000288,GO:0005730,GO:0005634,GO:0017091,GO:0010467,GO:0006364,GO:0005652,GO:0010468,GO:0034475,GO:0071051,GO:0031125,GO:0000460,GO:0035327,GO:0043928,GO:0016075,GO:0090503,GO:0000178,GO:0045006,GO:0051607,GO:0005829,GO:0000176,GO:0000177,GO:0000175,GO:0034427,GO:0000956	CG15481-PB						PF01138				G3DSA:3.30.230.70	SSF55666,SSF54211			REACT_21257						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly83113.1	Heat shock 70 kDa protein cognate 5	GO:0070584,GO:0006457,GO:0000422,GO:0005811,GO:0005739,GO:0010918,GO:0051082,GO:0016887,GO:0009408,GO:0005875,GO:0005524	CG8542-PB						PF00012		PR00301,PR00301,PR00301	PS01036	G3DSA:3.30.420.40,G3DSA:2.60.34.10	SSF53067,SSF100920									
aly8316.1	Serine protease snake	GO:0004252,GO:0009950,GO:0005576,GO:0007311,GO:0008063,GO:0016485,GO:0006508,GO:0008233,GO:0008236	CG7996-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly8316.2	Unknown		n/a																				
aly8316.3	Unknown		n/a																				
aly8334.1	Chymotrypsin BI	GO:0004252,GO:0005615,GO:0030574,GO:0006508	CG6467-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly8334.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly83396.1	Unknown		n/a																				
aly8351.1	Unknown		n/a																				
aly8351.10	Akirin	GO:0016203,GO:0007517,GO:0045089,GO:0045088,GO:0005634,GO:0003712,GO:0005700,GO:0009790,GO:0045944,GO:0005515,GO:0006366,GO:0050829,GO:0005719,GO:0045087,GO:0007526	CG8580-PA																				
aly8351.11	Charged multivesicular body protein 1b	GO:0005770,GO:0007034,GO:0000815,GO:0005829,GO:0032509,GO:0003674,GO:0015031,GO:0031902	CG4108-PA						PF03357						10~37,110~130								
aly8351.12	Spermine synthase	GO:0070062,GO:0006597,GO:0005575,GO:0004766,GO:0016768,GO:0008295	CG4300-PA						PF01564	PS51006		PS01330	G3DSA:3.40.50.150,G3DSA:3.30.160.110	SSF53335		00480+2.5.1.16,00410+2.5.1.16,00330+2.5.1.16,00270+2.5.1.16			UPA00248				
aly8351.13	Eukaryotic translation initiation factor 4E	GO:0030307,GO:0031594,GO:0048102,GO:0007067,GO:0005875,GO:0005737,GO:0006325,GO:0097482,GO:0016281,GO:0005845,GO:0005515,GO:0035071,GO:0000339,GO:0016321,GO:0007052,GO:0001558,GO:0007076,GO:0043234,GO:0022008,GO:0031370,GO:0016070,GO:0000340,GO:0006413,GO:0005829,GO:0000932,G	CG4035-PA						PF01652			PS00813	G3DSA:3.30.760.10	SSF55418										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8351.14	Eukaryotic translation initiation factor 4E	GO:0030307,GO:0031594,GO:0048102,GO:0007067,GO:0005875,GO:0005737,GO:0006325,GO:0097482,GO:0016281,GO:0000340,GO:0005845,GO:0005515,GO:0035071,GO:0000339,GO:0016321,GO:0007052,GO:0001558,GO:0045995,GO:0007076,GO:0022008,GO:0031370,GO:0016070,GO:0009790,GO:0005829,GO:0000932,GO:0003723,GO:0000022,GO:0006417,GO:0002191,GO:0006413,GO:0006412,GO:0003743	CG4035-PA						PF01652			PS00813	G3DSA:3.30.760.10	SSF55418										
aly8351.15	X-linked retinitis pigmentosa GTPase regulator	GO:0005737,GO:0005794,GO:0042384,GO:0036064,GO:0005813,GO:0005634,GO:0005085,GO:0042073,GO:0007601,GO:0042787,GO:0036126,GO:0004842,GO:0050896	CG9153-PC						PF00415,PF00415,PF00415,PF00415	PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012,PS50012	PR00633,PR00633,PR00633,PR00633,PR00633,PR00633,PR00633,PR00633	PS00626,PS00626,PS00626	G3DSA:2.130.10.30	SSF50985	405~425,578~598,838~858									
aly8351.16	Asialoglycoprotein receptor 1	GO:0006897,GO:0016021,GO:0046872,GO:0042246,GO:0030246	CG6014-PB				SM00034		PF00059	PS50041			G3DSA:3.10.100.10	SSF56436									
aly8351.2	Protein amnionless	GO:0045177,GO:0008104,GO:0015889,GO:0007588,GO:0016324,GO:0005615,GO:0016021,GO:0006898,GO:0030139,GO:0043001,GO:0046331,GO:0005102,GO:0007275,GO:0070062	CG11592-PA						PF14828														
aly8351.3	Unknown	GO:0007157,GO:0005576,GO:0003674	CG10134-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8351.4	Interferon-related developmental regulator 1	GO:0005737,GO:0051091,GO:0048671,GO:0046427,GO:0005634,GO:0014706,GO:0045944,GO:0005488,GO:0030517,GO:0043403,GO:0061629,GO:0042692	CG31694-PA						PF04836,PF05004				G3DSA:1.25.10.10	SSF48371	40~60								
aly8351.5	DNA-binding protein RFX2	GO:0043565,GO:0007399,GO:0007605,GO:0005634,GO:0006355,GO:0048813,GO:0006357,GO:0003700,GO:0000978,GO:0006351	CG6312-PH						PF02257	PS51526			G3DSA:1.10.10.10	SSF46785									
aly8351.6	Ubiquitin-like protein 4A	GO:0071818,GO:0005829,GO:0006810,GO:0005515,GO:0071816	CG7215-PA				SM00213		PF00240	PS50053	PR00348,PR00348,PR00348	PS00299	G3DSA:3.10.20.90	SSF54236									
aly8351.7	DDB1- and CUL4-associated factor 15	GO:0016567	CG6325-PA						PF14939														
aly8351.8	Nucleoporin NUP53	GO:0051028,GO:0005643,GO:0031965,GO:0005811,GO:0044613,GO:0006999,GO:0015031,GO:0005487,GO:0007476,GO:0055085	CG6540-PA			PIRSF038119			PF05172	PS51472				SSF54928									
aly8351.9	Glucose-induced degradation protein 8 homolog	GO:0005654,GO:0030054	CG6617-PA				SM00757,SM00667,SM00668		PF10607,PF08513	PS50897,PS50896													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly83580.1	Unknown		n/a																				
aly837.1	Cytoplasmic polyadenylation element-binding protein 2	GO:0045900,GO:0007616,GO:1990124,GO:0071243,GO:0008187,GO:0045202,GO:0032869,GO:0008049,GO:0008356,GO:0005737,GO:0043679,GO:1900248,GO:0000900,GO:0005634,GO:0000166,GO:0003730,GO:0071456,GO:0043023,GO:2000766,GO:0043024,GO:0044292,GO:0044822,GO:0044297,GO:0034260,GO:0005095,GO:0034599,GO:0005844,GO:0043022,GO:0003723,GO:0017148,GO:0035925,GO:0003729	CG43782-PD				SM00360,SM00360		PF16366,PF16367	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928									
aly837.2	Transcription factor Sp9	GO:0043565,GO:0007380,GO:0030326,GO:0007376,GO:0003700,GO:0006355,GO:0008134,GO:0000122,GO:0003705,GO:0035288,GO:0035289,GO:0007480,GO:0006357,GO:0045944,GO:0045743,GO:0003677,GO:0046872,GO:0035118,GO:0005634,GO:0006351	CG12653-PA				SM00355,SM00355		PF00096	PS50157,PS50157		PS00028	G3DSA:3.30.160.60	SSF57667									
aly8371.1	Unknown		n/a																				
aly8371.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8371.3	Unknown		n/a																				
aly838.1	Fibroblast growth factor homolog	GO:0000187,GO:0007424,GO:0007427,GO:0007426,GO:0006935,GO:0007430,GO:0007429,GO:0035231,GO:0035152,GO:0005104,GO:0007428,GO:0035215,GO:0005576,GO:0001763,GO:0050918,GO:0046847,GO:0008543,GO:0008347,GO:0008083	CG4608-PA				SM00442		PF00167		PR00263,PR00263,PR00263,PR00262,PR00262		G3DSA:2.80.10.50	SSF50353									
aly838.10	Unknown		n/a						PF16009														
aly838.11	Unknown		n/a						PF16009														
aly838.12	Unknown		n/a						PF16009	PS51257					42~62								
aly838.13	Phosphatidylinositol 4-kinase type 2-beta	GO:0005737,GO:0016020,GO:0005802,GO:0004430,GO:0016773,GO:0005770,GO:0033339,GO:0032252,GO:0046854,GO:0005524	CG2929-PA						PF00454														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly838.14	Protein FAM160B1	GO:0005575,GO:0003674,GO:0008150	CG3558-PC						PF10257,PF10257														
aly838.15	Tuftelin-interacting protein 11	GO:0071011,GO:0071013,GO:0000398,GO:0008380,GO:0006355,GO:0003676,GO:0003677,GO:0005578,GO:0005681,GO:0006397	CG7238-PA				SM00443		PF07842,PF01585	PS50174					104~131,37~58								
aly838.16	Mitochondrial pyruvate carrier 2	GO:0050833,GO:0016021,GO:0006850,GO:0044237,GO:0031305,GO:0005743,GO:0005739,GO:0006090,GO:0005634,GO:0044281	CG9399-PB						PF03650														
aly838.17	Unknown		CG6945-PA						PF11819						6~33								
aly838.18	Unknown		n/a																				
aly838.19	UDP-glucuronosyltransferase 2B1	GO:0052696,GO:0071361,GO:0070980,GO:0016021,GO:0071385,GO:0009813,GO:0071394,GO:0005789,GO:0071378,GO:0008152,GO:0016758,GO:0015020,GO:0017144,GO:0032496,GO:0043231	CG6649-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly838.2	Unknown		n/a																				
aly838.20	UPF0160 protein MYG1, mitochondrial	GO:0005654,GO:0070062,GO:0005739,GO:0005575,GO:0035641,GO:0008150,GO:0003674	CG11980-PB						PF03690														
aly838.21	PiggyBac transposable element-derived protein 4		CG9839-PA						PF13843,PF13843														
aly838.22	Unknown		n/a																				
aly838.23	Phosphatidylinositol 4-kinase type 2-beta	GO:0005737,GO:0016020,GO:0005802,GO:0004430,GO:0016773,GO:0005770,GO:0033339,GO:0032252,GO:0046854,GO:0005524	CG2929-PA						PF00454														
aly838.24	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG6633-PB						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756,SSF53756									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly838.3	Calcium uptake protein 3, mitochondrial	GO:0016021,GO:0005509,GO:0005739	CG4662-PD							PS50222,PS50222		PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473										
aly838.4	Protein phosphatase methylesterase 1	GO:0051721,GO:0006482,GO:0051722,GO:0034047,GO:0052689,GO:0019903,GO:0004864,GO:0008601,GO:0043086	CG5068-PA			PIRSF022950			PF12697				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474,SSF53474									
aly838.5	Zinc finger protein 154	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG17359-PA				SM00868,SM00355,SM00355,SM00355		PF07776,PF00096	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667									
aly838.6	Polycomb group RING finger protein 3	GO:0031519,GO:0005634,GO:0005654,GO:0006355,GO:0006351,GO:0008270	CG4195-PB				SM00184		PF16207,PF00097	PS50089		PS00518	G3DSA:3.30.40.10	SSF57850									
aly838.7	Coiled-coil domain-containing protein R3HCC1L	GO:0035145,GO:0003676,GO:0000166	CG2162-PE						PF01424	PS51061			G3DSA:3.30.70.330,G3DSA:3.30.1370.50	SSF54928,SSF82708	366~371								
aly838.8	Unknown		n/a						PF16009						398~418								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly838.9	Unknown		n/a																				
aly839.1	Voltage-dependent T-type calcium channel subunit alpha-1G	GO:0005262,GO:0008332,GO:0030425,GO:0005891,GO:0016020,GO:0045956,GO:0048471,GO:0043025,GO:0006811,GO:0060402,GO:0005216,GO:0044297,GO:0014824,GO:0034220,GO:0005886,GO:0086010,GO:0055085,GO:0071549,GO:0005829,GO:0051924,GO:0070588,GO:0007204,GO:0070509	CG15899-PF						PF00520,PF00520,PF00520,PF00520		PR01629,PR01629,PR01629		G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350	SSF81324,SSF81324,SSF81324,SSF81324,SSF81324	1975~1995,1676~1696		REACT_18266						
aly839.10	Unknown		CG13857-PA						PF16027														
aly839.11	Protein CLEC16A	GO:0016197,GO:0008333,GO:0016021,GO:0005770,GO:0005765,GO:0006914,GO:0010008	CG12753-PA						PF09758														
aly839.12	Unknown	GO:0005575,GO:0008150,GO:0003674	CG42784-PF																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly839.13	Unknown		n/a																				
aly839.14	Unknown		n/a																				
aly839.15	STIP1 homology and U box-containing protein 1	GO:0032436,GO:0005783,GO:0042405,GO:0000209,GO:0030018,GO:0032091,GO:0045111,GO:0070062,GO:0004842,GO:0005654,GO:0006511,GO:0071218,GO:0070534,GO:0042803,GO:0031943,GO:0034450,GO:0006281,GO:0005886,GO:0016874,GO:0030579,GO:0090035,GO:0030968,GO:0051443,GO:0000151,GO:0016567,GO:0051865,GO:0006515,GO:0043161	CG5203-PA				SM00504,SM00028,SM00028,SM00028		PF13414,PF04564,PF07719	PS50293,PS51698			G3DSA:1.25.40.10,G3DSA:3.30.40.10	SSF48452,SSF57850	181~201,157~177				UPA00143				
aly839.16	Unknown	GO:0005515	n/a						PF00646	PS50181			G3DSA:1.20.1280.50	SSF81383									
aly839.17	Endothelin-converting enzyme 1	GO:0004175,GO:0004222,GO:0016021,GO:0016020,GO:0016529,GO:0005886,GO:0016485,GO:0006508,GO:0016486,GO:0046872,GO:0042803	CG4058-PA						PF01431,PF05649		PR00786,PR00786,PR00786,PR00786		G3DSA:3.40.390.10,G3DSA:3.40.390.10	SSF55486,SSF55486									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly839.18	Unknown		n/a																				
aly839.19	Prostaglandin reductase 1	GO:0005737,GO:0036132,GO:0008270,GO:0047522,GO:0032440	n/a				SM00829		PF00107,PF16884				G3DSA:3.40.50.720,G3DSA:3.90.180.10	SSF51735,SSF50129									
aly839.2	Unknown		n/a										G3DSA:3.40.630.30,G3DSA:3.40.630.30	SSF55729									
aly839.20	Prostaglandin reductase 1	GO:0005737,GO:0036132,GO:0006631,GO:0005739,GO:0008270,GO:0047522,GO:0032440,GO:0019166,GO:0005875,GO:0055114	CG16935-PB				SM00829		PF16884,PF00107				G3DSA:3.90.180.10,G3DSA:3.40.50.720	SSF50129,SSF51735,SSF50129									
aly839.21	Prostaglandin reductase 1	GO:0005737,GO:0036132,GO:0008270,GO:0047522,GO:0032440,GO:0055114	n/a				SM00829		PF00107,PF16884				G3DSA:3.90.180.10,G3DSA:3.40.50.720	SSF50129,SSF50129,SSF51735									
aly839.22	Prostaglandin reductase 1	GO:0005737,GO:0036132,GO:0008270,GO:0047522,GO:0032440	n/a						PF16884				G3DSA:3.40.50.720,G3DSA:3.90.180.10	SSF50129,SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly839.23	Prostaglandin reductase 1	GO:0005737,GO:0036132,GO:0008270,GO:0047522,GO:0032440	n/a										G3DSA:3.40.50.720	SSF50129									
aly839.24	Histone-binding protein N1/N2	GO:0005575,GO:0003674,GO:0005634,GO:0008150	CG8223-PA				SM00028,SM00028		PF10516	PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452									
aly839.25	Unknown	GO:0005575,GO:0003674,GO:0008150	CG11768-PA																				
aly839.26	Small subunit processome component 20 homolog	GO:0005737,GO:0008285,GO:0030688,GO:0005730,GO:0044822,GO:0030686,GO:0005654,GO:0006364,GO:0032040,GO:0005488,GO:0000447,GO:0000480,GO:0022008,GO:0000472	CG4554-PA						PF07539				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371,SSF48371	854~881,1718~1745									
aly839.27	Hydroxyacylglutathione hydrolase, mitochondrial	GO:0004416,GO:0019243,GO:0005759,GO:0008270,GO:0006750,GO:0005875	CG4365-PC	MF_01374		PIRSF005457	SM00849	TIGR03413	PF16123,PF00753				G3DSA:3.60.15.10	SSF56281		00620+3.1.2.6		PWY-5386	UPA00619				
aly839.28	TCF3 fusion partner homolog	GO:0006310,GO:0005737,GO:0005730,GO:0006281,GO:0019901,GO:0097190,GO:0005634,GO:0006915,GO:0031011,GO:0005575,GO:0006355,GO:0003674,GO:0006351,GO:0003677,GO:0008150,GO:0005654,GO:0031965	CG32202-PA				SM00398			PS50118			G3DSA:1.10.30.10	SSF47095	31~58								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly839.29	Heparan sulfate glucosamine 3-O-sulfotransferase 3A1	GO:0030203,GO:0008587,GO:0008586,GO:0007474,GO:0007040,GO:0001745,GO:0008467,GO:0007219,GO:0016021,GO:0033872,GO:0007476,GO:0008407,GO:0050768,GO:0048190,GO:0016348,GO:0008146,GO:0051036,GO:0007032,GO:0005975,GO:0000139,GO:0006024,GO:0044281	CG7890-PA						PF00685				G3DSA:3.40.50.300	SSF52540										
aly839.3	Unknown		n/a																				
aly839.30	tRNA-splicing endonuclease subunit Sen54	GO:0090502,GO:0090501,GO:0005730,GO:0004017,GO:0000214,GO:0006388,GO:0000379,GO:0006397	CG5626-PA						PF12928						534~561								
aly839.31	Unknown		n/a																				
aly839.4	Alpha-(1,3)-fucosyltransferase C	GO:0036065,GO:0006486,GO:0016021,GO:0016020,GO:0008417,GO:0005886,GO:0032580,GO:0046920	CG40305-PB						PF17039,PF00852					SSF53756					UPA00378				
aly839.5	Alpha-(1,3)-fucosyltransferase C	GO:0036065,GO:0006486,GO:0016021,GO:0016020,GO:0008417,GO:0005886,GO:0032580,GO:0046920	CG40305-PB						PF17039,PF00852					SSF53756					UPA00378				
aly839.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly839.7	Myophilin	GO:0035626,GO:0006939,GO:0003779,GO:0005515,GO:0005865,GO:0070594	CG14996-PB				SM00033		PF00307,PF00402	PS50021,PS51122	PR00888,PR00888,PR00888,PR00888,PR00888,PR00888,PR00888	PS01052	G3DSA:1.10.418.10	SSF47576									
aly839.8	Solute carrier family 25 member 38	GO:0030218,GO:0005215,GO:0016021,GO:0006810,GO:0005740,GO:0005743,GO:0022857,GO:0006783	CG14209-PB	MF_03064					PF00153,PF00153,PF00153	PS50920,PS50920,PS50920			G3DSA:1.50.40.10	SSF103506									
aly839.9	Soluble calcium-activated nucleotidase 1	GO:0070062,GO:0016021,GO:0017110,GO:0017111,GO:0005789,GO:0030166,GO:0016462,GO:0005509,GO:0004871,GO:0032580,GO:0045134,GO:0043123	CG5276-PA						PF06079					SSF101887									
aly84.1	Atrial natriuretic peptide-converting enzyme	GO:0004252,GO:0003050,GO:0016023,GO:0007565,GO:0005041,GO:0005576,GO:0008217,GO:0005887,GO:0005044,GO:0016485,GO:0006508,GO:0035813,GO:0016486	CG1632-PA				SM00192,SM00192,SM00063,SM00020		PF01390,PF00089,PF00057,PF01392	PS50068,PS50240,PS50068,PS50038	PR00261,PR00261	PS01209	G3DSA:4.10.1220.10,G3DSA:1.10.2000.10,G3DSA:3.30.70.960,G3DSA:4.10.400.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF82671,SSF50494,SSF57424,SSF63501									
aly84.10	Unknown	GO:0016203,GO:0007494,GO:0016339,GO:0035160,GO:0007160,GO:0035001,GO:0004872,GO:0007411,GO:0007298,GO:0005925,GO:0003344,GO:0007417,GO:0007517,GO:0007431,GO:0051492,GO:0007475,GO:0048803,GO:0016477,GO:0006930,GO:0005178,GO:0031589,GO:0007608,GO:0016340,GO:0030718,GO:0031252,GO:0008305,GO:0008360,GO:0005886,GO:0007155,GO:0008340,GO:0007157,GO:0050839,GO:0035099,GO:0007015,GO:0007427,GO:0007426,GO:0007377,GO:0007391,GO:0007508,GO:0005515,GO:0046982	CG1560-PA									PS00243	G3DSA:2.10.25.10				REACT_13552						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.100	Ras-related protein Rab-26	GO:0006904,GO:0055037,GO:0045202,GO:0031226,GO:0030667,GO:0031982,GO:0006886,GO:0045055,GO:0043001,GO:0017157,GO:0009306,GO:0003924,GO:0032482,GO:0035272,GO:0008152,GO:0005886,GO:0072659,GO:0016192,GO:0000139,GO:0019002,GO:0015031,GO:0005525,GO:0005768	CG34410-PC						PF00071	PS51419	PR00449,PR00449		G3DSA:3.40.50.300	SSF52540									
aly84.101	PiggyBac transposable element-derived protein 4	GO:0003677	CG13151-PA						PF13843														
aly84.102	Unknown		n/a										G3DSA:3.40.190.10	SSF53850									
aly84.11	Ribonuclease P protein subunit p25-like protein	GO:0022008,GO:0044822,GO:0005634,GO:0003676	CG9422-PA						PF01918				G3DSA:3.30.110.20	SSF82704									
aly84.12	MOB kinase activator-like 4	GO:0070374,GO:0043195,GO:0005813,GO:0005829,GO:0045886,GO:0046579,GO:0008088,GO:0019901,GO:0048812,GO:0000226,GO:0046872,GO:0090307	CG3403-PB						PF03637				G3DSA:1.20.140.30	SSF101152									
aly84.13	T-cell immunomodulatory protein	GO:0016021,GO:0070062	CG7739-PA						PF13517				G3DSA:2.130.10.130,G3DSA:2.130.10.130,G3DSA:2.130.10.130	SSF69318,SSF69318									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.14	Corepressor interacting with RBPJ 1	GO:0016607,GO:0000118,GO:0045892,GO:0006351,GO:0008380,GO:0006397	CG6843-PA				SM01083		PF10197						213~243,36~56									
aly84.15	Guanylate cyclase 32E	GO:0006468,GO:0016772,GO:0004383,GO:0016849,GO:0006182,GO:0005622,GO:0004872,GO:0005887,GO:0004672,GO:0035556,GO:0009190,GO:0005524,GO:0005525	CG42637-PA						PF01094				G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300	SSF53822										
aly84.16	Guanylate cyclase 32E	GO:0006468,GO:0016772,GO:0004383,GO:0016849,GO:0006182,GO:0005622,GO:0004872,GO:0005887,GO:0004672,GO:0035556,GO:0009190,GO:0005524,GO:0005525	CG42637-PA				SM00044		PF07714,PF00211,PF01094	PS50011,PS50125			G3DSA:3.30.70.1230,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300	SSF53822,SSF55073,SSF56112	898~932									
aly84.17	Guanylate cyclase 32E	GO:0045931,GO:0008284,GO:0006468,GO:0045792,GO:0016772,GO:0004383,GO:0005886,GO:0007030,GO:0005622,GO:0007165,GO:0005887,GO:0004672,GO:0005525,GO:0035556,GO:0006182,GO:0005524,GO:0004872	CG10738-PD				SM00044		PF01094,PF07714,PF00211	PS50011,PS50125		PS00452	G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:3.30.70.1230,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300	SSF55073,SSF53822,SSF56112	838~876									
aly84.18	Unknown	GO:0046983	n/a										G3DSA:4.10.280.10	SSF47459	69~89								
aly84.19	Syntenin-1	GO:0008022,GO:0019730,GO:0030036,GO:1903553,GO:0005895,GO:0007298,GO:0001948,GO:0070062,GO:0019838,GO:0072562,GO:0045545,GO:0046875,GO:0042803,GO:0005137,GO:0042043,GO:0046331,GO:0007268,GO:0007265,GO:0050839,GO:1903543,GO:0042470,GO:0042327,GO:0005515,GO:0046982	CG6509-PB				SM00228,SM00228		PF00595	PS50106,PS50106			G3DSA:2.30.42.10,G3DSA:2.30.42.10	SSF50156,SSF50156										
aly84.2	Unknown		CG42308-PA						PF14990														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.20	Sterol O-acyltransferase 2	GO:0034379,GO:0015485,GO:0010742,GO:0034736,GO:0016021,GO:0000062,GO:0005789,GO:0030299,GO:0005903,GO:0016746,GO:0034435,GO:0042632,GO:0008203,GO:0005783,GO:0004772,GO:0033344	CG8112-PB						PF03062														
aly84.21	Fungal protease inhibitor-1	GO:0004867	n/a						PF12190														
aly84.22	5-hydroxytryptamine receptor	GO:0007208,GO:0004930,GO:0016021,GO:0007615,GO:0001586,GO:0007210,GO:0007198,GO:0045187,GO:0005887,GO:0005886,GO:0008227,GO:0004993	CG16720-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly84.23	Unknown		n/a																				
aly84.24	Intraflagellar transport protein 81 homolog	GO:0036064,GO:0015631,GO:0042384,GO:0097228,GO:0030992,GO:0005813,GO:0030154,GO:0042073,GO:0007283,GO:0072372,GO:0035735,GO:0097225,GO:0005929,GO:0007275	n/a												527~561,582~609,208~228,467~487,356~383								
aly84.25	Trafficking kinesin-binding protein milt	GO:0019896,GO:0019895,GO:0048311,GO:0030382,GO:0005623,GO:0017022,GO:0005622,GO:0008152,GO:0005739,GO:0007287,GO:0007310,GO:0051654,GO:0003777	CG43227-PD						PF12448,PF04849						294~342,248~268,350~391								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.26	DNA primase small subunit	GO:1990077,GO:0003887,GO:0006260,GO:0003896,GO:0022008,GO:0046872,GO:0005658,GO:0006269,GO:0071897	CG7108-PA					TIGR00335	PF01896				G3DSA:3.90.920.10,G3DSA:3.90.920.10	SSF56747									
aly84.27	Peflin	GO:0005737,GO:0070062,GO:0044822,GO:0016020,GO:0051592,GO:0005509,GO:0006508,GO:0046983,GO:0046982,GO:0004198	CG17765-PA				SM00054,SM00054,SM00054		PF13499,PF13499	PS50222,PS50222,PS50222,PS50222		PS00018,PS00018,PS00018	G3DSA:1.10.238.10	SSF47473	208~208								
aly84.28	Leucine-rich repeats and immunoglobulin-like domains protein 3	GO:0005615,GO:0016021,GO:0008407,GO:0030659,GO:0005515,GO:0005886,GO:0032474,GO:0048477	CG8434-PB				SM00409,SM00409,SM00409,SM00082,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00408,SM00408,SM00408		PF00047,PF07679,PF07679,PF13855,PF13855,PF13855,PF13855	PS51450,PS51450,PS51450,PS51450,PS50835,PS51450,PS51450,PS51450,PS51450,PS51450,PS50835,PS51450,PS51450,PS51450,PS51450,PS51450,PS50835,PS51450		G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF52058									
aly84.29	NECAP-like protein CG9132	GO:0006897,GO:0016020,GO:0003674,GO:0005905,GO:0015031,GO:0030125	CG9132-PB						PF07933				G3DSA:2.30.29.30	SSF50729									
aly84.3	Small integral membrane protein 4	GO:0005575,GO:0008150,GO:0016021,GO:0003674	CG32736-PA						PF15114														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.30	Potassium voltage-gated channel subfamily H member 8	GO:0042391,GO:0005267,GO:0005887,GO:0071805,GO:0006813,GO:0000155,GO:0006357,GO:0008076,GO:0003705,GO:0043066,GO:0022843,GO:0005249,GO:0000160,GO:0005622,GO:0055085	CG5076-PA				SM00086,SM00100	TIGR00229	PF13426,PF00520	PS50042,PS50113	PR01465,PR01465,PR01465,PR01465,PR01465,PR01465,PR01463,PR01463,PR01463,PR01463,PR01463,PR01463,PR01463,PR01463,PR01463,PR01463		G3DSA:2.60.120.10,G3DSA:1.10.287.630,G3DSA:3.30.450.20,G3DSA:1.10.287.70	SSF81324,SSF81324,SSF55785,SSF51206	104~124									
aly84.31	Protein kintoun	GO:0005737,GO:0008157	CG1553-PC						PF08190						668~695								
aly84.32	rRNA methyltransferase 3, mitochondrial	GO:0005739,GO:0008173,GO:0003674,GO:0003723,GO:0008150,GO:0005875,GO:0006396,GO:0006364	CG14100-PA				SM00967		PF00588				G3DSA:3.30.1330.30,G3DSA:3.40.1280.10	SSF55315,SSF75217									
aly84.33	Transmembrane protein 132B	GO:0016021	CG14446-PE						PF16070,PF15706,PF15705														
aly84.34	39S ribosomal protein L16, mitochondrial	GO:0032543,GO:0005840,GO:0019843,GO:0003735,GO:0005743,GO:0005762,GO:0006412	CG3109-PA						PF00252		PR00060,PR00060		G3DSA:3.90.1170.10	SSF54686	186~206								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.35	Transmembrane protein 17B	GO:0035869,GO:0036038,GO:0042384,GO:0007224,GO:0060170,GO:0016021	n/a						PF09799														
aly84.36	Glycolipid transfer protein	GO:0005737,GO:0051861,GO:0046836,GO:0017089	CG6299-PB						PF08718				G3DSA:1.10.3520.10	SSF110004									
aly84.37	Putative zinc metalloproteinase YIL108W	GO:0005737,GO:0046872,GO:0008237	CG6294-PA						PF12044					SSF55486									
aly84.38	Unknown		n/a																				
aly84.39	Unknown		n/a																				
aly84.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.40	Cytochrome P450 306a1	GO:0005737,GO:0001700,GO:0016020,GO:0009055,GO:0043231,GO:0020037,GO:0017143,GO:0042738,GO:0016705,GO:0019825,GO:0005789,GO:0006805,GO:0016712,GO:0006082,GO:0006697,GO:0005506,GO:0035302,GO:0048477,GO:0007298,GO:0055114,GO:0005783	CG6578-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385		G3DSA:1.10.630.10,G3DSA:1.10.630.10	SSF48264,SSF48264			REACT_13433						
aly84.41	Cytochrome P450 18a1	GO:0046344,GO:0005789,GO:0006805,GO:0007304,GO:0005737,GO:0016020,GO:0016021,GO:0016705,GO:0005506,GO:0035074,GO:0020037,GO:0035210,GO:0055114,GO:0009055,GO:0019825,GO:0043231,GO:0006082,GO:0042738,GO:0016712,GO:0007480,GO:0006694,GO:0007552,GO:0008395	CG6816-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00385,PR00385,PR00385,PR00385	PS00086	G3DSA:1.10.630.10	SSF48264	280~300		REACT_13433						
aly84.42	Cytochrome P450 18a1	GO:0046344,GO:0005789,GO:0006805,GO:0007304,GO:0005737,GO:0016020,GO:0016021,GO:0016705,GO:0005506,GO:0035074,GO:0020037,GO:0035210,GO:0055114,GO:0009055,GO:0019825,GO:0043231,GO:0006082,GO:0042738,GO:0016712,GO:0007480,GO:0006694,GO:0007552,GO:0008395	CG6816-PA						PF00067		PR00463,PR00463,PR00463,PR00463,PR00463		G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly84.43	Serine/threonine-protein kinase fused	GO:0043234,GO:0005737,GO:0006468,GO:0007228,GO:0007367,GO:0007224,GO:0010600,GO:0042073,GO:0007293,GO:0031398,GO:0030162,GO:0005515,GO:0004674,GO:0005929,GO:0035301,GO:0030514,GO:0042993,GO:0005524,GO:0031647	CG6551-PA				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.44	Troponin C, isoform 3	GO:0005509	CG7930-PA				SM00054,SM00054,SM00054,SM00054		PF13499,PF13833	PS50222,PS50222,PS50222,PS50222		PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473									
aly84.45	BMP-binding endothelial regulator protein	GO:0048839,GO:0045446,GO:0005615,GO:0042118,GO:0009986,GO:0070374,GO:0007476,GO:0036122,GO:0060393,GO:0010594,GO:0043395,GO:0001657,GO:0070700,GO:0007474,GO:0002043,GO:0030514,GO:0030510	CG15671-PA				SM00832,SM00216,SM00214,SM00214,SM00214,SM00215		PF00093,PF00093,PF00093,PF08742,PF00094	PS51233,PS50184,PS50184,PS50184		PS01208,PS01208,PS01208	G3DSA:2.10.70.10,G3DSA:2.10.70.10	SSF57603,SSF57603,SSF57603									
aly84.46	Unknown		n/a																				
aly84.47	DNA polymerase delta catalytic subunit	GO:0003887,GO:0006297,GO:0051539,GO:0008310,GO:0006287,GO:0045004,GO:0006273,GO:0006272,GO:0008296,GO:0000166,GO:0006974,GO:0090305,GO:0006260,GO:0006261,GO:0003676,GO:0003677,GO:0022008,GO:0046872,GO:0043625,GO:0071897,GO:0005875	CG5949-PA				SM00486	TIGR00592	PF14260,PF03104,PF00136		PR00106,PR00106,PR00106	PS00116	G3DSA:3.30.420.10,G3DSA:3.90.1600.10,G3DSA:3.90.1600.10,G3DSA:1.10.287.690	SSF53098,SSF56672		00240+2.7.7.7,00230+2.7.7.7							
aly84.48	Pleckstrin homology domain-containing family A member 8	GO:0035621,GO:0070273,GO:0006869,GO:0016020,GO:0097001,GO:0051861,GO:0015031,GO:0017089,GO:0005802	n/a							PS50003			G3DSA:2.30.29.30	SSF50729									
aly84.49	Unknown	GO:0005737,GO:0035151,GO:0035633,GO:0019991,GO:0042060,GO:0060856	CG2813-PA										G3DSA:2.10.60.10	SSF57302									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.5	Unknown		CG34398-PA												1060~1065								
aly84.50	Endoplasmic reticulum resident protein 44	GO:0006986,GO:0006457,GO:0070062,GO:0005793,GO:0009986,GO:0005788,GO:0005789,GO:0003756,GO:0045454,GO:0009100,GO:0034976	CG9911-PD						PF13848,PF00085	PS51352			G3DSA:3.40.30.10,G3DSA:3.40.30.10	SSF52833,SSF52833,SSF52833									
aly84.51	Transcription factor Sp3	GO:0030324,GO:0030224,GO:0005886,GO:0001503,GO:0001889,GO:0001078,GO:0043565,GO:0016605,GO:0005634,GO:0030183,GO:0030851,GO:0000987,GO:0003690,GO:0046872,GO:0005794,GO:0048706,GO:0017053,GO:0007480,GO:0030219,GO:0048596,GO:0045893,GO:0060216,GO:0001779,GO:0003682,GO:0003700,GO:0030217,GO:0043353,GO:0006355,GO:0006351,GO:0000979	CG1343-PF				SM00355,SM00355,SM00355		PF00096	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									
aly84.52	Unknown		n/a																				
aly84.53	Transcription factor Sp9	GO:0043565,GO:0030326,GO:0007480,GO:0003700,GO:0005634,GO:0006355,GO:0045743,GO:0003677,GO:0046872,GO:0035118,GO:0006351	CG1343-PF				SM00355,SM00355,SM00355		PF13894,PF00096	PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.54	Obg-like ATPase 1	GO:0005737,GO:0043022,GO:0005575,GO:0003674,GO:0016887,GO:0008150,GO:0043023,GO:0046872,GO:0005524,GO:0005525	CG1354-PE	MF_00944					PF03669,PF06071,PF01926	PS51710	PR00326,PR00326,PR00326,PR00326		G3DSA:3.10.20.30,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.10.150.300,G3DSA:1.10.150.300	SSF81271,SSF52540		00970+6.1.1.3							
aly84.55	Protein PTHB1	GO:0005737,GO:0042384,GO:0060170,GO:0005815,GO:0003674,GO:0005929,GO:0034464	CG15666-PD						PF14727,PF14728						650~677,378~398								
aly84.56	Caspase-1	GO:0010165,GO:0035070,GO:0035103,GO:0012501,GO:0006915,GO:0016322,GO:0046672,GO:0004197,GO:0046668,GO:0048515,GO:0045476,GO:0010623,GO:0006508,GO:0008234	CG7788-PA				SM00115		PF00656	PS50207,PS50208	PR00376,PR00376,PR00376,PR00376,PR00376,PR00376	PS01121,PS01122	G3DSA:3.40.50.1460	SSF52129									
aly84.57	DEP domain-containing protein 5	GO:0009593,GO:0043547,GO:0048471,GO:0016021,GO:0005096,GO:0015276,GO:1990130,GO:0005764,GO:0005765,GO:0008150,GO:0034198,GO:0032007,GO:0035556,GO:0035859,GO:0005829,GO:0032403	CG12090-PA						PF12257,PF00610				G3DSA:1.10.10.10	SSF46785									
aly84.58	Sugar transporter SWEET1	GO:0006310,GO:0007431,GO:0016021,GO:0051119,GO:0000139,GO:0003674,GO:0005886,GO:0034219	CG8717-PA						PF03083,PF03083														
aly84.59	Unknown	GO:0003824,GO:0008152	CG7120-PF						PF02995				G3DSA:3.40.720.10	SSF53649									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.6	NIF3-like protein 1	GO:0005575,GO:0003674,GO:0008150,GO:0005739,GO:0005737	CG4278-PA						PF01784				G3DSA:3.40.1390.30,G3DSA:3.40.1390.30	SSF102705		00790+3.5.4.16		PWY-5663,PWY-6147,PWY-7442,PWY-5664,PWY-6703,PWY-6983					
aly84.60	Unknown	GO:0003824,GO:0008152	CG7120-PF						PF02995				G3DSA:3.40.720.10	SSF53649									
aly84.61	Low-density lipoprotein receptor-related protein	GO:0030334,GO:0006897,GO:0042395,GO:0040017,GO:0016324,GO:0040018,GO:0016021,GO:0002119,GO:0007561,GO:0015918,GO:0019898,GO:0030139,GO:0003674,GO:0005905,GO:0015248,GO:0005509	CG32356-PA				SM00192,SM00192,SM00192,SM00192		PF01683,PF00057,PF00057,PF00057	PS50068,PS50068,PS50068,PS50068	PR00261,PR00261,PR00261,PR00261	PS01209,PS01209	G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10	SSF57424,SSF57424,SSF57424,SSF57424									
aly84.62	Isocitrate dehydrogenase [NADP] cytoplasmic	GO:0005811,GO:0051287,GO:0008585,GO:0006099,GO:0006097,GO:0014070,GO:0050661,GO:0001561,GO:0070062,GO:0000287,GO:0005777,GO:0005739,GO:0006749,GO:0071071,GO:0006979,GO:0055114,GO:0016616,GO:0005829,GO:0004450,GO:0006103,GO:0006102,GO:0060696,GO:0048545	CG7176-PC			PIRSF000108		TIGR00127	PF00180			PS00470	G3DSA:3.40.718.10	SSF53659		00020+1.1.1.42,00720+1.1.1.42,00480+1.1.1.42	REACT_1046	PWY-5913,PWY-7268,PWY-6969,PWY-6728,PWY-6549,PWY-7254,PWY-7124					
aly84.63	Deoxynucleotidyltransferase terminal-interacting protein 1	GO:0031491,GO:0005730,GO:0005634,GO:0000118,GO:0006355,GO:0006351,GO:0003677	CG42304-PB																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.64	RNA-binding protein Musashi homolog Rbp6	GO:0005737,GO:0005844,GO:0048864,GO:0000166,GO:0008266,GO:0003727,GO:0003676,GO:0003729	CG32169-PB				SM00360,SM00360		PF00076,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									
aly84.65	Sorting nexin-13	GO:0038032,GO:0043547,GO:0035091,GO:0006886,GO:0032266,GO:0008340,GO:0005769,GO:0031901	CG1514-PA				SM00312,SM00313		PF08628,PF02194,PF00787	PS50195,PS51207			G3DSA:3.30.1520.10	SSF64268	321~341								
aly84.66	Protein rogdi	GO:0048149,GO:0005635,GO:0007611,GO:0005575,GO:0003674,GO:0008355	CG7725-PB						PF10259						2~22								
aly84.67	Unknown		CG30415-PA																				
aly84.68	TBC1 domain family member 9	GO:0032313,GO:0005096,GO:0005097,GO:0005509	CG7324-PA				SM00568,SM00568,SM00164		PF02893,PF02893,PF00566	PS50086			G3DSA:1.10.238.10,G3DSA:1.10.8.270	SSF47923,SSF47923									
aly84.69	TBC1 domain family member 8	GO:0005096	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.7	Probable cytosolic iron-sulfur protein assembly protein Ciao1	GO:0097361,GO:0016226,GO:0005575,GO:0003674,GO:0005515,GO:0022008	CG12797-PA	MF_03037			SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF04762,PF12894	PS50082,PS50082,PS50082,PS50294,PS50082,PS50082,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10	SSF50978									
aly84.70	Putative alpha-L-fucosidase	GO:0005737,GO:0016139,GO:0005575,GO:0004560,GO:0042742,GO:0006004,GO:0042806,GO:0006027	CG6128-PB			PIRSF001092	SM00812		PF01120,PF16757		PR00741,PR00741,PR00741,PR00741,PR00741,PR00741,PR00741,PR00741		G3DSA:3.20.20.80,G3DSA:2.60.40.1180	SSF51445		00511+3.2.1.51							
aly84.71	Putative alpha-L-fucosidase	GO:0005737,GO:0016139,GO:0005575,GO:0004560,GO:0042742,GO:0006004,GO:0042806,GO:0006027	CG6128-PB			PIRSF001092	SM00812		PF16757,PF01120		PR00741,PR00741,PR00741,PR00741,PR00741,PR00741,PR00741,PR00741		G3DSA:3.20.20.80	SSF51445		00511+3.2.1.51							
aly84.72	Unknown		CG11504-PB				SM00595		PF10545	PS51029													
aly84.73	Chromobox protein homolog 7	GO:0035064,GO:0035102,GO:0000785,GO:0005737,GO:0031519,GO:0005730,GO:0006342,GO:0005634,GO:0007385,GO:0005654,GO:0016458,GO:0016322,GO:0000792,GO:0000790,GO:0045892,GO:0042060,GO:0001047,GO:2001229,GO:0022008,GO:0035186,GO:0048733,GO:0005725,GO:0000122,GO:0042493,GO:0006355,GO:0006351,GO:0003682,GO:0016568,GO:0003727	CG32443-PA				SM00298		PF00385	PS50013	PR00504,PR00504,PR00504	PS00598	G3DSA:2.40.50.40	SSF54160									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.74	Unknown		CG10904-PA				SM00595		PF10545	PS51029					84~111								
aly84.75	Ras-related protein Rab-26	GO:0030667,GO:0072659,GO:0031982,GO:0009306,GO:0006904,GO:0055037,GO:0003924,GO:0017157,GO:0032482,GO:0045202,GO:0008152,GO:0005886,GO:0015031,GO:0005525,GO:0031226,GO:0006886,GO:0016192	CG7605-PA				SM00176,SM00174,SM00175,SM00173	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly84.76	Unknown		n/a																				
aly84.77	Zinc finger protein Xfin	GO:0045931,GO:0005737,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0003723,GO:0003676,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00868		PF12874,PF12874,PF12874,PF12874,PF00096,PF07776,PF13912,PF13912	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57716,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667										
aly84.78	Protein Tob2	GO:0005737,GO:0008285,GO:0045778,GO:0005634,GO:0007292,GO:0045671,GO:0010468	CG9214-PA				SM00099		PF07742		PR00310,PR00310,PR00310			SSF160696									
aly84.79	Tctex1 domain containing protein 3	GO:0005737,GO:0006810,GO:0042623,GO:0016020,GO:0007018,GO:0003774,GO:0030286,GO:0005874,GO:0005875	CG14763-PA						PF03645														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.8	Methylosome protein 50	GO:0007031,GO:0006909,GO:0005829,GO:0005777,GO:0005053,GO:0035097,GO:0005515,GO:0034709	CG6486-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320			PS50082,PS50294,PS50082			G3DSA:2.130.10.10	SSF50978										
aly84.80	Unknown	GO:0005515	n/a										G3DSA:2.130.10.10										
aly84.81	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.82	Armadillo segment polarity protein	GO:0035147,GO:0007367,GO:0016020,GO:0016337,GO:0016055,GO:0007616,GO:0030720,GO:0060429,GO:0071896,GO:0048754,GO:0030424,GO:0030139,GO:0003136,GO:0007163,GO:0045296,GO:0004871,GO:0001745,GO:0030057,GO:0030018,GO:0005737,GO:0014017,GO:0000902,GO:0060914,GO:0000122,GO:0007472,GO:0045294,GO:0005634,GO:0001709,GO:0003713,GO:0030707,GO:0005198,GO:0014019,GO:0030877,GO:0007293,GO:0032403,GO:0046667,GO:0048477,GO:0001105,GO:0048599,GO:0035153,GO:0016342,GO:0005667,GO:0005912,GO:0007370,GO:0016324,GO:0060232,GO:0008134,GO:0016327,GO:0035257,GO:0019903,GO:0016323,GO:0019901,GO:0019900,GO:0005915,GO:0005914,GO:0009898,GO:0035017,GO:0005886,GO:0007155,GO:0072659,GO:0035293,GO:0007400,GO:0007507,GO:0007016,GO:0007399,GO:0005916,GO:0005829,GO:0008092,GO:0035019,GO:0045186,GO:0007391,GO:0046530,GO:0008360,GO:0045944,GO:0005515,GO:0048526,GO:0045893	CG11579-PA				SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185		PF00514,PF00514,PF00514,PF13646	PS50176,PS50176,PS50176,PS50176,PS50176,PS50176,PS50176,PS50176	PR01869,PR01869,PR01869,PR01869,PR01869,PR01869,PR01869,PR01869		G3DSA:1.25.10.10	SSF48371			REACT_20676							
aly84.83	Myelin transcription factor 1-like protein	GO:0007399,GO:0003700,GO:0005634,GO:0030154,GO:0006355,GO:0008270,GO:0003677,GO:0006351	CG43689-PE						PF01530,PF01530					SSF103637,SSF103637	226~246								
aly84.84	Myelin transcription factor 1	GO:0005737,GO:0007399,GO:0003700,GO:0005634,GO:0030154,GO:0001228,GO:0001158,GO:0005654,GO:0006355,GO:0045944,GO:0008270,GO:0006366,GO:0000977	CG43689-PE						PF01530,PF01530,PF01530					SSF103637,SSF103637,SSF103637	223~257								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.85	WD repeat-containing protein 46	GO:0032040,GO:0005730,GO:0044822,GO:0030686,GO:0000462,GO:1903955,GO:0005515,GO:0022008	CG2260-PA				SM00320,SM00320,SM00320,SM01033		PF08149	PS50082,PS50294		PS00678	G3DSA:2.130.10.10	SSF50978	51~71								
aly84.86	Transcription factor E2F5	GO:0008284,GO:0035206,GO:0030030,GO:0003677,GO:0000082,GO:0000083,GO:0001077,GO:0007307,GO:0005737,GO:0043565,GO:0019730,GO:0000122,GO:0005634,GO:0007476,GO:0005654,GO:0010467,GO:0006367,GO:0000981,GO:0048666,GO:0005730,GO:0045850,GO:0000278,GO:0001012,GO:0008134,GO:0009987,GO:0005667,GO:0042023,GO:0045893,GO:0045476,GO:0009887,GO:0007179,GO:0040007,GO:0051726,GO:0003700,GO:0007444,GO:0048813,GO:0010628,GO:0045944,GO:0006351,GO:0005515,GO:0060537,GO:0035189	CG6376-PD							PF16421,PF02319			G3DSA:1.10.10.10	SSF144074,SSF46785									
aly84.87	Unknown		n/a						PF13837						140~177								
aly84.88	B-cell receptor associated protein 29	GO:0070973,GO:0016020,GO:0006888,GO:0005783,GO:0016021,GO:0006915,GO:0005789,GO:0006886,GO:0001649	CG13887-PC						PF05529						204~231,153~187,112~132								
aly84.89	Putative nuclease HARBI1	GO:0005737,GO:0004518,GO:0005634,GO:0046872	CG43088-PA						PF13359				G3DSA:1.10.10.10										
aly84.9	Tyrosine decarboxylase	GO:0005737,GO:0007626,GO:0018991,GO:0043204,GO:0048148,GO:0043025,GO:0006520,GO:0004058,GO:0030424,GO:0030170,GO:0004837,GO:0006589	CG30446-PA						PF00282		PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800,PR00800		G3DSA:1.20.1340.10,G3DSA:3.90.1150.10,G3DSA:3.40.640.10	SSF53383									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.90	Unknown		n/a						PF13837						242~262,213~233								
aly84.91	ATP-binding cassette sub-family F member 3	GO:0043190,GO:0042626,GO:0051607,GO:0005215,GO:0016020,GO:0016887,GO:0005524	CG9330-PA				SM00382,SM00382		PF00005,PF00005,PF12848	PS50893,PS50893		PS00211	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	113~140,411~431								
aly84.92	Cerebellar degeneration-related protein 2-like	GO:0005813,GO:0032154,GO:0005515,GO:0040016	CG1962-PA										G3DSA:1.20.5.340		266~307,106~133,176~217,408~428,820~840,148~168								
aly84.93	Four-domain proteases inhibitor	GO:0004867	n/a				SM00280		PF00050	PS51465			G3DSA:3.30.60.30,G3DSA:3.30.60.30	SSF100895,SSF100895									
aly84.94	U4/U6 small nuclear ribonucleoprotein Prp31	GO:0046540,GO:0000244,GO:0071011,GO:0000398,GO:0003723,GO:0022008,GO:0071339,GO:0005681,GO:0060041	CG6876-PA				SM00931		PF09785,PF01798	PS51358				SSF89124									
aly84.95	Probable nuclear transport factor 2	GO:0005737,GO:0002807,GO:0006810,GO:0006606,GO:0008320,GO:0015031,GO:0005622	CG1740-PA						PF02136	PS50177			G3DSA:3.10.450.50	SSF54427									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly84.96	Unknown	GO:0005515	n/a				SM00028			PS50293,PS50005			G3DSA:1.25.40.10	SSF48452	161~188								
aly84.97	Transcription initiation factor TFIID subunit 2	GO:0043565,GO:0007221,GO:0051123,GO:0046427,GO:0006355,GO:0060261,GO:0008134,GO:0001075,GO:0006352,GO:0008270,GO:0006367,GO:0006366,GO:0005669,GO:0022008,GO:0001129,GO:0005634,GO:0008237	CG6711-PA						PF01433				G3DSA:1.10.390.10	SSF55486,SSF63737,SSF63737									
aly84.98	Kynurenine 3-monooxygenase	GO:0043420,GO:0050660,GO:0004502,GO:0019674,GO:0034354,GO:0016021,GO:0048072,GO:0006727,GO:0006726,GO:0005741,GO:0006569,GO:0019805	CG1555-PB	MF_01971					PF01494		PR00420,PR00420,PR00420,PR00420		G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905		00380+1.14.13.9		PWY-5651,PWY-6309	UPA00253				
aly84.99	Adenylate kinase 9	GO:0005737,GO:0005730,GO:0061565,GO:0061571,GO:0061566,GO:0061570,GO:0061568,GO:0061569,GO:0005634,GO:0061567,GO:0031965,GO:0005654,GO:0050145,GO:0004550,GO:0006756,GO:0006174,GO:0061508,GO:0006186,GO:0005524,GO:0006757	n/a						PF13207,PF04945,PF00406,PF00406				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540									
aly84425.1	Unknown		n/a																				
aly84581.1	Unknown		n/a												63~82								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly846.1	Unknown	GO:0048102,GO:0035071	CG14995-PA																				
aly846.2	40S ribosomal protein S21	GO:0005737,GO:0042127,GO:0043022,GO:0005840,GO:0042274,GO:0005622,GO:0003735,GO:0000461,GO:0048542,GO:0000447,GO:0006414,GO:0006412,GO:0022627	CG2986-PF			PIRSF002148			PF01249			PS00996											
aly8462.1	Unknown		n/a																				
aly8462.2	Unknown		n/a																				
aly8478.1	THAP domain containing protein 1	GO:0043565,GO:0005654,GO:0006355,GO:0006351,GO:0003676,GO:0046872,GO:0007049	n/a				SM00980,SM00692		PF05485	PS50950				SSF57716	269~310								
aly8478.10	WD repeat-containing protein 74	GO:0016070,GO:0001825,GO:0046716,GO:0005730	CG7845-PA				SM00320,SM00320,SM00320,SM00320,SM00320						G3DSA:2.130.10.10	SSF50978	368~395								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8478.11	Aldose reductase	GO:0005737,GO:0004032,GO:0055114,GO:0016491	CG6084-PB						PF00248		PR00069,PR00069,PR00069,PR00069	PS00062,PS00798	G3DSA:3.20.20.100	SSF51430									
aly8478.12	Unknown		n/a																				
aly8478.13	Transcription elongation regulator 1	GO:0005730,GO:0070064,GO:0015629,GO:0006355,GO:0071011,GO:0005634,GO:0000122,GO:0044822,GO:0000398,GO:0006354,GO:0003700,GO:0001106,GO:0006351,GO:0005515,GO:0001103,GO:0071013	CG42724-PC				SM00456		PF00397	PS50020		PS01159	G3DSA:2.20.70.10	SSF51045									
aly8478.14	Unknown		n/a																				
aly8478.15	Transcription elongation regulator 1	GO:0005730,GO:0015629,GO:0006355,GO:0071011,GO:0003713,GO:0005634,GO:0000122,GO:0044822,GO:0006366,GO:0000398,GO:0006354,GO:0003700,GO:0001106,GO:0001103,GO:0071013	CG33097-PA						PF01846				G3DSA:1.10.10.440	SSF81698									
aly8478.16	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8478.2	Krueppel-like factor 6	GO:0043565,GO:0071409,GO:0003700,GO:0071407,GO:0005634,GO:0070301,GO:0042060,GO:0006355,GO:0045944,GO:1901653,GO:0022008,GO:0046872,GO:0003690,GO:0006351	CG42741-PA				SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										
aly8478.3	Unknown	GO:0003677	CG3995-PA				SM00614		PF02892	PS50808				SSF57667									
aly8478.4	Unknown	GO:0003677	n/a						PF02892	PS50808				SSF57667									
aly8478.5	Suppressor of fused homolog	GO:0001501,GO:0007165,GO:0004871,GO:0007275,GO:0005737,GO:0072372,GO:0000122,GO:0005634,GO:0003714,GO:2000059,GO:0001947,GO:0005654,GO:1901621,GO:0006508,GO:0001843,GO:0045668,GO:0043588,GO:0008134,GO:0045879,GO:0019901,GO:0021776,GO:0035301,GO:0042994,GO:0042992,GO:0043433,GO:0043234,GO:0021775,GO:0005829,GO:0006355,GO:0097542,GO:0097546	CG6054-PA			PIRSF011844			PF05076,PF05076,PF12470				SSF103359										
aly8478.6	Transmembrane emp24 domain-containing protein 5	GO:0070971,GO:0005794,GO:0005783,GO:0005793,GO:0048193,GO:0090263,GO:0005215,GO:0016021,GO:0006810,GO:0033116,GO:0090161,GO:0005789,GO:0061357,GO:0005801,GO:0048042,GO:0015031,GO:0022008,GO:0000003	CG9053-PC						PF01105	PS50866				SSF101576	159~179								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8478.7	Myoneurin	GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG15436-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57716,SSF57667,SSF57667	165~192								
aly8478.8	Zinc finger protein 45	GO:0003700,GO:0005634,GO:0005654,GO:0006355,GO:0010467,GO:0008270,GO:0006367,GO:0003677,GO:0046872,GO:0007275	CG15436-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00868		PF07776,PF13894	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57716									
aly8478.9	Zinc finger protein 26	GO:0005737,GO:0005819,GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0005876	CG8474-PA				SM00355,SM00355,SM00355,SM00355,SM00868,SM00868		PF07776	PS50157,PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57716	62~82,196~216,164~184								
aly848.1	Helicostatins	GO:0005179,GO:0007218,GO:0005184,GO:0005615,GO:0005576,GO:0071855	CG13633-PA						PF05953,PF05953,PF05953,PF05953,PF05953,PF05953,PF05953,PF05953,PF05953														
aly848.10	GDP-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase	GO:0044267,GO:0004377,GO:0006488,GO:0018279,GO:0016021,GO:0016020,GO:0005789,GO:0009058,GO:0022008,GO:0043687,GO:0000026	CG11306-PA						PF00534,PF15924				G3DSA:3.40.50.2000	SSF53756									
aly848.11	Ubiquitin-fold modifier 1		CG34191-PB						PF03671				G3DSA:3.10.20.90	SSF54236									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly848.12	Tigger transposable element-derived protein 6	GO:0005634,GO:0003677	n/a						PF03184					SSF46689									
aly848.2	Dynein heavy chain 1, axonemal	GO:0009331,GO:0007018,GO:0009612,GO:0016887,GO:0030286,GO:0004368,GO:0005874,GO:0005875,GO:0042623,GO:0036126,GO:0005858,GO:0000166,GO:0003351,GO:0006072,GO:0003774,GO:0005524,GO:0007605,GO:0030317,GO:0001539,GO:0008152,GO:0055114,GO:0036156,GO:0036159,GO:0060294,GO:0003777	CG5526-PB				SM00382,SM00382		PF12774,PF12780,PF12775,PF03028,PF07728,PF08393,PF12777,PF12781				G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540,SSF52540	2832~2852,2979~3048,2751~2785								
aly848.3	Apoptosis-inducing factor 1, mitochondrial	GO:0016174,GO:0030261,GO:0006309,GO:0003677,GO:0010623,GO:0071949,GO:0016491,GO:0050660,GO:0032981,GO:0005634,GO:0005739,GO:0006308,GO:0043065,GO:0005758,GO:0048471,GO:0030182,GO:0006919,GO:0006915,GO:0050832,GO:0051402,GO:0045454,GO:0042775,GO:1902510,GO:0009055,GO:0070059,GO:0005829,GO:0005743,GO:0016651,GO:0046983	CG7263-PB						PF14721,PF14721,PF07992		PR00411,PR00411,PR00411,PR00411,PR00368,PR00368,PR00368,PR00368		G3DSA:3.30.390.30,G3DSA:3.40.50.720,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF55424,SSF51905,SSF51905,SSF51905									
aly848.4	Unknown		n/a												270~290								
aly848.5	RING finger protein 121	GO:0030968,GO:0016021,GO:0005789,GO:0016567,GO:0008270,GO:0005515,GO:0030433,GO:0000139,GO:0061630	CG15814-PB				SM00184		PF13639	PS50089			G3DSA:3.30.40.10	SSF57850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly848.6	Lipase 1	GO:0004806,GO:0006629,GO:0007586,GO:0016788,GO:0016042,GO:0048812,GO:0005576	CG31871-PA			PIRSF000862			PF00561				G3DSA:3.40.50.1820	SSF53474,SSF53474									
aly848.7	Protein cramped	GO:0006351,GO:0003700,GO:0005634,GO:0006355,GO:0000790,GO:0006260,GO:0008270,GO:0005515,GO:0003677,GO:0007379,GO:0003682,GO:0043035	CG2714-PB				SM00717			PS51293				SSF46689									
aly848.8	Protein cramped	GO:0006351,GO:0003700,GO:0005634,GO:0006355,GO:0000790,GO:0006260,GO:0008270,GO:0005515,GO:0003677,GO:0007379,GO:0003682,GO:0043035	CG2714-PB																				
aly848.9	Unknown		n/a																				
aly84888.1	E3 ubiquitin-protein ligase RNF123	GO:0005737,GO:0016567,GO:0016874,GO:0008270	n/a																				
aly8493.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8493.2	Ankyrin repeat and protein kinase domain containing protein 1	GO:0005261,GO:0005262,GO:0007605,GO:0006812,GO:0006816,GO:0004674,GO:0009270,GO:0034703,GO:0055085,GO:0005524	CG31284-PA				SM00248,SM00248,SM00248,SM00248		PF12796	PS50088,PS50297			G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403	1046~1066								
aly8493.3	Kelch-like protein 5	GO:0005737,GO:0016758,GO:0032580,GO:0005856,GO:0005515	CG43313-PA				SM00612,SM00225		PF00651,PF01344,PF01344,PF05679,PF05679	PS50097			G3DSA:2.120.10.80,G3DSA:3.30.710.10	SSF54695,SSF117281									
aly8493.4	Unknown		n/a												23~50								
aly85.1	Protein PRRC2A	GO:0005737,GO:0005634,GO:0010378,GO:0005575,GO:0003674,GO:0009649	CG17255-PC						PF07001						344~364,1135~1158								
aly85.10	Unknown	GO:0005575,GO:0008150,GO:0003674,GO:0003677	CG14103-PA																				
aly85.11	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly85.12	DNA-3-methyladenine glycosylase 1	GO:0006284,GO:0046872,GO:0008725	n/a					TIGR00624	PF03352				G3DSA:1.10.340.30	SSF48150			REACT_216						
aly85.13	DNA-3-methyladenine glycosylase 1	GO:0003824,GO:0006284,GO:0046872,GO:0008725,GO:0006281	n/a					TIGR00624	PF03352				G3DSA:1.10.340.30	SSF48150			REACT_216						
aly85.14	Nucleoside diphosphate kinase	GO:0018105,GO:0016334,GO:0034332,GO:0009142,GO:0006468,GO:0007067,GO:0005874,GO:0046777,GO:0006220,GO:0006228,GO:0042981,GO:0000287,GO:0005875,GO:0006241,GO:0005524,GO:0005525,GO:0035152,GO:0008017,GO:0016301,GO:0005880,GO:0009117,GO:0005886,GO:0006183,GO:0007424,GO:0007427,GO:0007017,GO:0005829,GO:0005622,GO:0006163,GO:0004550,GO:0006165	CG2210-PC	MF_00451			SM00562		PF00334		PR01243,PR01243,PR01243,PR01243,PR01243	PS00469	G3DSA:3.30.70.141	SSF54919		00230+2.7.4.6,00240+2.7.4.6		PWY-7210,PWY-7198,PWY-7176,PWY-7220,PWY-7184,PWY-7187,PWY-7205,PWY-7224,PWY-7197,PWY-7226,PWY-7227,PWY-7221,PWY-6545,PWY-7222						
aly85.15	Zinc finger protein 234	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG1832-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly85.16	General transcription factor 3C polypeptide 6	GO:0005654,GO:0000127,GO:0006383,GO:0006351,GO:0003677	CG42516-PA						PF10419														
aly85.17	Endothelial differentiation-related factor 1 homolog	GO:0005737,GO:0007424,GO:0030674,GO:0070062,GO:0005730,GO:0008327,GO:0005669,GO:0005634,GO:0003713,GO:0043565,GO:0006355,GO:0048813,GO:0045944,GO:0006351,GO:0003677,GO:0043388,GO:0044822,GO:0007417	CG4143-PE				SM00530		PF08523,PF01381	PS50943			G3DSA:1.10.260.40	SSF47413										
aly85.18	Probable nucleoporin Nup54	GO:0005643,GO:0006606,GO:0006913,GO:0006607,GO:0006605,GO:0005487,GO:0051028	CG8831-PA						PF13874														
aly85.19	Zinc finger protein GLIS2 homolog	GO:0016607,GO:0003676,GO:0000122,GO:0031670,GO:0048009,GO:0045892,GO:0045893,GO:0042594,GO:0003677,GO:0046872,GO:0007275,GO:0006351	CG3850-PA				SM00355,SM00355,SM00355,SM00355,SM00355		PF00096	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly85.2	Dynamin	GO:0007637,GO:0050803,GO:0007614,GO:0032956,GO:0007612,GO:0007613,GO:0000281,GO:0007293,GO:0007291,GO:0036465,GO:0045202,GO:0007298,GO:0070864,GO:0001661,GO:0005875,GO:0048488,GO:0008355,GO:0005737,GO:0090148,GO:0007435,GO:0034334,GO:0016185,GO:0005874,GO:0040008,GO:0007349,GO:0003779,GO:0045747,GO:0048489,GO:0003777,GO:0005525,GO:0035152,GO:0060429,GO:0008017,GO:0032970,GO:0003924,GO:0072583,GO:0072659,GO:0007017,GO:0048172,GO:0008152,GO:0005886,GO:0009408,GO:0046667,GO:0048499,GO:0001738,GO:0007424,GO:0007427,GO:0030536,GO:0006897,GO:0016192,GO:0006898,GO:0030866,GO:0030198,GO:0046843	CG18102-PN						PF00350	PS51718			G3DSA:3.40.50.300	SSF52540										
aly85.20	UPF0676 protein C1494.01	GO:0005737,GO:0016706,GO:0005829,GO:0045544,GO:0005634,GO:0055114	CG33099-PA						PF14226,PF03171	PS51471			G3DSA:2.60.120.330	SSF51197										
aly85.21	NEDD8-conjugating enzyme Ubc12	GO:0005737,GO:0045116,GO:0045879,GO:0006464,GO:0019788,GO:0005575,GO:0016567,GO:0004842,GO:0005524,GO:0018169	CG7375-PC				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				
aly85.22	Death domain-associated protein 6	GO:2001235,GO:0042393,GO:0019901,GO:0031072,GO:0050681,GO:0019899,GO:0042981,GO:0001741,GO:0005737,GO:0007257,GO:0016605,GO:0008625,GO:0070603,GO:0030521,GO:0071356,GO:0005874,GO:0005634,GO:0003714,GO:0000281,GO:0006979,GO:0071454,GO:0043005,GO:0031396,GO:0008134,GO:0042803,G	CG9537-PA												721~748,493~523,756~776								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly85.23	Collagen alpha 1(XXVII) chain B	GO:0005201,GO:0005587,GO:0005581,GO:0048570,GO:0007391,GO:0005578,GO:0001501,GO:0005604,GO:0046872,GO:0030282,GO:0035848	CG4145-PC				SM00038,SM00210		PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF01391,PF01410	PS51461			G3DSA:2.60.120.200	SSF49899									
aly85.24	Probable maleylacetoacetate isomerase 1	GO:0005737,GO:0006572,GO:0004364,GO:0006559,GO:0016034,GO:0006749,GO:0009072	CG9362-PA					TIGR01262	PF13417	PS50405,PS50404,PS51257			G3DSA:3.40.30.10,G3DSA:1.20.1050.10	SSF47616,SSF52833									
aly85.25	Unknown		n/a																				
aly85.26	Kynurenine formamidase	GO:0005737,GO:0019441,GO:0016272,GO:0034354,GO:0005829,GO:0004061,GO:0005634	CG9542-PA						PF07859				G3DSA:3.40.50.1820	SSF53474									
aly85.27	Kynurenine formamidase	GO:0019441,GO:0016272,GO:0034354,GO:0005829,GO:0004061,GO:0005634	CG9542-PA										G3DSA:3.40.50.1820	SSF53474									
aly85.28	Carbohydrate sulfotransferase 3	GO:0098779,GO:0005975,GO:0050698,GO:0030206,GO:0016021,GO:0008459,GO:0008146,GO:0000139,GO:0043029,GO:0002230,GO:0006790	CG31637-PA						PF00685				G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly85.29	Beta-1,4-glucuronyltransferase 1	GO:0005794,GO:0035269,GO:0016021,GO:0008109,GO:0000139,GO:0002121,GO:0046872,GO:0015020	CG9171-PC						PF13896														
aly85.3	Dynamin	GO:0007637,GO:0050803,GO:0007614,GO:0032956,GO:0007612,GO:0007613,GO:0000281,GO:0007293,GO:0007291,GO:0036465,GO:0045202,GO:0007298,GO:0070864,GO:0001661,GO:0005875,GO:0048488,GO:0008355,GO:0005737,GO:0090148,GO:0007435,GO:0034334,GO:0016185,GO:0005874,GO:0040008,GO:0007349,GO:0003779,GO:0045747,GO:0048489,GO:0003777,GO:0005525,GO:0035152,GO:0060429,GO:0008017,GO:0032970,GO:0003924,GO:0072583,GO:0072659,GO:0007017,GO:0048172,GO:0008152,GO:0005886,GO:0009408,GO:0046667,GO:0048499,GO:0001738,GO:0007424,GO:0007427,GO:0030536,GO:0006897,GO:0016192,GO:0006898,GO:0030866,GO:0030198,GO:0046843	CG18102-PN				SM00302,SM00233,SM00053		PF00350,PF02212,PF00169,PF01031	PS50003,PS51718,PS51388	PR00195,PR00195,PR00195,PR00195,PR00195,PR00195	PS00410	G3DSA:2.30.29.30,G3DSA:3.40.50.300	SSF52540,SSF50729										
aly85.30	Unknown	GO:0006030,GO:0005576,GO:0008061,GO:0016490	CG11142-PB				SM00494,SM00494		PF01607,PF01607	PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625	55~75,323~343								
aly85.31	Chondroitin proteoglycan 2	GO:0000281,GO:0009790,GO:0005576,GO:0008061,GO:0006030,GO:0016490	CG11142-PB				SM00494,SM00494,SM00494		PF01607,PF01607,PF01607	PS50940,PS50940,PS50940			G3DSA:2.170.140.10,G3DSA:2.170.140.10,G3DSA:2.170.140.10	SSF57625,SSF57625,SSF57625									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly85.32	Unknown		n/a								PR01217,PR01217,PR01217,PR01217,PR01217,PR01217												
aly85.33	Zinc finger protein 568	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0003676,GO:0003677,GO:0046872,GO:0006351	CG9233-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF13912,PF00096,PF07776	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57716,SSF57667,SSF57667	80~100									
aly85.34	Peptidyl-prolyl cis-trans isomerase-like 3	GO:0000413,GO:0006457,GO:0071013,GO:0003755,GO:0008380,GO:0006397	CG11777-PA			PIRSF001467			PF00160	PS50072	PR00153,PR00153,PR00153,PR00153,PR00153	PS00170	G3DSA:2.40.100.10	SSF50891									
aly85.35	Sarcosine dehydrogenase, mitochondrial	GO:0005737,GO:0004047,GO:0050660,GO:0006545,GO:0005542,GO:0006546,GO:0035999,GO:0005739,GO:0005759,GO:0008480,GO:0042426,GO:0055114,GO:0016491	CG6385-PA						PF16350,PF08669,PF01266,PF01571				G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.30.9.10,G3DSA:3.30.9.10,G3DSA:3.30.70.1400,G3DSA:2.40.30.110,G3DSA:3.30.1360.120,G3DSA:3.30.1360.120,G3DSA:3.30.1360.120	SSF103025,SSF101790,SSF54373,SSF51905,SSF51905		00260+2.1.2.10,00670+2.1.2.10							
aly85.36	Myotubularin-related protein 2	GO:0008021,GO:0016311,GO:0006470,GO:0032288,GO:0030425,GO:0030424,GO:0044281,GO:0005737,GO:0097062,GO:0070062,GO:0005634,GO:0016020,GO:0009611,GO:0051262,GO:0005774,GO:0046856,GO:0046855,GO:0030031,GO:0006661,GO:2000645,GO:2000643,GO:0031901,GO:0048666,GO:0097060,GO:0006644,GO:0000278,GO:0008138,GO:0005938,GO:0002091,GO:0007059,GO:0097481,GO:0043197,GO:0090394,GO:0032456,GO:0004725,GO:0052629,GO:0030866,GO:0031642,GO:0004438,GO:0005515,GO:0045806,GO:0005829	CG9115-PA				SM00568,SM00404		PF06602	PS51339		PS00383	G3DSA:3.90.190.10,G3DSA:2.30.29.30	SSF50729,SSF52799									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly85.37	T-complex-associated testis-expressed protein 1		CG14325-PB				SM00368,SM00368,SM00368						G3DSA:3.80.10.10	SSF52047									
aly85.38	Formin-binding protein 1-like	GO:0051126,GO:0008104,GO:0007498,GO:0008582,GO:0017048,GO:0045886,GO:0007165,GO:0035317,GO:0005856,GO:0030837,GO:0016023,GO:0005543,GO:0007349,GO:0006914,GO:0032154,GO:0008289,GO:0005938,GO:0012506,GO:0005886,GO:0006897,GO:0030496,GO:0097320,GO:0005515	CG15015-PB				SM00055		PF00611	PS50002,PS51741			G3DSA:2.30.30.40	SSF103657,SSF50044	428~455,178~198,206~282								
aly85.39	Unknown		n/a																				
aly85.4	Unknown		n/a																				
aly85.40	Nose resistant to fluoxetine protein 6	GO:0007275,GO:0016021,GO:0006869,GO:0016747,GO:0008289	CG32645-PB						PF01757														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly85.5	Homeobox protein B-H1	GO:0043565,GO:0007479,GO:0000122,GO:0003700,GO:0007455,GO:0005634,GO:0007601,GO:0008407,GO:0003705,GO:0006355,GO:0008052,GO:0045892,GO:0008057,GO:0003677,GO:0001751,GO:0050896	CG5529-PA				SM00389		PF00046	PS50071	PR00031,PR00031,PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly85.6	Probable ATP-dependent RNA helicase CG8611	GO:0004004,GO:0010501,GO:0005524,GO:0003676,GO:0003723	CG8611-PB				SM00490,SM00487		PF00271,PF13959,PF00270	PS51195,PS51194,PS51192		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540,SSF52540	534~554,978~978								
aly85.7	Dynein light chain 1, axonemal	GO:0005515	CG8800-PA				SM00365,SM00365,SM00365,SM00365			PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									
aly85.8	ATP-binding cassette sub-family F member 1	GO:0005737,GO:0043190,GO:0042626,GO:0005635,GO:0005215,GO:0044822,GO:0016020,GO:0043022,GO:0005654,GO:0045727,GO:0016887,GO:0042788,GO:0006413,GO:0005524,GO:0008494	CG1703-PA				SM00382,SM00382		PF00005,PF00005	PS50893,PS50893		PS00211,PS00211	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	644~671,494~514,309~336,358~378								
aly85.9	Granzyme-like protein 1	GO:0005737,GO:0004252,GO:0060545,GO:0045087,GO:0006955,GO:0016485,GO:0008626,GO:0050832,GO:0010942,GO:0050830,GO:0005576,GO:0045752,GO:0050829,GO:0006508,GO:0005769	CG2056-PB				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly851.1	Unknown		n/a												592~612								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly851.10	Mitogen-activated protein kinase kinase kinase kinase 5	GO:0000185,GO:0048149,GO:0031931,GO:0005083,GO:0032147,GO:0042059,GO:0035556,GO:0042981,GO:0005737,GO:0007254,GO:0040009,GO:0000165,GO:0031098,GO:0043065,GO:0004674,GO:0004672,GO:0005524,GO:0032008,GO:0006468,GO:0070328,GO:0006915,GO:0007346,GO:0046626,GO:0008349,GO:0008361,GO:0005886,GO:0007030,GO:0046330,GO:0004702,GO:0032006	CG7097-PA				SM00036		PF00780,PF00780														
aly851.11	Mitogen-activated protein kinase kinase kinase kinase 5	GO:0000185,GO:0048149,GO:0031931,GO:0005083,GO:0032147,GO:0042059,GO:0035556,GO:0042981,GO:0005737,GO:0007254,GO:0040009,GO:0000165,GO:0031098,GO:0043065,GO:0004674,GO:0004672,GO:0005524,GO:0032008,GO:0006468,GO:0070328,GO:0006915,GO:0007346,GO:0046626,GO:0008349,GO:0008361,GO:0005886,GO:0007030,GO:0046330,GO:0004702,GO:0032006	CG7097-PA				SM00220		PF00069	PS50011			G3DSA:1.10.510.10	SSF56112									
aly851.12	Unknown		n/a																				
aly851.13	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly851.2	ALK tyrosine kinase receptor	GO:0000187,GO:0000186,GO:0048565,GO:0042051,GO:0007498,GO:0016310,GO:0038061,GO:0018108,GO:0007165,GO:0007169,GO:0007411,GO:0090328,GO:0042981,GO:0046777,GO:0070062,GO:0040008,GO:0016020,GO:0004716,GO:0004714,GO:0042802,GO:0004713,GO:0071212,GO:0005524,GO:0048666,GO:0006468,GO:0008283,GO:0043410,GO:0061177,GO:0061176,GO:0005887,GO:0005886,GO:0007522,GO:0043234,GO:0051092,GO:0045792,GO:0005622,GO:0004704,GO:1900074,GO:0070374,GO:0045610	CG8250-PA				SM00137,SM00192		PF00629,PF00629,PF12810	PS50060,PS50060,PS50068			G3DSA:4.10.400.10	SSF49899,SSF57424,SSF49899,SSF49899	76~99								
aly851.3	Transmembrane channel-like protein 7	GO:0016021,GO:0006811	CG3280-PC						PF07810														
aly851.4	ADP-ribosylation factor-like protein 13B	GO:0006996,GO:0001947,GO:0021830,GO:0042384,GO:0000819,GO:0021532,GO:0007224,GO:0060170,GO:0070986,GO:0021943,GO:0005764,GO:0031514,GO:0072372,GO:0005929,GO:0009953,GO:0035058,GO:0007264,GO:0005930,GO:0005525	CG7891-PA				SM00178,SM00177	TIGR00231	PF00025	PS51417	PR00328,PR00328,PR00328,PR00328		G3DSA:3.40.50.300	SSF52540									
aly851.5	Tubulin-specific chaperone E	GO:0007021,GO:0005737,GO:0007023,GO:0008582,GO:0005856,GO:0046785,GO:0005515,GO:0022008,GO:0007274	CG7861-PB				SM01052		PF01302	PS51450,PS50245,PS51450,PS51450,PS51450		PS00845	G3DSA:3.80.10.10,G3DSA:2.30.30.190,G3DSA:3.80.10.10	SSF52058,SSF74924,SSF54236									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly851.6	Protein enabled	GO:0032433,GO:0007409,GO:0008258,GO:0017124,GO:0030036,GO:0030424,GO:0008064,GO:0007303,GO:0003382,GO:0007411,GO:0007298,GO:0031346,GO:0005856,GO:0060288,GO:0051491,GO:0003779,GO:0071212,GO:0048749,GO:0030335,GO:1990255,GO:0051489,GO:0030027,GO:0031252,GO:0008360,GO:0005912,GO:0005911,GO:0032956,GO:0010591,GO:0035262,GO:0030425,GO:0007015,GO:0007010,GO:0007396,GO:0005829,GO:0007391,GO:0007390,GO:0048813,GO:0045886,GO:0005515	CG15112-PF				SM00461		PF00568	PS50229			G3DSA:2.30.29.30	SSF50729										
aly851.7	Protein enabled	GO:0032433,GO:0007409,GO:0008258,GO:0017124,GO:0030036,GO:0030424,GO:0008064,GO:0007303,GO:0003382,GO:0007411,GO:0007298,GO:0031346,GO:0005856,GO:0060288,GO:0051491,GO:0003779,GO:0071212,GO:0048749,GO:0030335,GO:1990255,GO:0051489,GO:0030027,GO:0031252,GO:0008360,GO:0005912,GO:0005911,GO:0032956,GO:0010591,GO:0035262,GO:0030425,GO:0007015,GO:0007010,GO:0007396,GO:0005829,GO:0007391,GO:0007390,GO:0048813,GO:0045886,GO:0005515	CG15112-PF						PF08776					SSF118370	183~203,716~96		REACT_18266,REACT_6900							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly851.8	Protein kinase C zeta type	GO:0046628,GO:0032148,GO:0050732,GO:0006954,GO:0016363,GO:0007616,GO:0008286,GO:0006468,GO:0018105,GO:0000226,GO:0004672,GO:0030010,GO:0046326,GO:0060081,GO:0035556,GO:0004697,GO:0005923,GO:2000553,GO:0005737,GO:0043203,GO:0072659,GO:0070062,GO:0019992,GO:0005634,GO:0005635,GO:0045179,GO:0005815,GO:0004674,GO:0043066,GO:2000664,GO:2000667,GO:0048471,GO:0016477,GO:0005524,GO:0008284,GO:2000463,GO:0031941,GO:2001181,GO:1990138,GO:0016324,GO:0035748,GO:0015459,GO:0031333,GO:0051291,GO:0031252,GO:0031584,GO:0001954,GO:0005938,GO:0005911,GO:0005886,GO:0046627,GO:0051346,GO:0043234,GO:0051092,GO:0046872,GO:0060291,GO:0005829,GO:0045121,GO:0031532,GO:0070528,GO:0005515,GO:0032753,GO:0045630,GO:0070374,GO:0005768,GO:0047496	CG10737-PT				SM00109,SM00239		PF00130,PF00168	PS50081		PS00479	G3DSA:2.60.40.150,G3DSA:2.60.40.150,G3DSA:3.30.60.20	SSF49562,SSF57889									
aly851.9	DNA polymerase epsilon subunit 3	GO:0043565,GO:0042766,GO:0008622,GO:0008623,GO:0006338,GO:0004402,GO:0006974,GO:0005671,GO:0005515,GO:0003887,GO:0046982,GO:0016573	CG13399-PB						PF00808				G3DSA:1.10.20.10	SSF47113									
aly853.1	Mitogen-activated protein kinase kinase kinase kinase 3	GO:0000185,GO:0048149,GO:0031931,GO:0005083,GO:0032147,GO:0042059,GO:0009411,GO:0035556,GO:0042981,GO:0005737,GO:0007254,GO:0040009,GO:0000165,GO:0031098,GO:0043065,GO:0004674,GO:0004672,GO:0005524,GO:0032008,GO:0006468,GO:0070328,GO:0034612,GO:0006915,GO:0007346,GO:0046626,GO:0008349,GO:0008361,GO:0007030,GO:0046330,GO:0005622,GO:0004702,GO:0032006	CG7097-PA				SM00220		PF00069	PS50011		PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly853.2	Putative ribosomal protein S6 kinase alpha-2	GO:0006468,GO:0000287,GO:0009651,GO:0045793,GO:0005622,GO:0004674,GO:0008360,GO:0004672,GO:0007155,GO:0046328,GO:0035556,GO:0005524	CG3086-PB										G3DSA:1.10.510.10	SSF56112									
aly853.3	Ribosomal protein S6 kinase alpha-5	GO:0031936,GO:0006468,GO:0000287,GO:0051276,GO:0006325,GO:0016456,GO:0005634,GO:0035175,GO:0016321,GO:0005700,GO:0005703,GO:0004674,GO:0000790,GO:0004672,GO:0035556,GO:0048477,GO:0016572,GO:0005524	CG6297-PB				SM00220,SM00133		PF00069,PF00069,PF00433	PS50011,PS51285,PS50011		PS00107,PS00108,PS00107	G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:3.30.200.20	SSF56112,SSF56112									
aly853.4	CCAAT/enhancer-binding protein zeta	GO:0003700,GO:0005634,GO:0006366,GO:0044822,GO:0006355,GO:0001077,GO:0045944,GO:0003677,GO:0000978,GO:0022008	CG7839-PA						PF03914														
aly853.5	CCAAT/enhancer-binding protein zeta	GO:0003700,GO:0005634,GO:0044822,GO:0006355,GO:0001077,GO:0045944,GO:0006366,GO:0000978,GO:0022008	CG7839-PA						PF03914				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371									
aly853.6	Actin-related protein 2	GO:0005737,GO:0003779,GO:0005200,GO:0007010,GO:0015629,GO:0007015,GO:0072553,GO:0008064,GO:0045887,GO:0051489,GO:0005885,GO:0005884,GO:0034314,GO:0005524,GO:0000902	CG9901-PC				SM00268		PF00022,PF00022		PR00190,PR00190,PR00190,PR00190,PR00190	PS01132	G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:3.90.640.10	SSF53067,SSF53067									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly853.7	Nephrin	GO:0061321,GO:0007286,GO:0030036,GO:0007520,GO:0001745,GO:0072015,GO:0007254,GO:0042995,GO:0070062,GO:0097206,GO:0030838,GO:0007519,GO:0007588,GO:0032836,GO:0005917,GO:0036059,GO:0017022,GO:0005887,GO:0005886,GO:0007155,GO:0007157,GO:0007156,GO:0036057,GO:0044062,GO:0005622,GO:0007523,GO:0005515	CG33141-PB				SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00060		PF08205,PF08205,PF00041,PF13895,PF07679,PF07679,PF07679,PF07679	PS50835,PS50835,PS50835,PS50835,PS50853,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF48726										
aly853.8	Unknown		n/a																				
aly8530.1	Unknown		n/a												329~349								
aly8533.1	Cuticle protein 6	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG12045-PA						PF00379	PS51155													
aly8533.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8533.3	Unknown		n/a																				
aly85370.1	Hemolymph lipopolysaccharide-binding protein	GO:0005576,GO:0030246	n/a										G3DSA:3.10.100.10	SSF56436									
aly85438.1	Unknown		n/a																				
aly8554.1	Unknown		n/a																				
aly8554.2	Unknown		n/a						PF03732														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly856.1	Roundabout homolog 2	GO:0016319,GO:0001657,GO:0030424,GO:0007419,GO:0008046,GO:0007411,GO:0007417,GO:0070062,GO:0016021,GO:0008406,GO:0031290,GO:0042802,GO:0009986,GO:0008038,GO:0032870,GO:0048036,GO:0001656,GO:0005886,GO:0007156,GO:0021891,GO:0007420,GO:0030673,GO:0050925,GO:0050772,GO:0016199,GO:0005515,GO:0051964,GO:0061364	CG5423-PA				SM00060,SM00060,SM00060,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408		PF07679,PF07679,PF07679,PF07679,PF07679,PF00041,PF00041	PS50835,PS50835,PS50853,PS50853,PS50835,PS50835,PS50853,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF49265,SSF48726									
aly856.10	Cytochrome P450 4d2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG3466-PA						PF00067				G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly856.11	Unknown		n/a												95~115								
aly856.2	Juvenile hormone esterase	GO:0005575,GO:0004453,GO:0007476,GO:0052689	CG1131-PC						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly856.3	Venom carboxylesterase-6	GO:0005737,GO:0005811,GO:0052689,GO:0005576,GO:0019915,GO:0008340,GO:0046683	CG1112-PA						PF00135				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly856.4	Esterase E4	GO:0005575,GO:0008150,GO:0052689	CG4382-PB						PF00135			PS00941,PS00122	G3DSA:3.40.50.1820	SSF53474									
aly856.5	Venom carboxylesterase-6	GO:0005575,GO:0005576,GO:0008150,GO:0052689,GO:0008152	CG10175-PD						PF00135				G3DSA:3.40.50.1820	SSF53474									
aly856.6	Unknown	GO:0005575,GO:0009631,GO:0003674	CG13510-PA				SM00714		PF10601														
aly856.7	39S ribosomal protein L27, mitochondrial	GO:0044822,GO:0005739,GO:0032543,GO:0003735,GO:0005762,GO:0006412	CG33002-PA						PF01016		PR00063,PR00063,PR00063		G3DSA:2.40.50.100	SSF110324									
aly856.8	Cytochrome P450 4d2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG3466-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly856.9	Cytochrome P450 4d2	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0005506,GO:0055114,GO:0009055	CG3466-PA						PF00067				G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly8567.1	Protein son of sevenless	GO:0005089,GO:0005088,GO:0003677,GO:0046579,GO:0035022,GO:0035023,GO:0005737,GO:2000134,GO:0043547,GO:0045500,GO:0007480,GO:0008595,GO:0008360,GO:0007265,GO:0007264,GO:0031234,GO:0030676,GO:0007015,GO:0007426,GO:0007399,GO:0005829,GO:0016199,GO:0005515,GO:0008293,GO:0046982	CG7793-PA				SM00325		PF00621	PS50010			G3DSA:1.20.900.10	SSF48065									
aly85725.1	Unknown		n/a																				
aly85726.1	Diacylglycerol kinase eta	GO:0005737,GO:0051259,GO:0019992,GO:0016310,GO:0007205,GO:0008152,GO:0003951,GO:0035556,GO:0046872,GO:0004143,GO:0005768,GO:0005524	CG34384-PE						PF00609					SSF111331		00561+2.7.1.107,00564+2.7.1.107	REACT_14797,REACT_604	PWY-7039					
aly85783.1	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0005576,GO:0046693,GO:0008364,GO:0006006,GO:0045455,GO:0055114,GO:0016491	CG9514-PA						PF00732			PS00623	G3DSA:3.50.50.60	SSF51905									
aly85875.1	Unknown	GO:0031594,GO:0051124,GO:0009986,GO:0052689,GO:0007528,GO:0042043,GO:0004872,GO:0005887,GO:0007416	CG31146-PD										G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly859.1	Protein Dok-7	GO:0005158,GO:0008289,GO:0019901,GO:0045202,GO:0005886,GO:0061098,GO:0030054	n/a						PF02174	PS51064			G3DSA:2.30.29.30	SSF50729									
aly8591.1	V-type proton ATPase subunit e 2	GO:0015992,GO:0055085,GO:0015991,GO:0016021,GO:0016020,GO:0016471,GO:0033179,GO:0000220,GO:0046961,GO:0005886,GO:0015078	CG1268-PB			PIRSF038097			PF05493														
aly86.1	Sorting nexin-4	GO:1990459,GO:0019898,GO:0031201,GO:0005737,GO:0006886,GO:0016020,GO:0061357,GO:0005886,GO:1990460,GO:0031901,GO:0005154,GO:0005158,GO:0042147,GO:0005868,GO:0043234,GO:0006897,GO:0035091,GO:0016050,GO:0030904,GO:1903595,GO:0032456,GO:0015031,GO:0005768	CG2774-PA				SM00312		PF00787	PS50195			G3DSA:3.30.1520.10	SSF103657,SSF64268	287~317,259~279,350~370,398~418								
aly86.10	Peroxiredoxin-4	GO:0005783,GO:0097190,GO:0008584,GO:0042744,GO:0008379,GO:0005737,GO:0005615,GO:0005634,GO:0005739,GO:0030198,GO:0042803,GO:0005790,GO:0016209,GO:2000255,GO:0072593,GO:0006974,GO:0022417,GO:0045454,GO:0055114,GO:0070062,GO:0005829,GO:0019471,GO:0007283,GO:0051920,GO:0005576,GO:0005515,GO:0004601	CG1274-PA						PF00578,PF10417	PS51352			G3DSA:3.40.30.10	SSF52833		00480+1.11.1.15							
aly86.11	Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 3	GO:0004792,GO:0006457,GO:0051082	CG6000-PD				SM00450		PF00581	PS50206			G3DSA:3.40.250.10	SSF52821									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly86.12	Putative thiosulfate sulfurtransferase, mitochondrial	GO:0004792,GO:0006457,GO:0005739,GO:0051082	CG6000-PD				SM00450		PF00581	PS50206			G3DSA:3.40.250.10	SSF52821									
aly86.13	Angiomotin	GO:0009897,GO:0042074,GO:0030036,GO:0030139,GO:0007043,GO:0004872,GO:0005923,GO:0043532,GO:0005737,GO:0001725,GO:0001726,GO:0003365,GO:0051496,GO:0016021,GO:0001702,GO:0030334,GO:0006935,GO:0030027,GO:0009986,GO:0034613,GO:0034260,GO:0043536,GO:0001701,GO:0005884,GO:0035329,GO:0001570,GO:0045793,GO:0040019,GO:0005829,GO:0043534,GO:0043116,GO:0016525	n/a						PF12240		PR01807,PR01807,PR01807,PR01807,PR01807,PR01807				543~570,460~480,621~648,494~529,320~364,425~445,593~613							
aly86.14	BCL-6 corepressor	GO:0035518,GO:0070171,GO:0031072,GO:0060021,GO:0003674,GO:0030502,GO:0005876,GO:0000415,GO:0031519,GO:0000122,GO:0005634,GO:0003714,GO:0065001,GO:0042826,GO:0048190,GO:0044212,GO:0008134,GO:0045892,GO:0051572,GO:0004842,GO:0007507,GO:0042476,GO:0006351,GO:0005515	CG14073-PB				SM00248,SM00248,SM00248		PF12796	PS50088,PS50297,PS50088			G3DSA:1.25.40.20	SSF48403									
aly86.15	Contactin	GO:0019991,GO:0045197,GO:0030246,GO:0031225,GO:0061343,GO:0060857,GO:0008366,GO:0005515,GO:0005886,GO:0007155,GO:0005918,GO:0005919,GO:0021682	CG1084-PA				SM00408,SM00408,SM00408,SM00408,SM00408,SM00409,SM00409,SM00409,SM00409,SM00409,SM00060,SM00060,SM00060,SM00060,SM00034		PF13927,PF07679,PF07679,PF07679,PF07679,PF07679,PF00041,PF00041,PF00041	PS50853,PS50835,PS50853,PS50835,PS50853,PS50853,PS50835,PS50853,PS50041,PS50835,PS50835,PS50835			G3DSA:3.10.100.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF56436,SSF48726,SSF48726,SSF49265,SSF48726,SSF48726,SSF48726,SSF49265									
aly86.16	Protein bric-a-brac 2	GO:0007478,GO:0007480,GO:0003700,GO:0007455,GO:0005634,GO:0008585,GO:0005701,GO:0006355,GO:0061040,GO:0006351,GO:0005515,GO:0003677,GO:0003680,GO:0005700	CG9102-PA				SM00225		PF00651	PS50097			G3DSA:3.30.710.10	SSF54695									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly86.17	Disintegrin and metalloprotease domain-containing protein 10 (Fragment)	GO:0007162,GO:0008270,GO:0008237,GO:0005737,GO:0007219,GO:0005634,GO:0016020,GO:0006509,GO:0006508,GO:0046872,GO:0042803,GO:0005794,GO:0006468,GO:0004222,GO:0009986,GO:0005798,GO:0019901,GO:0001701,GO:0008593,GO:0005802,GO:0045670,GO:0016021	CG1964-PA				SM00050		PF01562,PF13574	PS50215			G3DSA:4.10.70.10,G3DSA:3.40.390.10	SSF55486,SSF57552										
aly86.18	Unknown		n/a																				
aly86.2	Unknown		CG34309-PA										G3DSA:1.10.240.10		55~95								
aly86.3	Unknown		n/a																				
aly86.4	Cytosolic carboxypeptidase-like protein 5	GO:0005737,GO:0015631,GO:0072686,GO:0035608,GO:0004181,GO:0030496,GO:0005739,GO:0002164,GO:0003407,GO:0008270,GO:0017076,GO:0006508,GO:0035611,GO:0005634,GO:0005829,GO:0007005	CG44533-PH						PF00246				G3DSA:3.40.630.10	SSF53187									
aly86.5	Cytosolic carboxypeptidase-like protein 5	GO:0015631,GO:0072686,GO:0035608,GO:0004181,GO:0030496,GO:0005739,GO:0002164,GO:0003407,GO:0008270,GO:0017076,GO:0006508,GO:0035611,GO:0005634,GO:0005829,GO:0007005	CG44533-PH										G3DSA:3.40.630.10	SSF53187									
aly86.6	40S ribosomal protein S14	GO:0003735,GO:0022627,GO:0005840,GO:0006412	CG1527-PA	MF_01310		PIRSF002131			PF00411			PS00054	G3DSA:3.30.420.80	SSF53137									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly86.7	GTP-binding protein SAR1b	GO:0048081,GO:0005789,GO:0070863,GO:0030134,GO:0070971,GO:0040003,GO:0000902,GO:0007029,GO:0006886,GO:0005811,GO:0046872,GO:0005525,GO:0009306,GO:0003924,GO:0035050,GO:0008363,GO:0032580,GO:0035293,GO:0030127,GO:0050774,GO:0016192,GO:0003400,GO:0097110	CG7073-PE				SM00177,SM00178	TIGR00231	PF00025	PS51422	PR00328,PR00328,PR00328,PR00328,PR00328		G3DSA:3.40.50.300	SSF52540									
aly86.8	Histone-lysine N-methyltransferase trr	GO:0048749,GO:0006351,GO:0035332,GO:0042054,GO:0007458,GO:0007224,GO:0042800,GO:0005634,GO:0003677,GO:0003713,GO:0005700,GO:0016571,GO:0045893,GO:0051568,GO:0005102,GO:0044666,GO:1900114,GO:0008270	CG3848-PD				SM00249,SM00508,SM00541,SM00317,SM00542		PF13832,PF00856,PF05964,PF05965	PS51543,PS50280,PS51542,PS50868			G3DSA:2.170.270.10	SSF82199	2700~2730,498~518,459~479,157~184,2241~2261	00310+2.1.1.43							
aly86.9	Histone-lysine N-methyltransferase 2C	GO:0042393,GO:0006909,GO:0051568,GO:0035097,GO:0003677,GO:0008230,GO:0035576,GO:0006325,GO:0005634,GO:0007474,GO:0005654,GO:0042800,GO:0044822,GO:1900114,GO:0035076,GO:0071390,GO:0030374,GO:0018990,GO:0005700,GO:0006355,GO:0006351,GO:0003682,GO:0044666,GO:0008270	CG5591-PA				SM00249,SM00249,SM00249,SM00249,SM00249,SM00249		PF00628	PS50016,PS50016,PS50016			G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57903,SSF47095,SSF57903,SSF57903,SSF57903,SSF57903,SSF57903	286~306								
aly860.1	Unknown		n/a																				
aly860.10	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly860.2	Hypoxia-inducible factor 1-alpha	GO:0035774,GO:0007595,GO:0001076,GO:0001077,GO:0043524,GO:0007165,GO:0030502,GO:0003151,GO:0031514,GO:0048514,GO:0070244,GO:0070243,GO:0042127,GO:0000989,GO:0006366,GO:0019901,GO:0001755,GO:0010870,GO:0010634,GO:0051216,GO:0042826,GO:0005829,GO:0005667,GO:1903377,GO:0060574,GO:0046716,GO:0035162,GO:0003674,GO:0003677,GO:1903715,GO:0061419,GO:0016607,GO:0001666,GO:0045648,GO:0001568,GO:0003208,GO:0097411,GO:0006110,GO:0071456,GO:0051879,GO:0000981,GO:2000378,GO:0050790,GO:0035257,GO:0030279,GO:0042541,GO:0030949,GO:0032364,GO:0048546,GO:0002052,GO:0032007,GO:0046983,GO:0046982,GO:0019896,GO:0030308,GO:0030154,GO:0019899,GO:0090575,GO:0032963,GO:0043619,GO:0008542,GO:0005737,GO:0043565,GO:0005730,GO:0005634,GO:0001944,GO:0001947,GO:0006879,GO:0008134,GO:0035035,GO:0006974,GO:0045893,GO:0046886,GO:0001892,GO:0061298,GO:0031625,GO:0010575,GO:0010573,GO:0006089,GO:0045944,GO:0071347,GO:0048477,GO:0045926,GO:0032909,GO:0060438,GO:2001054,GO:0042593,GO:0004871,GO:0032869,GO:0001525,GO:0021987,GO:0051541,GO:0006355,GO:0010508,GO:0043066,GO:0001922,GO:0010468,GO:0002248,GO:0030334,GO:0021502,GO:0061030,GO:0051726,GO:0003700,GO:0071542,GO:0003705,GO:0001837,GO:0014850,GO:1903599	CG45051-PD				SM00353,SM00086,SM00091,SM00091	TIGR00229	PF08447,PF00989	PS50112,PS50888,PS50112	PR00785,PR00785,PR00785		G3DSA:3.30.450.20,G3DSA:3.30.450.20	SSF55785,SSF55785,SSF47459									
aly860.3	Unknown	GO:0005575,GO:0003674,GO:0008150	CG9795-PE												361~388,117~137,420~440,246~280								
aly860.4	Unknown		n/a																				
aly860.5	Silk gland factor 1	GO:0030308,GO:0009790,GO:0043565,GO:0007435,GO:0007432,GO:0000122,GO:0005634,GO:0007439,GO:0043066,GO:0045944,GO:0003690,GO:0043069,GO:0035072,GO:0007389,GO:0008134,GO:0042023,GO:0008301,GO:0019904,GO:0001706,GO:0007443,GO:0051090,GO:0040015,GO:0003700,GO:0007431,GO:0003705,G	CG10002-PC				SM00339		PF08430,PF09354,PF00250	PS50039	PR00053,PR00053,PR00053	PS00657,PS00658	G3DSA:1.10.10.10	SSF46785									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly860.6	Unknown		n/a																				
aly860.7	Chromosome-associated kinesin KIF4	GO:0007018,GO:0003677,GO:0005871,GO:0007067,GO:0005874,GO:0005875,GO:0007140,GO:0005737,GO:0005818,GO:0005819,GO:0005634,GO:0007088,GO:0005694,GO:0005524,GO:0008017,GO:0016321,GO:0007052,GO:0007338,GO:0007059,GO:0007131,GO:0051233,GO:0051231,GO:0000910,GO:0008574,GO:0030496,G	CG8590-PA				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10	SSF52540	469~489,907~952,380~407,825~845,701~728,851~871,562~596,422~449,599~657,665~699,778~814								
aly860.8	Putative epidermal cell surface receptor	GO:0005515,GO:0016324,GO:0004872,GO:0005887,GO:0007411,GO:0002168	CG2507-PB				SM00214,SM00214		PF00041	PS50853,PS50184,PS50853			G3DSA:2.60.40.10	SSF49265									
aly860.9	Neuroendocrine convertase 2	GO:0004252,GO:0030425,GO:0002165,GO:0034231,GO:0008233,GO:0030070,GO:0030133,GO:0035180,GO:0035187,GO:0005615,GO:0016020,GO:0033500,GO:0032403,GO:0006508,GO:0043025,GO:0016485,GO:0016486,GO:0043204,GO:0007399,GO:0016540,GO:0034230,GO:0005576	CG6438-PA						PF01483,PF00082		PR00723,PR00723	PS00138,PS00137	G3DSA:2.60.120.260,G3DSA:3.40.50.200	SSF49785,SSF52743									
aly861.1	Unknown		n/a																				
aly862.1	Bifunctional glutamate/proline--tRNA ligase	GO:0005737,GO:0006424,GO:0004827,GO:0006433,GO:0004818,GO:0017101,GO:0003723,GO:0005524	CG5394-PA	MF_01571			SM00991,SM00991,SM00946	TIGR00408	PF09180,PF03129,PF00587,PF00458,PF00458	PS51185,PS50862,PS51185	PR01046,PR01046,PR01046,PR01046	PS00762,PS00762	G3DSA:3.30.110.30,G3DSA:3.40.50.800,G3DSA:1.10.287.10,G3DSA:1.10.287.10,G3DSA:3.30.930.10	SSF55681,SSF47060,SSF52954,SSF64586,SSF47060	124~144	00970+6.1.1.15	REACT_71						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly862.10	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	GO:0070328,GO:0000159,GO:0006470,GO:0006914,GO:0007528,GO:0045498,GO:0043066,GO:0007165,GO:0008601,GO:0007274,GO:0005634	CG7913-PB						PF01603				G3DSA:1.25.10.10	SSF48371	457~477		REACT_6900,REACT_152,REACT_11045,REACT_383						
aly862.11	Protein phosphatase 1 regulatory subunit 21	GO:0019902	CG6607-PA						PF10212,PF10205						141~186,373~400,232~273,62~89,331~351								
aly862.12	DNA polymerase iota	GO:0071494,GO:0042276,GO:0006281,GO:0005634,GO:0005654,GO:0019985,GO:0005622,GO:0003887,GO:0006260,GO:0046872,GO:0003684,GO:0043231	CG7602-PB						PF11799,PF00817	PS50173			G3DSA:3.30.1490.100,G3DSA:1.10.150.20,G3DSA:3.30.70.270	SSF56672,SSF100879		00240+2.7.7.7,00230+2.7.7.7							
aly862.13	Conserved oligomeric Golgi complex subunit 2	GO:0008565,GO:0006891,GO:0006887,GO:0017119,GO:0016020,GO:0007030,GO:0000139,GO:0033227,GO:0015031,GO:0005802	CG6177-PA						PF12022,PF06148						615~635								
aly862.14	Odorant receptor Or1	GO:0005549,GO:0007608,GO:0042048,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984	CG17584-PA						PF02949														
aly862.15	Odorant receptor Or1	GO:0005549,GO:0007608,GO:0042048,GO:0016021,GO:0016020,GO:0050911,GO:0005886,GO:0004984	CG15377-PA						PF02949														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly862.16	Spastin	GO:0019226,GO:0031117,GO:0050803,GO:0030154,GO:0034214,GO:0048167,GO:0000226,GO:0016887,GO:0000022,GO:0005874,GO:0051301,GO:0005737,GO:0005819,GO:0005813,GO:0016021,GO:0008568,GO:0005694,GO:0005524,GO:0007626,GO:0051013,GO:0008017,GO:0000091,GO:0008152,GO:0007079,GO:0008344,GO:0035099,GO:0000070,GO:0043195,GO:0007399,GO:0036078,GO:0005634	CG5977-PA	MF_03021			SM00745,SM00382		PF09336,PF00004			PS00674	G3DSA:1.20.58.280,G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540,SSF116846										
aly862.17	Tryptophan--tRNA ligase, cytoplasmic	GO:0005737,GO:0006436,GO:0070062,GO:0005634,GO:0045765,GO:0048813,GO:0022008,GO:0004830,GO:0005524	CG9735-PB					TIGR00233	PF00579		PR01039,PR01039,PR01039,PR01039	PS00178	G3DSA:3.40.50.620,G3DSA:1.10.240.10	SSF52374		00970+6.1.1.2	REACT_71						
aly862.18	Unknown		n/a																				
aly862.19	Unknown		n/a																				
aly862.2	Unknown		n/a						PF06632				G3DSA:1.20.5.370,G3DSA:2.170.210.10	SSF50809,SSF58022	189~207,153~173								
aly862.20	Unknown		n/a						PF15884														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly862.21	Papilin	GO:0005201,GO:0005604,GO:0004222,GO:0007275,GO:0030198,GO:0008270,GO:0004867,GO:0005578	CG33103-PE				SM00131,SM00131,SM00131,SM00131,SM00131,SM00131,SM00131,SM00131,SM00131,SM00131,SM00131,SM00131,SM00409,SM00409,SM00209,SM00209,SM00209,SM00209,SM00209,SM00209,SM00209,SM00209,SM00408,SM00408,SM00217		PF08686,PF05986,PF07679,PF07679,PF00090,PF00090,PF00090,PF00090,PF00090,PF00090,PF00014,PF00014,PF00014,PF00014,PF00014,PF00014,PF00014,PF00014,PF00014,PF00014,PF00014,PF00014,PF00014,PF13927	PS50279,PS50092,PS50092,PS50279,PS50279,PS50279,PS50279,PS50279,PS50279,PS50279,PS50900,PS50092,PS50835,PS50279,PS50279,PS51390,PS50279,PS50835,PS50835,PS50279,PS50092,PS50092	PR01857,PR01857,PR01857,PR00759,PR00759,PR00759	PS00280,PS00280,PS00280,PS00280,PS00280,PS00280,PS00280,PS00280,PS00280	G3DSA:2.60.40.10,G3DSA:4.10.410.10,G3DSA:4.10.410.10,G3DSA:4.10.410.10,G3DSA:4.10.410.10,G3DSA:2.60.40.10,G3DSA:4.10.410.10,G3DSA:4.10.410.10,G3DSA:4.10.410.10,G3DSA:4.10.410.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:2.20.100.10,G3DSA:4.10.410.10,G3DSA:4.10.410.10,G3DSA:4.10.410.10,G3DSA:4.10.410.10,G3DSA:2.60.40.10	SSF82895,SSF57362,SSF48726,SSF57362,SSF57362,SSF57362,SSF57362,SSF57362,SSF82895,SSF48726,SSF48726,SSF82895,SSF57256,SSF82895,SSF82895,SSF57362,SSF82895,SSF57362,SSF57362,SSF57362,SSF57362								
aly862.22	Baculoviral IAP repeat-containing protein 6	GO:0042127,GO:2001237,GO:0060711,GO:0060712,GO:0007291,GO:0007067,GO:0000922,GO:0051301,GO:0005737,GO:0016874,GO:0016020,GO:0005815,GO:0043066,GO:0032465,GO:0048477,GO:0016242,GO:0008284,GO:0006468,GO:0006915,GO:0012501,GO:0009267,GO:0007286,GO:0010951,GO:0004869,GO:0004842,GO:0061631,GO:0005802,GO:0030496,GO:0016567,GO:0005768	CG6303-PB				SM00212		PF00179	PS50127			G3DSA:3.10.110.10	SSF54495									
aly862.23	Unknown		n/a																				
aly862.24	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly862.25	Unknown	GO:0004867	n/a										G3DSA:4.10.410.10										
aly862.3	Ribosomal RNA processing protein 36 homolog	GO:0022008,GO:0006364,GO:0005730	CG8461-PA						PF06102						185~205								
aly862.4	Unknown		n/a																				
aly862.5	Unknown		n/a																				
aly862.6	Nidogen-2	GO:0005604,GO:0070062,GO:0004867,GO:0031012,GO:0007160,GO:0005576,GO:0005509,GO:0030414,GO:0071711,GO:0007155,GO:0005518,GO:0030198	CG5639-PA				SM00289,SM00289,SM00289,SM00217,SM00217,SM00217,SM00211,SM00211,SM00211,SM00211,SM00211,SM00211,SM00131		PF14625,PF14625,PF14625,PF00095,PF00095,PF00014,PF00086,PF00086,PF00086,PF00086,PF00086,PF00086,PF02822,PF02822	PS51390,PS51162,PS51162,PS51252,PS51252,PS51252,PS51390,PS50279,PS51252,PS51162,PS51390,PS51162,PS51252,PS51162,PS51162	PR00759,PR00759,PR00759	PS00484,PS00484,PS00280,PS00484,PS00484,PS00484	G3DSA:4.10.75.10,G3DSA:4.10.75.10,G3DSA:4.10.75.10,G3DSA:4.10.410.10,G3DSA:4.10.800.10,G3DSA:4.10.800.10,G3DSA:4.10.800.10,G3DSA:4.10.800.10,G3DSA:4.10.800.10,G3DSA:4.10.800.10,G3DSA:4.10.800.10,G3DSA:2.10.22.10,G3DSA:2.10.22.10,G3DSA:2.10.22.10,G3DSA:2.10.22.10	SSF57362,SSF57256,SSF57262,SSF57262,SSF57610,SSF57610,SSF57610,SSF57610,SSF57262,SSF57610,SSF57610									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly862.7	Egl nine homolog 1 (Fragment)	GO:0008104,GO:0060439,GO:0030307,GO:0019899,GO:0001666,GO:0031418,GO:0007430,GO:0051344,GO:0005634,GO:0016705,GO:0045765,GO:0005654,GO:0006611,GO:0071456,GO:0005506,GO:0006974,GO:0031545,GO:0031543,GO:0043433,GO:0055114,GO:0018401,GO:0030821,GO:0071731,GO:0005829,GO:0019511	CG44015-PC				SM00702		PF01753,PF13640	PS51471,PS50865				SSF144232	88~108									
aly862.8	IQ domain-containing protein G	GO:0070062	CG13972-PA				SM00015		PF00612	PS50096					298~339								
aly862.9	IQ domain-containing protein G	GO:0005515	CG13972-PA				SM00015		PF00612	PS50096													
aly8630.1	Unknown		CG14609-PA												48~68								
aly8630.2	Venom allergen 5	GO:0008150,GO:0005576,GO:0003674	CG8483-PA				SM00198		PF00188		PR00837,PR00837,PR00837		G3DSA:3.40.33.10,G3DSA:3.40.33.10	SSF55797,SSF55797									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8630.3	TBC1 domain family member 13	GO:0032313,GO:0006451,GO:0001514,GO:0005096,GO:0005097	CG5978-PA				SM00164		PF00566	PS50086			G3DSA:1.10.8.270,G3DSA:1.10.8.270,G3DSA:1.10.8.270	SSF47923,SSF47923,SSF47923									
aly8630.4	Sterol regulatory element-binding protein cleavage-activating protein	GO:0032933,GO:0015485,GO:0000042,GO:0016021,GO:0000139,GO:0035103,GO:0012507,GO:0016485,GO:0005789,GO:0008203	CG33131-PA				SM00320,SM00320,SM00320,SM00320		PF12349,PF00400,PF00400	PS50082,PS50294,PS50082,PS50294,PS50082,PS50156		PS00678,PS00678	G3DSA:1.20.1640.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF82866									
aly8630.5	Unknown		n/a										G3DSA:1.10.472.10	SSF47954									
aly8630.6	Unknown	GO:0005634,GO:0045892,GO:0008039	CG8780-PB						PF15926														
aly8630.7	Unknown		n/a																				
aly8630.8	Unknown	GO:0000042,GO:0035103,GO:0016021,GO:0016485	CG33131-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly864.1	Fructose-bisphosphate aldolase A	GO:0031430,GO:0007498,GO:0004332,GO:0007095,GO:0006096,GO:0030018	CG6058-PE						PF00274,PF00274				G3DSA:3.20.20.70,G3DSA:3.20.20.70	SSF51569,SSF51569		00030+4.1.2.13,00710+4.1.2.13,00010+4.1.2.13,00051+4.1.2.13,00680+4.1.2.13	REACT_474	PWY-1042,PWY-6142,PWY-5484,PWY-1861,PWY-7385	UPA00109				
aly8640.1	Protein SCAF8	GO:0016363,GO:0043175,GO:0000398,GO:0000166,GO:0005654,GO:0003723,GO:0003676,GO:0006397,GO:0008380,GO:0005681,GO:0003729	CG4266-PB				SM00582		PF04818	PS51391			G3DSA:1.25.40.90	SSF48464									
aly8640.2	Tubulin-folding cofactor B	GO:0005856,GO:0005737,GO:0007023,GO:0035089,GO:0007399,GO:0005813,GO:0005634,GO:0030154,GO:0031122,GO:0005654,GO:0072686,GO:0005938,GO:0007309,GO:0005874,GO:0005829	CG11242-PA				SM01052		PF01302,PF14560	PS50245			G3DSA:3.10.20.90,G3DSA:2.30.30.190	SSF54236,SSF74924	134~168								
aly8640.3	Pleiotropic regulator 1	GO:0016607,GO:0034504,GO:0007030,GO:0009306,GO:0005829,GO:0000398,GO:0008380,GO:0071011,GO:0005662,GO:0003674,GO:1900087,GO:0071013,GO:0006397	CG1796-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50294,PS50082	PR00320,PR00320,PR00320	PS00678,PS00678	G3DSA:2.130.10.10	SSF50978									
aly8640.4	Unknown		CG9919-PA																				
aly8661.1	Acyl-CoA:lysophosphatidylglycerol acyltransferase 1	GO:0005737,GO:0006644,GO:0016021,GO:0016020,GO:0036148,GO:0005789,GO:0016746,GO:0044281,GO:0046474	n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8661.2	Plexin A3	GO:0048675,GO:0005886,GO:0060272,GO:0016021,GO:0016020,GO:0048696,GO:0016199,GO:0005622,GO:0071889,GO:0008046,GO:0007165,GO:0005515,GO:0008045,GO:0007411,GO:2000305,GO:0048755,GO:0017154,GO:0008201,GO:0042803	CG11081-PA				SM00429,SM00429,SM00429,SM00429,SM00423,SM00423,SM00630		PF01403,PF08337,PF01833,PF01833,PF01833,PF01437,PF01437	PS51004			G3DSA:2.60.40.10,G3DSA:3.30.1680.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:3.10.20.90,G3DSA:3.30.1680.10,G3DSA:2.130.10.10	SSF81296,SSF81296,SSF48350,SSF48350,SSF81296,SSF101912,SSF103575	1272~1292		REACT_18266							
aly8661.3	Fumarate hydratase, mitochondrial	GO:0005737,GO:0045239,GO:0005739,GO:0006099,GO:0006106,GO:0004333	CG4094-PA	MF_00743				TIGR00979	PF00206,PF10415		PR00149,PR00149,PR00149,PR00149	PS00163	G3DSA:1.10.40.30,G3DSA:1.20.200.10,G3DSA:1.10.275.10	SSF48557		00020+4.2.1.2,00720+4.2.1.2,00620+4.2.1.2		PWY-561,PWY-5913,PWY-7384,PWY-5392,PWY-6969,PWY-6728,PWY-7254,PWY-5690	UPA00223				
aly8661.4	RUN domain-containing protein 1	GO:0048812	CG3703-PA				SM00593		PF06809,PF02759	PS50826				SSF140741									
aly868.1	Unknown		n/a																				
aly86892.1	Unknown		n/a																				
aly87.1	Myotubularin-related protein 10-B	GO:0016311,GO:0050829,GO:0016791	CG14411-PA						PF06602,PF06602	PS51339			G3DSA:2.30.29.30	SSF50729,SSF52799									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly87.10	Sorbitol dehydrogenase	GO:0003939,GO:0031514,GO:0030317,GO:0031966,GO:0008270,GO:0055114	CG4649-PA				SM00829		PF08240,PF00107			PS00059	G3DSA:3.90.180.10,G3DSA:3.40.50.720	SSF51735,SSF50129									
aly87.11	Serine/threonine-protein kinase RIO2	GO:0006468,GO:0060252,GO:0004674,GO:0004672,GO:0022008,GO:0005524	CG11859-PA				SM00090		PF09202,PF01163			PS01245	G3DSA:1.10.10.10,G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112,SSF46785	444~464								
aly87.12	Arrestin domain-containing protein 3	GO:0031651,GO:0051443,GO:0043588,GO:0090327,GO:0060613,GO:0005886,GO:0001659,GO:0005768,GO:0044252,GO:0071879	CG1105-PA				SM01017		PF00339,PF02752					SSF81296,SSF81296									
aly87.13	Arrestin domain-containing protein 4	GO:0051443,GO:0005768,GO:0005886	CG1105-PA				SM01017		PF02752,PF00339					SSF81296,SSF81296									
aly87.14	Bumetanide-sensitive sodium-(potassium)-chloride cotransporter	GO:0016021,GO:0006813,GO:0003333,GO:0008511,GO:0006814,GO:0006821,GO:0015377,GO:0005886,GO:0035826,GO:0015378,GO:0015171	CG4357-PE					TIGR00930	PF00324,PF03522						979~999		REACT_15518						
aly87.15	Receptor-type tyrosine-protein phosphatase C	GO:0009897,GO:2000473,GO:0016311,GO:0006470,GO:0044770,GO:0006933,GO:0007166,GO:0035335,GO:0007411,GO:0005925,GO:0050857,GO:0048864,GO:0070062,GO:0016020,GO:0006469,GO:0051209,GO:0002244,GO:0001960,GO:0048539,GO:0050852,GO:0050853,GO:2000648,GO:0030890,GO:0030217,GO:0009986,G	CG42327-PE				SM00194		PF00102	PS50055	PR00700,PR00700		G3DSA:3.90.190.10	SSF52799	1433~1433								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly87.16	Unknown	GO:0005575,GO:0008150,GO:0003674	CG10014-PA				SM00015			PS50096			G3DSA:1.20.890.10	SSF47391									
aly87.17	Zinc transporter ZIP3	GO:0001701,GO:0048701,GO:0000902,GO:0060173,GO:0016021,GO:0016020,GO:0016323,GO:0043029,GO:0030001,GO:0005385,GO:0046873,GO:0005622,GO:0055085	CG4334-PB						PF02535														
aly87.18	Unknown		n/a										G3DSA:2.10.90.10	SSF57501	197~217								
aly87.2	Metaxin-1	GO:0005743,GO:0006626,GO:0015031,GO:0005741,GO:0006839,GO:0016021	CG9393-PA						PF13410,PF11801,PF10568				G3DSA:1.20.1050.10,G3DSA:1.20.1050.10	SSF47616,SSF47616,SSF52833									
aly87.3	Ral GTPase-activating protein subunit beta	GO:0060178,GO:0051056,GO:0090630,GO:0005096,GO:0005622,GO:0061024,GO:0032484,GO:0046982	CG2967-PA											SSF111347									
aly87.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly87.5	Unknown		n/a												792~812								
aly87.6	Unknown	GO:0005730	CG10496-PA																				
aly87.7	Mitochondrial import inner membrane translocase subunit TIM50-C	GO:0006470,GO:0016021,GO:0004722,GO:0005739,GO:0005743,GO:0003674,GO:0004725,GO:0005744,GO:0015031,GO:0035335,GO:0007067,GO:0007006,GO:0007005	CG2713-PA				SM00577		PF03031	PS50969			G3DSA:3.40.50.1000	SSF56784	67~97								
aly87.8	Bloom syndrome protein homolog	GO:0008094,GO:0006303,GO:0006302,GO:0045003,GO:0000403,GO:0004003,GO:0032508,GO:0000724,GO:0000731,GO:0000732,GO:0004386,GO:0006974,GO:0006260,GO:0043140,GO:1901291,GO:0003678,GO:0007131,GO:0000733,GO:0006281,GO:0005634,GO:0005524	CG6920-PA				SM00341,SM00487,SM00490,SM00956	TIGR00614	PF00570,PF00271,PF16124,PF00270,PF09382	PS51192,PS51194,PS50967		PS00690	G3DSA:3.40.50.300,G3DSA:1.10.10.10,G3DSA:1.10.150.80,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF47819,SSF52540									
aly87.9	Sorbitol dehydrogenase	GO:0003939,GO:0008270,GO:0055114,GO:0016491	CG4649-PA				SM00829		PF08240,PF00107			PS00059	G3DSA:3.90.180.10,G3DSA:3.40.50.720	SSF50129,SSF51735									
aly8710.1	Unknown		n/a												71~105								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8715.1	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6467-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly8715.2	Unknown		n/a												140~160								
aly8734.1	Cytoplasmic aconitate hydratase	GO:0005737,GO:0010040,GO:0006879,GO:0051539,GO:0006447,GO:0030350,GO:0006099,GO:0006101,GO:0008152,GO:0003994,GO:0005506,GO:0046872,GO:0003729	CG6342-PA						PF00694				G3DSA:3.20.19.10	SSF52016		00290+4.2.1.33			UPA00048				
aly8734.2	Lysosomal alpha-mannosidase	GO:0005764,GO:0015923,GO:0030246,GO:0007611,GO:0006013,GO:0005576,GO:0008270,GO:0004559	CG6206-PA						PF07748				G3DSA:2.60.40.1360,G3DSA:2.60.40.1180,G3DSA:2.70.98.30	SSF74650,SSF74650									
aly8734.3	Lysosomal alpha-mannosidase	GO:0005764,GO:0030246,GO:0006013,GO:0005576,GO:0008270,GO:0004553,GO:0004559	CG6206-PA				SM00872		PF09261,PF07748,PF01074				G3DSA:1.20.1270.50,G3DSA:3.20.110.10,G3DSA:2.70.98.30	SSF88713,SSF88688,SSF74650									
aly8734.4	Lysosomal alpha-mannosidase	GO:0005764,GO:0005975,GO:0070062,GO:0030246,GO:0006464,GO:0007611,GO:0006013,GO:0003824,GO:0005576,GO:0008270,GO:0004559,GO:0005537	CG6206-PA						PF07748				G3DSA:2.60.40.1180	SSF74650									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly87486.1	Probable C-mannosyltransferase DPY19L1	GO:0005637,GO:0016021,GO:0016020,GO:0018406,GO:0000030	CG6659-PA						PF10034														
aly8749.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0005215,GO:0016021,GO:0005886,GO:0055085	CG1208-PC					TIGR00879	PF00083	PS50850	PR00171,PR00171,PR00171,PR00171	PS00216,PS00217,PS00216	G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473	252~272		REACT_15518						
aly8749.2	Unknown		n/a												91~111								
aly876.1	Aminoacylase-1	GO:0004046,GO:0005737,GO:0070062,GO:0006520,GO:0006508,GO:0046872,GO:0008237	CG6465-PA			PIRSF036696		TIGR01880	PF01546,PF07687			PS00758	G3DSA:3.40.630.10,G3DSA:3.30.70.360	SSF55031,SSF53187		00330+3.5.1.14							
aly876.10	KAT8 regulatory NSL complex subunit 1	GO:0005705,GO:0005737,GO:0000123,GO:0006325,GO:0005634,GO:0030727,GO:0005654,GO:0048477,GO:0071339,GO:0035035,GO:0007528,GO:0045893,GO:0001047,GO:0030100,GO:0007526,GO:0000777,GO:0030718,GO:0043982,GO:0044545,GO:0043981,GO:0043984,GO:0005515,GO:0007095	CG4699-PM																				
aly876.11	Lipoma-preferred partner homolog	GO:0005856,GO:0001725,GO:0045572,GO:0005925,GO:0005515,GO:0007430,GO:0005634,GO:0007593,GO:0005737,GO:0035002,GO:0035003,GO:0007155,GO:0008270,GO:0005911,GO:0045805,GO:0035329,GO:0048526	CG32018-PB				SM00132,SM00132		PF00412,PF00412	PS50023,PS50023		PS00478	G3DSA:2.10.110.10,G3DSA:2.10.110.10	SSF57716,SSF57716									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly876.12	Lipoma-preferred partner	GO:0005856,GO:0001725,GO:0045572,GO:0005925,GO:0005515,GO:0007430,GO:0005634,GO:0007593,GO:0005737,GO:0035002,GO:0035003,GO:0007155,GO:0008270,GO:0005911,GO:0005886,GO:0045805,GO:0035329,GO:0048526	CG32018-PB				SM00132		PF00412	PS50023			G3DSA:2.10.110.10	SSF57716										
aly876.13	Unknown		n/a																				
aly876.14	Methionine synthase reductase	GO:0030586,GO:0050821,GO:0003958,GO:0046655,GO:0071949,GO:0016491,GO:0005737,GO:0006306,GO:0045111,GO:0050660,GO:0050667,GO:0016709,GO:0005654,GO:0033353,GO:0010181,GO:0005506,GO:0047138,GO:0016723,GO:0008150,GO:0043418,GO:0055114,GO:0050444,GO:1904042,GO:0005829,GO:0070402,GO:0009086	CG14882-PA						PF00667,PF00175	PS51384	PR00371,PR00371,PR00371,PR00371,PR00371,PR00371,PR00371,PR00371		G3DSA:3.40.50.80,G3DSA:1.20.990.10,G3DSA:2.40.30.10,G3DSA:2.40.30.10,G3DSA:2.40.30.10	SSF63380,SSF52343										
aly876.15	Serine/threonine-protein kinase PAK 1	GO:0000186,GO:0016020,GO:0033138,GO:0060244,GO:0032956,GO:0031941,GO:0030036,GO:0030424,GO:0014704,GO:0032869,GO:0043507,GO:0030425,GO:0005925,GO:0042981,GO:0035556,GO:0030018,GO:0005737,GO:0007346,GO:0001666,GO:0031532,GO:0051496,GO:0006887,GO:0000165,GO:0031098,GO:0046777,GO:0004674,GO:0004672,GO:0016477,GO:0001726,GO:0005524,GO:0005794,GO:0006468,GO:0032587,GO:0006915,GO:0031965,GO:0033148,GO:0042060,GO:0019901,GO:0048754,GO:0005911,GO:0005886,GO:0007520,GO:0007266,GO:0007264,GO:0010033,GO:0007015,GO:0005829,GO:0048365,GO:0048812,GO:0004702,GO:0005518,GO:0004709,GO:0001934	CG14895-PD				SM00220		PF00069,PF00786	PS50011		PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10,G3DSA:3.90.810.10	SSF56112										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly876.16	Unknown	GO:0003700,GO:0006355,GO:0043565	CG42599-PH												28~73,290~324,157~199,107~134,681~715,542~562,625~662								
aly876.17	Unknown	GO:0003700,GO:0006355,GO:0043565	CG42599-PH												70~90,204~245,250~270,24~44,154~188,105~125								
aly876.18	Unknown		n/a												1067~1087,852~879								
aly876.19	Zinc finger protein 845	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG5245-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667,SSF57667									
aly876.2	Unknown		n/a																				
aly876.20	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly876.21	Unknown	GO:0005515	n/a							PS50835													
aly876.22	Zinc finger protein 564	GO:0051726,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG11247-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12874	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667										
aly876.23	Unknown		n/a																				
aly876.24	Probable methylthioribulose-1-phosphate dehydratase	GO:0005737,GO:0046570,GO:0008270,GO:0019509,GO:0046872,GO:0019284	CG11134-PA	MF_03116			SM01007	TIGR03328	PF00596				G3DSA:3.40.225.10	SSF53639		00270+4.2.1.109		PWY-4361	UPA00904				
aly876.25	Unknown		n/a												121~144,265~324,78~98,173~211								
aly876.26	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly876.27	Unknown		n/a																				
aly876.28	Spondin-2	GO:1901739,GO:0045087,GO:0031012,GO:0007155,GO:0005102,GO:0046872,GO:0005578	CG10145-PA				SM00209		PF06468,PF00090	PS50092,PS51020			G3DSA:2.20.100.10	SSF82895									
aly876.29	Spondin-2	GO:1901739,GO:0045087,GO:0031012,GO:0007155,GO:0005102,GO:0046872,GO:0005578	CG10145-PA						PF06468	PS51020,PS50092			G3DSA:2.20.100.10	SSF82895									
aly876.3	Unknown		n/a																				
aly876.30	Unknown	GO:0009593,GO:0016021,GO:0016020,GO:0015276,GO:0005234,GO:0004970	CG11775-PA										G3DSA:3.40.190.10	SSF53850,SSF53850									
aly876.4	Glutamate receptor 2	GO:0008021,GO:0030666,GO:0032281,GO:0045211,GO:0035235,GO:0016021,GO:0016020,GO:0007165,GO:0015276,GO:0005234,GO:0005789,GO:0034220,GO:0007268,GO:0030054,GO:0050907,GO:0005887,GO:0005886,GO:0030425,GO:0035249,GO:0004970,GO:0004971	CG42315-PD						PF00060		PR00177,PR00177		G3DSA:3.40.190.10,G3DSA:1.10.287.70	SSF53850,SSF53850									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly876.5	UDP-N-acetylglucosamine transferase subunit ALG13 homolog	GO:0016758,GO:0004577,GO:0005783,GO:0030259,GO:0030246	CG14512-PA						PF04101				G3DSA:3.40.50.2000	SSF53756		00550+2.4.1.227		PWY-6385,PWY-6470,PWY-6471,PWY-5265	UPA00219				
aly876.6	Transmembrane emp24 domain-containing protein eca	GO:0005794,GO:0007030,GO:0034389,GO:0009953,GO:0000003,GO:0048193,GO:0090263,GO:0005215,GO:0016021,GO:0006810,GO:0035220,GO:0005789,GO:0061357,GO:0048042,GO:0006888,GO:0002121,GO:0070863	CG33104-PA						PF01105	PS50866					135~162								
aly876.7	DDRGK domain-containing protein 1		CG5862-PA						PF09756					SSF46785	96~131,48~68								
aly876.8	Nuclear pore complex protein Nup107	GO:0034399,GO:0006810,GO:0031080,GO:0005643,GO:0005635,GO:0031965,GO:0051292,GO:0017056,GO:0000776,GO:0015031,GO:0005487,GO:0000777,GO:0006406,GO:0007184	CG6743-PA						PF04121														
aly876.9	KAT8 regulatory NSL complex subunit 1	GO:0005705,GO:0005737,GO:0000123,GO:0006325,GO:0005634,GO:0030727,GO:0005654,GO:0048477,GO:0071339,GO:0035035,GO:0007528,GO:0045893,GO:0001047,GO:0030100,GO:0007526,GO:0000777,GO:0030718,GO:0043982,GO:0044545,GO:0043981,GO:0043984,GO:0005515,GO:0007095	CG4699-PM												394~414								
aly87600.1	Unknown		n/a						PF03392				G3DSA:1.10.2080.10	SSF100910									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly87648.1	Serpin B11	GO:0005737,GO:0005615,GO:0030162,GO:0004867,GO:0010951,GO:0045861	CG9460-PA						PF00079			PS00284	G3DSA:2.30.39.10,G3DSA:3.30.497.10	SSF56574									
aly8768.1	Voltage-dependent calcium channel type D subunit alpha-1	GO:0046872,GO:0042045,GO:0006936,GO:0034220,GO:0016324,GO:0008331,GO:0070588,GO:0006816,GO:0016323,GO:0009790,GO:0005891,GO:0070509,GO:0005886,GO:0005245,GO:0086010	CG4894-PC				SM01062		PF08763,PF00520,PF00520,PF00520,PF16905		PR00167,PR00167,PR00167,PR00167,PR01630,PR01630,PR01630		G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350	SSF81324,SSF81324,SSF81324,SSF81324,SSF81324,SSF81324			REACT_18266						
aly8768.2	Unknown		n/a												211~235								
aly8768.3	Voltage-dependent L-type calcium channel subunit alpha-1S	GO:0008331,GO:0006941,GO:0009790,GO:0005891,GO:0007411,GO:0043501,GO:0005737,GO:0007029,GO:0031674,GO:0016324,GO:0048741,GO:0046872,GO:0042045,GO:0006936,GO:0030315,GO:0006816,GO:0016323,GO:0007528,GO:0034220,GO:0005886,GO:0007520,GO:0086010,GO:0001501,GO:0070588,GO:0016529,GO:0070509,GO:0005245,GO:0002074	CG4894-PC																				
aly877.1	Unknown		n/a						PF13358				G3DSA:3.40.50.150										
aly877.2	Unknown	GO:0005549	n/a				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly877.3	Myotubularin-related protein 8	GO:0000278,GO:0008138,GO:0016311,GO:0006470,GO:0004725,GO:0005635,GO:0052629,GO:0004438,GO:0046856,GO:0046872,GO:0010506	CG3530-PA				SM00404		PF06602	PS51339		PS00383		SSF50729,SSF52799									
aly877.4	Toll-interacting protein	GO:0035325,GO:0016310,GO:0045092,GO:0045321,GO:0045323,GO:0007165,GO:0004871,GO:0035556,GO:0005737,GO:0016604,GO:0070062,GO:0030855,GO:0048471,GO:0045087,GO:0033235,GO:0006914,GO:0019900,GO:0006954,GO:0007267,GO:0005829,GO:0036010,GO:0005515	n/a				SM00239		PF00168				G3DSA:2.60.40.150	SSF49562									
aly877.5	Unknown		n/a																				
aly877.6	Unknown		n/a																				
aly877.7	Probable ATP-dependent RNA helicase Dbp45A	GO:0000381,GO:0005634,GO:0004004,GO:0003723,GO:0003676,GO:0010501,GO:0005524	CG12759-PA				SM00487,SM00490		PF00271,PF00270	PS51194,PS51192,PS51195		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	434~473,398~418								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly877.8	Unknown	GO:0005575,GO:0003674,GO:0008150	CG3082-PB						PF05705				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474									
aly877.9	Unknown		n/a						PF14643						550~570								
aly8774.1	Receptor-type tyrosine-protein phosphatase kappa	GO:0005911,GO:0008285,GO:0006470,GO:0034644,GO:0030425,GO:0030424,GO:0007165,GO:0048041,GO:0035335,GO:0045786,GO:0016021,GO:0034394,GO:0016477,GO:0043025,GO:0030336,GO:0031256,GO:0009986,GO:0034614,GO:0008013,GO:0019901,GO:0045892,GO:0005912,GO:0005887,GO:0007155,GO:0001750,GO:0007179,GO:0010839,GO:0004725,GO:0045295,GO:0005001	CG7180-PA				SM00404,SM00404,SM00194,SM00194		PF00102,PF00102	PS50056,PS50056,PS50055,PS50055	PR00700,PR00700,PR00700,PR00700,PR00700,PR00700	PS00383	G3DSA:3.90.190.10,G3DSA:3.90.190.10	SSF52799,SSF52799									
aly8774.2	Putative uncharacterized transposon-derived protein F52C9.6		n/a																				
aly87946.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly88.1	Unknown	GO:0016021,GO:0055085	CG15890-PA						PF07690				G3DSA:1.20.1250.20	SSF103473									
aly88.10	Proteasome subunit alpha type-4	GO:0004175,GO:0090263,GO:0019773,GO:0000082,GO:0010499,GO:0042590,GO:0051439,GO:0044281,GO:0000022,GO:0051436,GO:0042981,GO:0005875,GO:0005737,GO:0002474,GO:0005839,GO:0043161,GO:0005634,GO:0002479,GO:0000209,GO:0005654,GO:0010467,GO:0043066,GO:0006508,GO:0002223,GO:0090090,GO:0000278,GO:0008283,GO:0045087,GO:0006915,GO:0031145,GO:0012501,GO:0007052,GO:0006977,GO:0005886,GO:0000502,GO:0070062,GO:0043231,GO:0005829,GO:0009932,GO:0034641,GO:0004298,GO:0006511,GO:0016032,GO:0006521,GO:0051437	CG9327-PA				SM00948		PF00227,PF10584	PS51475		PS00388,PS00854	G3DSA:3.60.20.10	SSF56235	235~255,174~194		REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045						
aly88.11	Vesicle transport protein USE1	GO:0007030,GO:0006890,GO:0005783,GO:0009306,GO:0061025,GO:0012505,GO:0005484,GO:0071458,GO:0022008,GO:0031201	CG14181-PA						PF09753														
aly88.12	Peptidyl-alpha-hydroxyglycine alpha-amidating lyase 2	GO:0004598,GO:0046872,GO:0005576,GO:0044237	CG5472-PA						PF01436,PF01436	PS51125,PS51125,PS51125,PS51125	PR00790,PR00790,PR00790,PR00790		G3DSA:2.120.10.30,G3DSA:2.120.10.30	SSF101898									
aly88.13	Unknown		CG7201-PA				SM00718		PF07841						255~275								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly88.14	Unknown		n/a												46~66								
aly88.15	RING finger protein nhl-1	GO:0030239,GO:0048747,GO:0006941,GO:0016567,GO:0003674,GO:0008270,GO:0004842,GO:0030018,GO:0046716	CG15105-PC				SM00184		PF01436,PF01436,PF00097	PS51125,PS51125,PS51125,PS51125,PS50089,PS51125,PS51125		PS00518	G3DSA:3.30.40.10,G3DSA:2.120.10.30,G3DSA:3.30.40.10	SSF101898,SSF57850	215~271								
aly88.16	Ras-related protein Rab-43	GO:0055037,GO:0045202,GO:1901998,GO:0070062,GO:0006886,GO:0090382,GO:0043025,GO:0019068,GO:0005525,GO:0005794,GO:0003924,GO:0005097,GO:0032482,GO:0045335,GO:0035526,GO:0008152,GO:0007264,GO:0031982,GO:0007030,GO:0016192,GO:0030670,GO:0005515,GO:0015031,GO:0005768	CG7062-PA				SM00175,SM00174,SM00176,SM00177,SM00173	TIGR00231	PF00071	PS51419	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044							
aly88.17	Putative GPI-anchor transamidase	GO:0003923,GO:0008234,GO:0004197,GO:0042765,GO:0006508,GO:0016255	CG4406-PA			PIRSF500138,PIRSF019663			PF01650		PR00776,PR00776,PR00776,PR00776,PR00776								UPA00196				
aly88.18	Carbohydrate sulfotransferase 11	GO:0030206,GO:0030204,GO:0030326,GO:0048704,GO:0016232,GO:0008146,GO:0009791,GO:0016051,GO:0048589,GO:0016021,GO:0016020,GO:0036342,GO:0043066,GO:0002063,GO:0033037,GO:0042127,GO:0005794,GO:0048703,GO:0007585,GO:0047756,GO:0051216,GO:0001537,GO:0030512,GO:0042733,GO:0050659,GO:0000139	CG13937-PF						PF03567														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly88.19	Unknown	GO:0009913,GO:0048800,GO:0003674,GO:0005938,GO:0035017,GO:0035316,GO:0035317	CG13209-PB																				
aly88.2	Proton-coupled folate transporter	GO:0016021,GO:0005542,GO:0055085	CG15890-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly88.20	Unknown	GO:0009913,GO:0048800,GO:0003674,GO:0005938,GO:0035017,GO:0035316,GO:0035317	CG13209-PB																				
aly88.21	DNA-directed RNA polymerases I, II, and III subunit RPABC1	GO:0005634,GO:0003677,GO:0006366,GO:0005665,GO:0006351,GO:0007095,GO:0003899	CG11979-PB	MF_00025		PIRSF000747			PF03871,PF01191			PS01110	G3DSA:3.40.1340.10,G3DSA:3.90.940.20	SSF55287,SSF53036									
aly88.22	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly88.23	Actin-related protein 3	GO:0005200,GO:0006909,GO:0015629,GO:0030589,GO:0030036,GO:0030037,GO:0008064,GO:0045887,GO:0034314,GO:0007413,GO:0005737,GO:0000902,GO:0006886,GO:0051491,GO:0003779,GO:0045747,GO:0005524,GO:0030027,GO:0022416,GO:0005885,GO:0005884,GO:0007520,GO:0010592,GO:0007010,GO:0030713,GO:0097320,GO:0072553	CG7558-PA				SM00268		PF00022,PF00022			PS01132	G3DSA:3.30.420.40,G3DSA:3.90.640.10,G3DSA:3.30.420.40	SSF53067,SSF53067										
aly88.3	Solute carrier family 46 member 3	GO:0016021,GO:0055085	CG15890-PA						PF07690				G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly88.4	Unknown		CG8818-PA																				
aly88.5	Unknown		n/a																				
aly88.6	Thrombospondin type-1 domain-containing protein 4	GO:0004222,GO:0070062,GO:0007508,GO:0031012,GO:0048251,GO:0008270,GO:0001527,GO:0005578,GO:1901203	CG6232-PA				SM00209,SM00209,SM00209,SM00209,SM00209,SM00209		PF05986,PF00090,PF00090	PS50092,PS50092,PS50092,PS50092,PS50092,PS50092	PR01857,PR01857		G3DSA:2.20.100.10,G3DSA:2.20.100.10	SSF82895,SSF82895,SSF82895,SSF82895,SSF82895										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly88.7	Unknown	GO:0016021	CG10165-PA				SM00665		PF03188														
aly88.8	Thrombospondin type-1 domain-containing protein 4	GO:0004222,GO:0070062,GO:0007508,GO:0031012,GO:0048251,GO:0008270,GO:0001527,GO:0005578,GO:1901203	CG6232-PA				SM00209,SM00209,SM00209,SM00209,SM00209		PF05986,PF08686	PS50092,PS50092,PS50092,PS50092,PS50092,PS50900,PS50092	PR01857,PR01857		G3DSA:2.20.100.10	SSF82895,SSF82895,SSF82895									
aly88.9	Unknown	GO:0016021	CG10165-PA				SM00665		PF03188	PS50939													
aly8810.1	Protein Cep89 homolog	GO:0005758,GO:0005829,GO:0046959,GO:0007005,GO:0007268	CG8214-PA												249~269,359~442,598~643,495~568,195~215								
aly8810.2	Venom serine protease 34	GO:0004252,GO:0005576,GO:0006508	CG30371-PA				SM00020,SM00020		PF00431,PF00089,PF00089	PS01180,PS50240,PS50240	PR00722,PR00722,PR00722	PS00134,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.60.120.290,G3DSA:2.40.10.10	SSF50494,SSF50494,SSF49854									
aly8810.3	Centrosomal protein of 104 kDa	GO:0005814,GO:0016596,GO:0016595,GO:0016594	CG10137-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8810.4	tRNA (cytosine(34)-C(5))-methyltransferase	GO:0005737,GO:0030488,GO:0000049,GO:0016428,GO:0007614,GO:0005730,GO:0005575,GO:0003723,GO:0001510,GO:0008168,GO:0005634	CG6133-PA						PF01189	PS51686	PR02008,PR02008,PR02008,PR02008,PR02011,PR02011	PS01153	G3DSA:3.40.50.150,G3DSA:3.40.50.150	SSF53335,SSF53335	421~441								
aly8810.5	5-oxoprolinase	GO:0017168,GO:0005524	CG4752-PA						PF05378,PF01968														
aly8810.6	5-oxoprolinase	GO:1901687,GO:0006805,GO:0005829,GO:0017168,GO:0003824,GO:0044281,GO:0006750,GO:0005524	CG4752-PA						PF02538														
aly8810.7	Serine/threonine-protein phosphatase 2A regulatory subunit B" subunit gamma	GO:0005737,GO:0045579,GO:0005819,GO:0005813,GO:0005634,GO:0032147,GO:0030865,GO:0002759,GO:0043029,GO:0048536,GO:0046331,GO:0000226,GO:0005509,GO:0050864,GO:0001782,GO:0008601,GO:0046872,GO:0051900	CG4733-PB									PS00018	G3DSA:1.10.238.10	SSF47473	33~53								
aly88137.1	MAU2 chromatid cohesion factor homolog	GO:0032116,GO:0034088,GO:0005634,GO:0005654,GO:0000785,GO:0005515,GO:0007411,GO:0051301	CG4203-PA						PF10345				G3DSA:1.25.40.10	SSF48452									
aly88161.1	Unknown	GO:0016787,GO:0046872,GO:0003676	CG3819-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly88172.1	Dynein heavy chain 6, axonemal	GO:0008152,GO:0042623,GO:0007018,GO:0005858,GO:0005875,GO:0001539,GO:0005524,GO:0016887,GO:0005874,GO:0003774,GO:0003777	CG7092-PA																				
aly8825.1	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG5065-PA						PF07993,PF03015				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly8825.2	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG5065-PA						PF03015,PF07993				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly8825.3	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG5065-PA						PF07993,PF03015	PS51257			G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly8825.4	Unknown		n/a				SM00249			PS50089,PS50016		PS01359	G3DSA:3.30.40.10	SSF57903									
aly8825.5	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG5065-PA						PF07993				G3DSA:3.40.50.720	SSF51735,SSF51735			REACT_22258						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8825.6	Unknown		n/a																				
aly8825.7	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG5065-PA						PF07993,PF03015				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly88343.1	Centaurin-gamma-1A	GO:0046872,GO:0043547,GO:0032312,GO:0005634,GO:0005096,GO:0005622,GO:0003924,GO:0008060,GO:0008270,GO:0008152,GO:0007264,GO:0043087,GO:0005525	CG31811-PB																				
aly884.1	Unknown		n/a																				
aly885.1	Protein CEPU-1	GO:0007606,GO:0005575,GO:0003674,GO:0005886,GO:0007155,GO:0031225	CG33512-PB				SM00409,SM00408		PF07679	PS50835			G3DSA:2.60.40.10	SSF48726									
aly8857.1	Calpain-D	GO:0005737,GO:0007632,GO:0007399,GO:0050896,GO:0007601,GO:0005622,GO:0008270,GO:0006508,GO:0004198	CG1391-PB				SM00230,SM00547,SM00547,SM00547,SM00547,SM00547		PF00641,PF00641,PF00641,PF00641,PF00648	PS50199,PS50199,PS50203,PS50199,PS50199,PS50199	PR00704,PR00704,PR00704,PR00704,PR00704	PS00139,PS01358,PS01358,PS01358,PS01358	G3DSA:3.90.70.10	SSF90209,SSF54001									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8857.2	Leucine-rich repeat, immunoglobulin-like domain and transmembrane domain-containing protein 2	GO:0016021,GO:0005886,GO:0005887,GO:0042059,GO:0030510	CG12199-PB				SM00409,SM00369,SM00369,SM00369,SM00369,SM00369,SM00082,SM00408		PF13855,PF07679	PS50835			G3DSA:2.60.40.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF48726,SSF52058									
aly88631.1	Protein son of sevenless	GO:0005088,GO:0003677,GO:0046579,GO:0035022,GO:0035023,GO:0005737,GO:2000134,GO:0043547,GO:0045500,GO:0007480,GO:0008595,GO:0008360,GO:0007265,GO:0007264,GO:0031234,GO:0030676,GO:0007015,GO:0007426,GO:0007399,GO:0005829,GO:0016199,GO:0005515,GO:0008293,GO:0046982	CG7793-PA										G3DSA:2.30.29.30										
aly8867.1	Unknown		n/a						PF15926														
aly88695.1	Unknown		n/a																				
aly887.1	Probable multidrug resistance-associated protein lethal(2)03659	GO:0043190,GO:0042626,GO:0048190,GO:0008514,GO:0016021,GO:0006855,GO:0001666,GO:0007275,GO:0005524,GO:0034059	CG14709-PB				SM00382,SM00382		PF00664,PF00664,PF00005,PF00005	PS50893,PS50929,PS50893,PS50929			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:1.20.1560.10	SSF90123,SSF52540,SSF52540,SSF90123									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly887.10	Unknown	GO:0005634,GO:0008270,GO:0003676	CG1231-PA				SM00451,SM00451,SM00451		PF12874,PF12874					SSF57667,SSF57667,SSF57667									
aly887.11	Decapping nuclease DXO homolog	GO:0004518,GO:0046872,GO:0003723,GO:0000166	CG9125-PA						PF08652														
aly887.12	Uncharacterized protein CG16817	GO:0003674,GO:0007030,GO:0031965,GO:0005634,GO:0005783	CG16817-PA						PF04969	PS51203			G3DSA:2.60.40.790	SSF49764									
aly887.13	Multidrug resistance-associated protein 4	GO:0043190,GO:0042626,GO:0016020,GO:0016404,GO:0005215,GO:0016021,GO:0007596,GO:0031088,GO:0016323,GO:0008559,GO:0055114,GO:0016887,GO:0005886,GO:0030168,GO:0055085,GO:0005524,GO:0002576	CG5789-PA				SM00382,SM00382		PF00664,PF00664,PF00005,PF00005	PS50893,PS50929,PS50893,PS50929		PS00211,PS00211	G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:1.20.1560.10	SSF90123,SSF90123,SSF90123,SSF52540,SSF52540										
aly887.14	Unknown		n/a												183~203,306~326,370~404								
aly887.15	Multidrug resistance-associated protein 4	GO:0043190,GO:0042626,GO:0016020,GO:0005215,GO:0016021,GO:0007596,GO:0031088,GO:0016323,GO:0055114,GO:0005886,GO:0030168,GO:0055085,GO:0005524,GO:0002576	CG4562-PE				SM00382,SM00382		PF00005,PF00005,PF00664,PF00664	PS50929,PS50893,PS50929,PS50893		PS00211,PS00211	G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF90123,SSF90123										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly887.16	Probable multidrug resistance-associated protein lethal(2)03659	GO:0043190,GO:0042626,GO:0005215,GO:0016021,GO:0006810,GO:0007275,GO:0055085,GO:0005524	CG4562-PE				SM00382,SM00382		PF00005,PF00005,PF00664,PF00664	PS50929,PS50893,PS50929,PS50893		PS00211,PS00211	G3DSA:1.20.1560.10,G3DSA:1.20.1560.10,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF90123,SSF90123,SSF52540									
aly887.17	Potassium voltage-gated channel subfamily H member 7	GO:0042391,GO:0007623,GO:0005887,GO:0071805,GO:0006813,GO:0016020,GO:0051291,GO:0008076,GO:0005242,GO:0004871,GO:0007605,GO:0022843,GO:0005249,GO:0055085	CG3182-PA				SM00100		PF00027,PF00520	PS50042	PR01470,PR01470,PR01470,PR01470,PR01470,PR01463,PR01463,PR01463,PR01463,PR01463,PR01463,PR01463,PR01463,PR014		G3DSA:2.60.120.10,G3DSA:1.10.287.70,G3DSA:1.10.287.630	SSF81324,SSF81324,SSF51206									
aly887.18	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase hpo-8	GO:0006633,GO:0016021,GO:0016829	CG6746-PA						PF04387							00062+4.2.1.134		PWY-7053,PWY-5353,PWY-7592,PWY-6433,PWY-7602,PWY-7049,PWY-7601,PWY-7606,PWY-6598,PWY-7036,PWY-	UPA00094				
aly887.19	Unknown		n/a						PF16984														
aly887.2	DNA replication complex GINS protein SLD5	GO:0005737,GO:0001833,GO:0000727,GO:0000278,GO:0032508,GO:0006270,GO:0000811,GO:0031298,GO:0046331,GO:0022008,GO:0043138,GO:0005634,GO:1900087	CG14549-PA			PIRSF007764			PF05916					SSF158573									
aly887.20	Bystin	GO:0005737,GO:0005730,GO:0045177,GO:0001829,GO:0008283,GO:0005634,GO:0016020,GO:0000462,GO:0003674,GO:0022008,GO:0044822	CG1430-PA						PF05291														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly887.21	60S ribosomal protein L30	GO:0040007,GO:0022625,GO:0007422,GO:0003735,GO:0007052,GO:0005840,GO:0000022,GO:0006412,GO:0051298	CG10652-PE	MF_00481					PF01248			PS00709,PS00993	G3DSA:3.30.1330.30	SSF55315									
aly887.22	Collagen alpha 5(VI) chain	GO:0005581,GO:0030574,GO:0005576,GO:0030198,GO:0007155,GO:0022617,GO:0005578	n/a																				
aly887.23	p53 and DNA damage-regulated protein 1	GO:0005737,GO:0006457,GO:0016272,GO:0051082	CG15863-PA						PF01920					SSF46579	84~104								
aly887.24	Serine/threonine-protein kinase mig-15	GO:0000185,GO:0004871,GO:0005083,GO:0001748,GO:0007411,GO:0007254,GO:0000003,GO:0033563,GO:0007476,GO:0009611,GO:0004674,GO:0016476,GO:0048477,GO:0005524,GO:0006468,GO:0030334,GO:0008349,GO:0008360,GO:0046580,GO:0010171,GO:0042656,GO:0001736,GO:0008594,GO:0002119,GO:0007391,GO:0048812,GO:0046529,GO:0004702,GO:0007097,GO:0005938	CG16973-PA				SM00036		PF00780	PS50219													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly887.25	Traf2 and NCK-interacting protein kinase	GO:0000185,GO:0000165,GO:0005083,GO:0030033,GO:0032147,GO:0031098,GO:0001748,GO:0007411,GO:0035556,GO:0042981,GO:0046777,GO:0007256,GO:0007254,GO:0072659,GO:0070062,GO:0031532,GO:0005634,GO:0007476,GO:0009611,GO:0005654,GO:0004674,GO:0002230,GO:0004672,GO:0016476,GO:0048477,GO:0055037,GO:0046529,GO:0048814,GO:0005737,GO:0006468,GO:0048471,GO:0016324,GO:0007346,GO:0008594,GO:0005856,GO:0008360,GO:0046580,GO:0042656,GO:0001736,GO:0008349,GO:0007010,GO:0016055,GO:0007391,GO:0048812,GO:0005524,GO:0004702,GO:0007097,GO:0001934,GO:0005938	CG16973-PA				SM00220		PF00069	PS50011		PS00108,PS00107	G3DSA:3.30.200.20,G3DSA:1.10.510.10	SSF56112,SSF56112										
aly887.26	Oocyte zinc finger protein XlCOF19 (Fragment)	GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG4374-PC				SM00355,SM00355		PF13894	PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667									
aly887.27	Heterochromatin-associated protein MENT	GO:0005654,GO:0005615,GO:0003677,GO:0030261,GO:0005576,GO:0030162,GO:0004867,GO:0010951,GO:0045751,GO:0045861,GO:0048526,GO:0005694,GO:0016568	CG18525-PA				SM00093		PF00079				G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:2.30.39.10	SSF56574									
aly887.28	Nicastrin	GO:0007219,GO:0007010,GO:0016021,GO:0005770,GO:0008594,GO:0070765,GO:0046331,GO:0045463,GO:0005886,GO:0007220,GO:0016485,GO:0045314,GO:0055037,GO:0006509	CG7012-PE						PF05450					SSF53187,SSF53187									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly887.29	E3 ubiquitin-protein ligase sina	GO:0005737,GO:0007423,GO:0007465,GO:0005634,GO:0010498,GO:0000151,GO:0007601,GO:0045676,GO:0016567,GO:0016874,GO:0006511,GO:0008270,GO:0005515,GO:0006508,GO:0004842,GO:0050896,GO:0043621	CG9949-PA							PS50089			G3DSA:3.30.40.10	SSF57850	403~423,329~349								
aly887.3	Opsin-1	GO:0008020,GO:0004930,GO:0016028,GO:0009881,GO:0000122,GO:0007605,GO:0016021,GO:0007601,GO:0018298,GO:0007602,GO:0007186	CG5192-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00238,PR00238,PR00238,PR00578,PR00578,PR00578,PR005	PS00237,PS00238	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly887.30	Unknown	GO:0046872	n/a				SM00868,SM00355		PF07776	PS50157		PS00028		SSF57716									
aly887.31	Mitochondrial chaperone BCS1	GO:0005750,GO:0033617,GO:0034551,GO:0032981,GO:0006461,GO:0005739,GO:0005743,GO:0007005,GO:0016887,GO:0005524	CG4908-PB				SM01024,SM00382		PF00004,PF08740			PS00674	G3DSA:3.40.50.300	SSF52540									
aly887.32	Unknown		n/a																				
aly887.33	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly887.34	Homeobox protein aristaless-like 4	GO:0005737,GO:0043565,GO:0021782,GO:0007399,GO:0007422,GO:0005634,GO:0001077,GO:0006355,GO:0006357,GO:0010628,GO:0000977,GO:0010001,GO:0003677,GO:0007275,GO:0006351	CG31240-PA				SM00389		PF00046	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689									
aly887.35	Unknown	GO:0006390,GO:0005739	CG7175-PA																				
aly887.36	Cytosolic non-specific dipeptidase	GO:0005737,GO:0070062,GO:0004180,GO:0016805,GO:0005576,GO:0034701,GO:0006508,GO:0046872,GO:0008237	CG17337-PA			PIRSF037242			PF07687,PF01546			PS00759	G3DSA:3.30.70.360,G3DSA:3.40.630.10,G3DSA:3.40.630.10	SSF53187,SSF53187									
aly887.37	Transmembrane protein 43 homolog	GO:0005575,GO:0003674,GO:0016021,GO:0008150	CG8111-PA						PF07787														
aly887.38	Beta-galactoside alpha-2,6-sialyltransferase 2	GO:0005794,GO:0006486,GO:0016021,GO:0009311,GO:0007528,GO:0003835,GO:0005576,GO:0032580,GO:0008373	CG4871-PB						PF00777														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly887.39	Matrix metalloproteinase-14	GO:0001503,GO:0030324,GO:0030307,GO:0007591,GO:0097094,GO:0030425,GO:0031012,GO:0048102,GO:0014070,GO:0035001,GO:0008270,GO:0048701,GO:0001525,GO:0005925,GO:0051895,GO:0002168,GO:0005737,GO:0043615,GO:0030574,GO:0001541,GO:0001666,GO:0016021,GO:0031638,GO:0009612,GO:0005509,GO:0006508,GO:0005178,GO:0030335,GO:0004222,GO:0035071,GO:0042470,GO:0035159,GO:0042060,GO:0048771,GO:0035988,GO:0048754,GO:0005886,GO:0007155,GO:0008584,GO:0035987,GO:0006979,GO:0007424,GO:0001958,GO:0003700,GO:0009725,GO:0042246,GO:0007561,GO:0030198,GO:0043627,GO:0071711,GO:0016504,GO:0001935,GO:0010952,GO:0034769	CG4859-PC			PIRSF001191	SM00235,SM00120,SM00120,SM00120,SM00120		PF00045,PF00045,PF00045,PF00045,PF00413,PF01471	PS51642,PS51642,PS51642,PS51642	PR00138,PR00138,PR00138,PR00138,PR00138	PS00024	G3DSA:3.40.390.10,G3DSA:2.110.10.10	SSF50923,SSF47090,SSF55486									
aly887.4	Zinc finger protein DZIP1L	GO:0036064,GO:0046872,GO:0042384	CG13617-PA						PF13815	PS50157		PS00028			206~233,372~423,325~345,104~124								
aly887.40	Unknown	GO:0005575,GO:0003674,GO:0008150	CG33988-PB																				
aly887.41	Lipopolysaccharide-induced tumor necrosis factor-alpha factor homolog	GO:0005794,GO:0071222,GO:0050699,GO:0006355,GO:0006915,GO:0001817,GO:0005654,GO:0005765,GO:0005576,GO:0006351,GO:0004871,GO:0005886,GO:0007568,GO:0042347,GO:0043123	CG13516-PA				SM00714		PF10601														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly887.42	Integrator complex subunit 8	GO:0016180,GO:0005634,GO:0003674,GO:0034472,GO:0032039	CG5859-PA																				
aly887.43	Sodium-dependent phosphate transporter 1	GO:0015293,GO:0044341,GO:0015321,GO:0016021,GO:0016020,GO:0005315,GO:0015114,GO:0006817	CG42575-PA						PF01384								REACT_15518						
aly887.44	Presenilins-associated rhomboid-like protein, mitochondrial	GO:0004252,GO:0004175,GO:0016021,GO:0005739,GO:0005743,GO:0008053,GO:0016485,GO:0006508,GO:0005634	CG8972-PA																				
aly887.45	ABC transporter C family member 10	GO:0043190,GO:0042626,GO:0005215,GO:0016021,GO:0006810,GO:0055085,GO:0005524	CG4562-PE										G3DSA:3.40.50.300	SSF52540									
aly887.5	60S ribosomal protein L8	GO:0048749,GO:0005737,GO:0008286,GO:0005840,GO:0022625,GO:0005730,GO:0007052,GO:0005622,GO:0003735,GO:0008361,GO:0000022,GO:0000228,GO:0019843,GO:0006412,GO:0051298	CG1263-PB			PIRSF002158			PF03947,PF00181			PS00467	G3DSA:2.30.30.30,G3DSA:2.40.50.140,G3DSA:4.10.950.10	SSF50249,SSF50104									
aly887.6	Cryptochrome 1	GO:0005737,GO:0009881,GO:0048511,GO:0006281,GO:0005634,GO:0006355,GO:0018298,GO:0000166,GO:0003914,GO:0006351,GO:0003913	CG2488-PA						PF00875,PF03441	PS51645			G3DSA:1.10.579.10,G3DSA:1.25.40.80,G3DSA:3.40.50.620	SSF48173,SSF52425									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly887.7	U7 snRNA-associated Sm-like protein LSm10	GO:0071208,GO:0005634,GO:0005654,GO:0005575,GO:0017069,GO:0003674,GO:0015030,GO:0008150,GO:1900087,GO:0005683,GO:0008380,GO:0006397	CG31913-PA						PF08695				G3DSA:2.30.30.100										
aly887.8	Golgin subfamily A member 4	GO:0005737,GO:0005794,GO:0005802,GO:0070062,GO:0048193,GO:0000042,GO:0043001,GO:0045773,GO:0017137,GO:0000138,GO:0000139,GO:0005654,GO:0030306,GO:0051020,GO:0043231,GO:0016192,GO:0042803	CG3493-PA				SM00755		PF01465	PS50913			G3DSA:1.10.220.60	SSF57997,SSF101283	354~381,860~887,547~567,814~841,168~202,1212~1295,288~336,895~915,951~1023,588~681,1096~1130,432~48								
aly887.9	Uncharacterized protein C9orf85 homolog		CG8675-PA						PF10217														
aly8874.1	Unknown	GO:0008150,GO:0003674,GO:0005615	CG31997-PA						PF15430														
aly8874.2	Synaptotagmin 7	GO:0008021,GO:0005886,GO:0030054,GO:0070062,GO:0016021,GO:0016020,GO:0005544,GO:0017158,GO:0045956,GO:0005509,GO:0005215,GO:0006810,GO:0031982,GO:0050796,GO:0030276,GO:0007269,GO:0031045,GO:0043195,GO:0001778,GO:0030672,GO:0016192,GO:0016079,GO:0048791,GO:0005764,GO:0016528,GO:0005515,GO:0019905	CG2381-PA				SM00239,SM00239		PF00168,PF00168	PS50004,PS50004	PR00360,PR00360,PR00360,PR00399,PR00399,PR00399,PR00399		G3DSA:2.60.40.150,G3DSA:2.60.40.150	SSF49562,SSF49562									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.1	PiggyBac transposable element-derived protein 2		n/a						PF13843,PF13843														
aly890.10	Unknown		CG4702-PB						PF07841														
aly890.11	Unknown		CG13407-PA																				
aly890.12	YLP motif-containing protein 1	GO:0016607,GO:0048812,GO:0005634,GO:0006355,GO:0008157,GO:0006351	CG32685-PE										G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	213~233								
aly890.13	Unknown		n/a																				
aly890.14	Ribokinase	GO:0019303,GO:0070062,GO:0005524,GO:0004747,GO:0006014	CG13369-PA						PF00294		PR00990,PR00990,PR00990,PR00990,PR00990	PS00584	G3DSA:3.40.1190.20	SSF53613									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.15	39S ribosomal protein L17, mitochondrial	GO:0070126,GO:0032543,GO:0070124,GO:0070125,GO:0000002,GO:0005840,GO:0006996,GO:0005622,GO:0003735,GO:0005743,GO:0019904,GO:0005762,GO:0006412	CG13880-PA						PF01196				G3DSA:3.90.1030.10	SSF64263	180~199								
aly890.16	Gamma-tubulin complex component 6	GO:0007020,GO:0000278,GO:0051298,GO:0000086,GO:0005813,GO:0005829,GO:0016020,GO:0000922,GO:0008274,GO:0007052,GO:0043015,GO:0007067,GO:0005874,GO:0008017,GO:0070062	CG5688-PA						PF04130						1086~1106,969~989,700~744,884~904,789~816		REACT_152						
aly890.17	Unknown		CG42240-PB																				
aly890.18	Niemann-Pick C1 protein	GO:0046718,GO:0005635,GO:0005783,GO:0071383,GO:0007591,GO:0030301,GO:0007291,GO:0004872,GO:0007041,GO:0070062,GO:0006486,GO:0032374,GO:0016021,GO:0016020,GO:0031579,GO:0005576,GO:0046686,GO:0048471,GO:0031902,GO:0005794,GO:0016125,GO:0060548,GO:0006914,GO:0007628,GO:0005887,GO:0045456,GO:0042632,GO:0008206,GO:0008158,GO:0015248,GO:0008203,GO:0006897,GO:0015485,GO:0090150,GO:0071404,GO:0045121,GO:0042493,GO:0016242,GO:0005764,GO:0005765,GO:0004888,GO:0033344,GO:2000189,GO:0007165	CG5722-PA						PF02460,PF02460,PF16414	PS50156			G3DSA:1.20.1640.10,G3DSA:1.20.1640.10	SSF82866,SSF82866									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.19	Protein Flattop homolog		CG3081-PA						PF16071						513~533,135~155								
aly890.2	Proteasome subunit alpha type-3	GO:0005737,GO:0004175,GO:0005839,GO:0043161,GO:0005634,GO:0010499,GO:0004298,GO:0006974,GO:0006511,GO:0019773,GO:0005875,GO:0070062	CG1519-PA				SM00948		PF00227,PF10584	PS51475		PS00388	G3DSA:3.60.20.10	SSF56235	82~102		REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_110						
aly890.20	Protein SMG9	GO:0000184,GO:0005622	n/a										G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540									
aly890.21	Cation-dependent mannose-6-phosphate receptor	GO:0015578,GO:0005765,GO:0016021,GO:0005537	n/a						PF02157														
aly890.22	Unknown	GO:0005549	n/a						PF01395				G3DSA:1.10.238.20	SSF47565									
aly890.23	General odorant-binding protein 72 (Fragment)	GO:0005549,GO:0006810,GO:0007608,GO:0042048,GO:0050896,GO:0007606,GO:0005576,GO:0019236	CG11748-PC				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.24	General odorant-binding protein 72 (Fragment)	GO:0005549,GO:0006810,GO:0007608,GO:0007619,GO:0042048,GO:0050896,GO:0007606,GO:0045471,GO:0005576,GO:0035275,GO:0035274,GO:0035276,GO:0019236	CG8807-PA				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly890.25	General odorant-binding protein 72 (Fragment)	GO:0005549,GO:0006810,GO:0007608,GO:0007619,GO:0042048,GO:0050896,GO:0007606,GO:0045471,GO:0005576,GO:0035275,GO:0035274,GO:0035276,GO:0019236	CG8807-PA				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly890.26	General odorant-binding protein 72 (Fragment)	GO:0005549,GO:0006810,GO:0007608,GO:0042048,GO:0050896,GO:0007606,GO:0005576,GO:0019236	CG11748-PC				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly890.27	Unknown	GO:0005549	n/a				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly890.28	Unknown	GO:0005549	n/a				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly890.29	General odorant-binding protein 19d	GO:0005549,GO:0007606,GO:0005576,GO:0008145,GO:0005550	CG1668-PA				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565	64~84								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.3	Apoptosis-stimulating of p53 protein 1	GO:0005737,GO:0045786,GO:0005634,GO:0005654,GO:0005912,GO:0005515,GO:0005886,GO:0061098,GO:0030296,GO:0072332	CG18375-PB				SM00248,SM00248,SM00326		PF00018,PF13637	PS50088,PS50297,PS50088,PS50002			G3DSA:1.25.40.20,G3DSA:2.30.30.40	SSF48403,SSF50044,SSF54236	161~188,206~233								
aly890.30	Unknown	GO:0005549,GO:0007606,GO:0005576,GO:0008145,GO:0005550	CG6641-PA				SM00708,SM00708		PF01395,PF01395				G3DSA:1.10.238.20,G3DSA:1.10.238.20	SSF47565,SSF47565									
aly890.31	Unknown	GO:0005549	n/a				SM00708		PF01395				G3DSA:1.10.238.20	SSF47565									
aly890.32	Unknown		CG13386-PA																				
aly890.33	Unknown		n/a																				
aly890.34	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.35	Protein sprint	GO:0032483,GO:0030139,GO:0006897,GO:0043547,GO:0005096,GO:0030971,GO:0005085,GO:0017112,GO:0017016,GO:0019901,GO:0007165,GO:0007298,GO:0007275,GO:0005938	CG34414-PO				SM00252		PF00017	PS50001	PR00401,PR00401,PR00401,PR00401		G3DSA:3.30.505.10	SSF55550	984~1004								
aly890.36	Protein sprint	GO:0032483,GO:0030139,GO:0006897,GO:0043547,GO:0005096,GO:0030971,GO:0005085,GO:0017112,GO:0017016,GO:0019901,GO:0007165,GO:0007298,GO:0007275,GO:0005938	CG33175-PA				SM00314,SM00167		PF00788,PF02204	PS51205,PS50200				SSF109993									
aly890.37	Unknown		n/a																				
aly890.38	GILT-like protein C02D5.2	GO:0016021	CG9427-PA						PF03227														
aly890.39	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG17572-PA				SM00020		PF00089,PF12032	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly890.4	Inositol-tetrakisphosphate 1-kinase	GO:0016853,GO:0047325,GO:0000287,GO:0005622,GO:0005524,GO:0032957,GO:0052725,GO:0052726	n/a			PIRSF038186			PF05770	PS50975				SSF56059		00562+2.7.1.134+2.7.1.159		PWY-6366,PWY-6362,PWY-6365,PWY-4661,PWY-6554					

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.40	Unknown		n/a																				
aly890.41	Unknown		n/a																				
aly890.42	Cilia- and flagella-associated protein 61		n/a										G3DSA:3.50.50.60										
aly890.43	Unknown		n/a						PF16092,PF16092														
aly890.44	Protein regulator of cytokinesis 1	GO:0000910,GO:0005737,GO:0019894,GO:0051298,GO:0000916,GO:0019901,GO:0005813,GO:0008017,GO:0000281,GO:0051533,GO:0005654,GO:0015630,GO:0000226,GO:0042802,GO:0005874,GO:0005886,GO:0022008,GO:0000922,GO:0051233,GO:0005819,GO:0043148	CG11207-PA						PF03999						215~242,100~120,53~80								
aly890.45	Unknown		CG14770-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.46	Unknown	GO:0005575,GO:0008150,GO:0003674	CG33299-PB																				
aly890.47	Unknown		CG7031-PA																				
aly890.48	Unknown		CG16885-PA																				
aly890.49	Unknown		n/a																				
aly890.5	Unknown		n/a						PF13847				G3DSA:3.40.50.150	SSF53335									
aly890.50	Unknown		CG11380-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.51	Unknown		n/a												20~40								
aly890.52	Unknown		n/a																				
aly890.53	Unknown		n/a																				
aly890.54	Unknown		n/a																				
aly890.55	Unknown		n/a																				
aly890.56	Mitochondrial ribonuclease P protein 3	GO:0008033,GO:0005739	CG15896-PA						PF16953														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.57	Protein crooked neck	GO:0007405,GO:0007417,GO:0016607,GO:0072686,GO:0000381,GO:0005813,GO:0005634,GO:0048663,GO:0007438,GO:0005737,GO:0051298,GO:0071011,GO:0071013,GO:0008366,GO:0022008,GO:0008347,GO:0007443,GO:0007422,GO:0000398,GO:0005622,GO:0006396,GO:0005681	CG3193-PA				SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386,SM00386		PF02184,PF02184,PF02184	PS50293,PS50293,PS50293			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452									
aly890.58	N-alpha-acetyltransferase 20	GO:0005737,GO:0005634,GO:0004596,GO:0008080,GO:0019186	CG14222-PB						PF00583	PS51186			G3DSA:3.40.630.30	SSF55729									
aly890.59	PHD finger protein 10	GO:0031936,GO:0006351,GO:0070604,GO:0046427,GO:0007399,GO:0007480,GO:0005634,GO:0005700,GO:0000792,GO:0006355,GO:0016458,GO:0000791,GO:0045892,GO:0008270,GO:0003682,GO:0048477,GO:0045893	CG12238-PC				SM00249,SM00249			PS50016			G3DSA:3.30.40.10,G3DSA:3.30.40.10	SSF57903,SSF57903									
aly890.6	CLK4-associating serine/arginine rich protein	GO:0005634,GO:0006397,GO:0008380,GO:0003729	CG6695-PA						PF09750														
aly890.60	Unknown		n/a																				
aly890.61	Unknown	GO:0005515	n/a				SM00249		PF00628	PS50016		PS01359	G3DSA:3.30.40.10	SSF57903									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.62	Diphthine--ammonia ligase	GO:0017183,GO:0017178,GO:0005524	CG1578-PA					TIGR00290	PF01902,PF01042				G3DSA:3.90.1490.10,G3DSA:3.40.50.620,G3DSA:3.30.1330.40	SSF52402,SSF55298	279~302			PWY-6482,PWY-7546	UPA00559				
aly890.63	REST corepressor 3	GO:0007221,GO:0017053,GO:0000122,GO:2000619,GO:0006355,GO:0005634,GO:0003714,GO:0045747,GO:0045892,GO:0006351,GO:0005515,GO:0003677,GO:0061086,GO:0003682	CG42687-PG				SM00717,SM00717		PF00249,PF01448	PS51293,PS51293,PS51156			G3DSA:1.10.10.60	SSF46689,SSF46689	316~343								
aly890.64	Unknown		n/a																				
aly890.65	Unknown		n/a						PF16092														
aly890.66	Unknown		n/a																				
aly890.67	Cilia- and flagella-associated protein 61	GO:0055114,GO:0016491	CG30275-PM										G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.68	ALX homeobox protein 1	GO:0043565,GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003677,GO:0007275	CG32532-PD				SM00389		PF00046	PS50071		PS00027	G3DSA:1.10.10.60	SSF46689									
aly890.69	Unknown	GO:0003700,GO:0006355,GO:0005634,GO:0003677,GO:0043565	CG32532-PD																				
aly890.7	Unknown		n/a																				
aly890.70	Multiple coagulation factor deficiency protein 2 homolog	GO:0005794,GO:0005783,GO:0032504,GO:0005793,GO:0019752,GO:0005576,GO:0005509,GO:0015031,GO:0016192,GO:0005615	CG17271-PA						PF13499	PS50222,PS50222		PS00018	G3DSA:1.10.238.10	SSF47473									
aly890.71	Unknown		CG12420-PA																				
aly890.72	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.73	Unknown		n/a																				
aly890.74	Transmembrane protein 151B	GO:0016021	n/a						PF14857														
aly890.75	Transmembrane protein 151B	GO:0016021	n/a						PF14857														
aly890.76	Unknown		n/a						PF03372				G3DSA:3.60.10.10	SSF56219									
aly890.77	Unknown		n/a												73~114,30~50								
aly890.78	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly890.79	Unknown		n/a																				
aly890.8	Unknown		CG14797-PC																				
aly890.80	Unknown		n/a																				
aly890.9	Unknown	GO:0005575,GO:0003674,GO:0008150	CG32040-PA																				
aly89255.1	Transport and Golgi organization protein 2	GO:0009306,GO:0005794,GO:0005829,GO:0003674,GO:0007030	CG11176-PB						PF05742														
aly89255.2	Unknown	GO:0046872	n/a							PS50157		PS00028											

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8933.1	Trimethylguanosine synthase	GO:0005737,GO:0071164,GO:0005615,GO:0036261,GO:0008283,GO:0005634,GO:0006355,GO:0009452,GO:0005654,GO:0008173,GO:0015030,GO:0006351,GO:0001510,GO:0008168	CG44890-PB						PF09445				G3DSA:3.40.50.150	SSF53335									
aly89340.1	Tankyrase	GO:0007016,GO:0005200,GO:0006471,GO:0090364,GO:0035220,GO:0022416,GO:0097110,GO:0003950	CG4719-PB						PF13637				G3DSA:1.25.40.20										
aly89367.1	Unknown		n/a												83~99								
aly8937.1	Probable dimethyladenosine transferase	GO:0005737,GO:0000179,GO:0005730,GO:0000154,GO:0005634,GO:0005575,GO:0052909,GO:0006364,GO:0022008,GO:0044822	CG11837-PA				SM00650	TIGR00755	PF00398	PS51689			G3DSA:3.40.50.150	SSF53335									
aly8937.10	Unknown		n/a																				
aly8937.11	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8937.2	Transportin-1	GO:0005737,GO:0006996,GO:0072372,GO:0006909,GO:0070062,GO:0008139,GO:0005643,GO:0008536,GO:0006886,GO:0000060,GO:0006606,GO:0008320,GO:0010467,GO:0044822,GO:0016032,GO:0022008,GO:0005634,GO:0005829	CG7398-PA				SM00913		PF03810,PF02985,PF13513	PS50166			G3DSA:1.25.10.10	SSF48371										
aly8937.3	Doublesex- and mab-3-related transcription factor 2	GO:0043565,GO:0048706,GO:0014807,GO:0006351,GO:0003700,GO:2000287,GO:0005634,GO:0006355,GO:0045944,GO:0000977,GO:0000987,GO:0046872,GO:0042803	CG15749-PA				SM00301		PF00751	PS50809		PS40000	G3DSA:4.10.1040.10	SSF82927									
aly8937.4	DNA ligase 4	GO:0006310,GO:0000723,GO:0007049,GO:0010212,GO:0071897,GO:0051301,GO:0006273,GO:0005634,GO:0051103,GO:0032807,GO:0006289,GO:0006266,GO:0006260,GO:0003910,GO:0005515,GO:0003677,GO:0006303,GO:0046872,GO:0005694,GO:0005524,GO:0070419	CG12176-PA						PF04679,PF01068,PF04675,PF11411	PS50172,PS50160,PS50172		PS00333	G3DSA:3.30.1490.70,G3DSA:3.30.1490.70,G3DSA:2.40.50.140,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190	SSF52113,SSF50249,SSF52113,SSF56091			REACT_216						
aly8937.5	General transcription factor 3C polypeptide 3	GO:0000127,GO:0005654,GO:0010467,GO:0006351,GO:0005515,GO:0003677,GO:0042797,GO:0006383,GO:0042791	CG8950-PA				SM00028,SM00028,SM00028,SM00028		PF13181,PF13181	PS50005,PS50293,PS50005,PS50293,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly8937.6	F-box/WD repeat-containing protein 9	GO:0008589,GO:0008588,GO:0046599,GO:0045849,GO:0007611,GO:0007293,GO:0030111,GO:0007304,GO:0007298,GO:0030178,GO:0008355,GO:0030708,GO:0030727,GO:0030720,GO:0030707,GO:0006508,GO:0007088,GO:0007623,GO:0060623,GO:0045879,GO:0060253,GO:0046627,GO:0030162,GO:0045475,GO:0004842,GO:0030512,GO:0030713,GO:0051219,GO:0000151,GO:0016322,GO:0019005,GO:0005515,GO:0032007,GO:0046983,GO:0046843	CG3412-PB				SM00320,SM00320,SM00320,SM00256		PF12937,PF00400,PF00400	PS50082,PS50294,PS50082,PS50181	PR00320,PR00320,PR00320	PS00678,PS00678	G3DSA:1.20.1280.50,G3DSA:2.130.10.10	SSF50978,SSF81383	5~25									
aly8937.7	Alpha/beta hydrolase domain-containing protein 17C	GO:0016787	CG33096-PC						PF12695				G3DSA:3.40.50.1820	SSF53474									
aly8937.8	Lipid droplet-associated hydrolase	GO:0016787,GO:0030730,GO:0005783,GO:0016021,GO:0005811,GO:0034389,GO:0012505	CG9186-PB						PF10230				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474									
aly8937.9	Low molecular weight phosphotyrosine protein phosphatase	GO:0005737,GO:0070062,GO:0004726,GO:0004725,GO:0009898,GO:0006470,GO:0003993	CG33748-PA				SM00226		PF01451		PR00720,PR00720,PR00720,PR00720,PR00719,PR00719,PR00719,PR00719,PR00719		G3DSA:3.40.50.270	SSF52788		00627+3.1.3.2		PWY-6348,PWY-6907,PWY-6357,PWY-6908					
aly89441.1	Unknown	GO:0019013	n/a																				
aly895.1	Cyclic nucleotide-gated cation channel alpha-3	GO:0030553,GO:0042391,GO:0050896,GO:1902495,GO:0005249,GO:0071805,GO:0005221,GO:0006812,GO:0005223,GO:0005222,GO:0046549,GO:0	CG43395-PJ				SM00100		PF00027,PF00520	PS50042		PS00888,PS00889	G3DSA:2.60.120.10,G3DSA:1.10.287.630,G3DSA:1.10.287.70	SSF81324,SSF51206	1898~1901,1387~1414,1755~1775								
aly895.2	Unknown		n/a										G3DSA:3.80.10.10	SSF52047,SSF52047									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly895.3	Histone deacetylase 3	GO:0005737,GO:0032041,GO:0016049,GO:0004407,GO:0005634,GO:0003714,GO:0043984,GO:1903507,GO:0016575,GO:0006355,GO:0043066,GO:0006351,GO:0005515,GO:0006342	CG2128-PA			PIRSF037913			PF00850		PR01270,PR01270,PR01270,PR01271,PR01271,PR01271,PR01271,PR01271,PR01271,PR01271		G3DSA:3.40.800.20	SSF52768									
aly895.4	Phosphatidylethanolamine-binding protein homolog	GO:0005575,GO:0008150,GO:0003674,GO:0008289,GO:0005739	CG6180-PA						PF01161				G3DSA:3.90.280.10	SSF49777									
aly89517.1	F-box only protein 21	GO:0003677	n/a				SM00992	TIGR02097	PF08755					SSF141255									
aly8968.1	60S ribosomal protein L44	GO:0005840,GO:0022625,GO:0005622,GO:0003735,GO:0007052,GO:0000022,GO:0006412	CG7424-PB	MF_01476					PF00935			PS01172	G3DSA:3.10.450.80	SSF57829									
aly897.1	Carboxypeptidase B	GO:0006508,GO:0004181,GO:0004180,GO:0008270,GO:0005576	CG8560-PA				SM00631		PF00246,PF02244		PR00765,PR00765,PR00765,PR00765		G3DSA:3.40.630.10,G3DSA:3.30.70.340	SSF54897,SSF53187									
aly897.2	Venom acid phosphatase Acph-1	GO:0005576,GO:0003993	CG9451-PA						PF00328			PS00616	G3DSA:3.40.50.1240,G3DSA:3.40.50.1240	SSF53254									
aly897.3	Unknown	GO:0003677	CG8359-PA				SM00595		PF10545,PF02944	PS51031,PS51029													
aly897.4	Unknown	GO:0003676,GO:0004523	n/a						PF00075	PS50879			G3DSA:3.30.420.10	SSF53098									
aly8990.1	Unknown		n/a																				
aly8990.2	NADH dehydrogenase [ubiqui] 1 alpha subcomplex assembly factor 3	GO:0005743,GO:0022008,GO:0005634,GO:0032981	CG5569-PA						PF04430				G3DSA:3.40.1230.10	SSF64076	110~130								
aly900.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly900.2	Unknown		n/a																				
aly900.3	23 kDa integral membrane protein	GO:0003674,GO:0016021,GO:0008150	CG11415-PA			PIRSF002419			PF00335		PR00259,PR00259,PR00259			SSF48652									
aly900.4	Transmembrane and TPR repeat-containing protein CG4050	GO:0016021,GO:0017122,GO:0008150,GO:0016262	CG4050-PA																				
aly900.5	Unknown		n/a																				
aly900.6	Unknown		n/a																				
aly90044.1	Protein slit	GO:0031012,GO:0001764,GO:0007411,GO:0050929,GO:0022409,GO:0003151,GO:0007432,GO:0008406,GO:0071666,GO:0005509,GO:0008078,GO:0035385,GO:0030182,GO:2000274,GO:0035050,GO:0048495,GO:0046331,GO:0005886,GO:0050919,GO:0008201,GO:0008347,GO:0007427,GO:0007502,GO:0010632,GO:0016199,GO:0007509,GO:0048813,GO:0005576,GO:0005515,GO:0005578	CG43758-PF				SM00082						G3DSA:3.80.10.10											
aly9009.1	Unknown		n/a												80~114,52~72								
aly902.1	PiggyBac transposable element-derived protein 4	GO:0003677	CG13151-PA						PF13843														
aly902.2	Unknown	GO:0016021	CG4984-PC						PF13903														
aly902.3	Coiled-coil domain-containing protein 96	GO:0005737,GO:0005815	n/a						PF13870						301~342,77~115								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly902.4	Putative inorganic phosphate cotransporter	GO:0051938,GO:0022857,GO:0015293,GO:0044341,GO:0015319,GO:0016021,GO:0006541,GO:0005314,GO:0006814,GO:0005316,GO:0015321,GO:0006820,GO:0005886,GO:0015114,GO:0055085,GO:0007005	CG5304-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473										
aly902.5	Putative inorganic phosphate cotransporter	GO:0051938,GO:0015293,GO:0044341,GO:0015319,GO:0016021,GO:0006541,GO:0005314,GO:0005316,GO:0015321,GO:0015114,GO:0005886,GO:0006814,GO:0055085,GO:0007005	CG5304-PA						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly902.6	Unknown		n/a																				
aly90291.1	Type I inositol 1,4,5-trisphosphate 5-phosphatase	GO:0042731,GO:0052658,GO:0070062,GO:0016311,GO:0016020,GO:0046030,GO:0043647,GO:0005575,GO:0046856,GO:0046855,GO:0004445,GO:0005886,GO:0044281,GO:0052659	CG42283-PF										G3DSA:3.60.10.10	SSF56219									
aly903.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly903.2	Titin	GO:0035206,GO:0007498,GO:0030017,GO:0005875,GO:0051301,GO:0007062,GO:0007517,GO:0007519,GO:0031674,GO:0003779,GO:0030018,GO:0016203,GO:0008307,GO:0045214,GO:0000794,GO:0007520,GO:0007522,GO:0005863,GO:0007525,GO:0040011,GO:0004687,GO:0005515,GO:0007076	CG1915-PP				SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00409		PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF07679,PF06582,PF06582,PF06582,PF06582	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726	2433~2453,1792~1826,1749~1769								
aly904.1	Unknown	GO:0005575,GO:0008150,GO:0003674	CG32204-PB						PF15860														
aly904.10	Mitochondrial import inner membrane translocase subunit Tim8	GO:0015450,GO:0006626,GO:0005739,GO:0005743,GO:0005744,GO:0015031,GO:0046872	CG1728-PB						PF02953				G3DSA:1.10.287.810	SSF144122									
aly904.11	UPF0568 protein C14orf166 homolog	GO:0005737,GO:0072669,GO:0005829,GO:0005575,GO:0045944,GO:0003674,GO:0003723,GO:0006388,GO:0008150,GO:0000993,GO:0005634,GO:0006351	CG31249-PA						PF10036														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly904.12	Dehydrodolichyl diphosphate syntase complex subunit DHDDS	GO:0044267,GO:0006909,GO:0006488,GO:0006489,GO:0043687,GO:0005789,GO:0016765,GO:0018279	CG10778-PA	MF_01139				TIGR00055	PF01255			PS01066	G3DSA:3.40.1180.10	SSF64005									
aly904.13	Protein FAM50 homolog	GO:0005575,GO:0005634,GO:0003674,GO:0022008	CG12259-PA						PF04921						80~122,14~38								
aly904.14	Gem-associated protein 5	GO:0005737,GO:0035075,GO:0016604,GO:0005829,GO:0071254,GO:0032797,GO:0005634,GO:0016020,GO:0007591,GO:0000387,GO:0007629,GO:0030374,GO:0005654,GO:0017069,GO:0044822,GO:0005515,GO:0034719,GO:0008344	CG30149-PB				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400	PS50082,PS50294,PS50082,PS50294		PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978	231~255,879~900								
aly904.15	Centromere-associated protein E	GO:0016020,GO:0051382,GO:0030496,GO:0007596,GO:0016887,GO:0005871,GO:0005874,GO:0005875,GO:0051301,GO:0005737,GO:0005634,GO:0000940,GO:0000775,GO:0007080,GO:0005694,GO:0003777,GO:0015630,GO:0000278,GO:0019886,GO:0008017,GO:1990023,GO:0000779,GO:0007052,GO:0008152,GO:0007079,GO:0043515,GO:0007059,GO:0022008,GO:0007264,GO:0051315,GO:0000776,GO:0000777,GO:0008574,GO:0005829,GO:0007018,GO:0030071,GO:0005524,GO:0007275,GO:0045860	CG6392-PC				SM00129		PF00225	PS50067	PR00380,PR00380,PR00380,PR00380	PS00411	G3DSA:3.40.850.10	SSF52540,SSF90257	894~942,1720~1757,1052~1079,818~879,2799~2833,538~593,728~762,1789~1865,1144~1178,2839~2873,2431~2472,2881~2915,511~531,3042~3042,2691~2725,2134~2189,615~635,341~378,954~974,2497~2538,2733~2753,2368~2416,1676~1696,2954~2981,1252~1321,1448~1510,2026~2067								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly904.16	Protein MAK16 homolog A	GO:0000022,GO:0022008,GO:0005730	CG10648-PA			PIRSF003352			PF01778,PF04874														
aly904.2	Carboxypeptidase Q	GO:0005737,GO:0005794,GO:0005783,GO:0004180,GO:0043171,GO:0005764,GO:0042803,GO:0070573,GO:0006508,GO:0046872,GO:0005615	n/a						PF02225,PF04389				G3DSA:3.50.30.30,G3DSA:3.40.630.10,G3DSA:3.40.630.10	SSF53187									
aly904.3	Carboxypeptidase Q	GO:0005737,GO:0005794,GO:0005783,GO:0004180,GO:0043171,GO:0005764,GO:0042803,GO:0070573,GO:0006508,GO:0046872,GO:0005615	n/a						PF04389,PF04389				G3DSA:3.50.30.30,G3DSA:3.50.30.30,G3DSA:3.40.630.10,G3DSA:3.40.630.10,G3DSA:3.40.630.10	SSF53187,SSF53187									
aly904.4	Cytochrome P450 CYP12A2	GO:0004497,GO:0020037,GO:0016705,GO:0005739,GO:0005506,GO:0055114,GO:0009055	CG11821-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly904.5	Ejaculatory bulb-specific protein 3	GO:0009615,GO:0045297,GO:0007552,GO:0005576	CG11390-PA						PF03392				G3DSA:1.10.2080.10	SSF100910									
aly904.6	Probable DNA directed RNA polymerases I and III subunit RPAC2	GO:0005736,GO:0005666,GO:0006360,GO:0006351,GO:0003677,GO:0003899,GO:0046983,GO:0006383,GO:0005875	CG10685-PD						PF13656			PS01154	G3DSA:3.30.1360.10	SSF55257		00240+2.7.7.6,00230+2.7.7.6							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly904.7	40S ribosomal protein S2	GO:0005737,GO:0005840,GO:0005730,GO:0007275,GO:0003735,GO:0015935,GO:0003723,GO:0000228,GO:0048477,GO:0006412,GO:0022627	CG5920-PA					TIGR01020	PF03719,PF00333	PS50881		PS00585	G3DSA:3.30.230.10,G3DSA:3.30.160.20	SSF54211,SSF54768									
aly904.8	N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase (Fragment)	GO:0005764,GO:0003948,GO:0008233	CG1827-PD						PF01112					SSF56235									
aly904.9	Adenosine deaminase-like protein	GO:0046872,GO:0004000,GO:0043101,GO:0006144,GO:0005575,GO:0009117,GO:0055086,GO:0043103,GO:0046103,GO:0017144,GO:0005829,GO:0006154,GO:0044281	CG11994-PA						PF00962				G3DSA:3.20.20.140	SSF51556									
aly905.1	Unknown		n/a						PF03372				G3DSA:3.60.10.10	SSF56219									
aly905.10	Unknown	GO:0005615	CG11854-PB				SM00700		PF06585														
aly905.11	Unknown		n/a						PF06585														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly905.12	Unknown	GO:0003676	n/a						PF00075	PS50879			G3DSA:3.30.420.10	SSF53098									
aly905.2	Juvenile hormone-binding protein (Fragment)	GO:0005576	n/a				SM00700		PF06585					SSF56808									
aly905.3	Unknown		n/a																				
aly905.4	Replication factor C subunit 3	GO:0005634,GO:0000166,GO:0003689,GO:0005663,GO:0006260,GO:0006261,GO:0016887,GO:0003677,GO:0046683,GO:0022008,GO:0005875	CG6258-PB				SM00382		PF13177,PF08542				G3DSA:3.40.50.300,G3DSA:1.10.8.60,G3DSA:1.20.272.10	SSF48019,SSF52540			REACT_152,REACT_216,REACT_22172,REACT_383,REACT_1538						
aly905.5	Beta-secretase 1	GO:0005794,GO:0001540,GO:0005783,GO:0035071,GO:0030659,GO:0009986,GO:0005802,GO:0030424,GO:0048102,GO:0004190,GO:0030163,GO:0005887,GO:0006509,GO:0006508,GO:0008233,GO:0050435,GO:0005768,GO:0005771	CG17283-PA						PF00026			PS00141	G3DSA:2.40.70.10,G3DSA:2.40.70.10	SSF50630,SSF50630									
aly905.6	Circadian clock-controlled protein	GO:0007623,GO:0003674,GO:0005615	CG2650-PA				SM00700		PF06585														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly905.7	Trace amine-associated receptor 1	GO:0004930,GO:0001594,GO:0010579,GO:0016021,GO:0007606,GO:0008227,GO:0005887,GO:0007191,GO:0007186,GO:0006171	CG13579-PB						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321,SSF81321			REACT_14797						
aly905.8	Circadian clock-controlled protein	GO:0007623,GO:0005615	CG13618-PA				SM00700		PF06585														
aly905.9	Unknown	GO:0005615	CG11854-PB				SM00700		PF06585														
aly90560.1	Unknown	GO:0008270	CG2991-PB																				
aly9061.1	Alpha-tocopherol transfer protein-like	GO:0016020,GO:0005215,GO:0008431,GO:0006810,GO:0005622	CG3823-PA						PF00650	PS50191			G3DSA:3.40.525.10	SSF52087									
aly9067.1	Unknown	GO:0008239,GO:0006508,GO:0016020,GO:0008236	CG17684-PC										G3DSA:3.40.50.1820										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9068.1	Unknown	GO:0007031,GO:0005777,GO:0007399	CG5325-PA						PF04614														
aly9068.2	Putative fatty acyl-CoA reductase CG5065	GO:0005778,GO:0080019,GO:0016021,GO:0005777,GO:0050062,GO:0010025,GO:0035336,GO:0008611	CG5065-PA						PF03015,PF07993				G3DSA:3.40.50.720	SSF51735			REACT_22258						
aly909.1	Unknown		n/a																				
aly909.2	Fat-like cadherin-related tumor suppressor homolog	GO:0016339,GO:0007293,GO:0004872,GO:0007295,GO:0050829,GO:0005925,GO:0007156,GO:0007431,GO:0016020,GO:0005509,GO:0009925,GO:0048477,GO:0045089,GO:0007442,GO:0060429,GO:0005887,GO:0005886,GO:0044331,GO:0050839,GO:0007424,GO:0007440,GO:0030950,GO:0042247,GO:0045571	CG7749-PD				SM00112,SM00112		PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF00028	PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49313	2761~2763								
aly909.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly909.4	Unknown		n/a																				
aly910.1	Unknown		n/a						PF13358														
aly910.2	Unknown		n/a																				
aly910.3	Transposable element Tcb2 transposase	GO:0015074,GO:0005634,GO:0006313,GO:0004803,GO:0003677	n/a						PF01498														
aly910.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly91140.1	PH-interacting protein	GO:0022604,GO:0045840,GO:2001237,GO:0033138,GO:0010800,GO:0006909,GO:0070062,GO:0005634,GO:0043568,GO:0070577,GO:0043066,GO:0008284,GO:0008286,GO:0046427,GO:0005158,GO:0006606,GO:0008360,GO:0045893,GO:0007010,GO:0045944,GO:0005515,GO:0007095,GO:0001932,GO:0040008	CG31132-PA										G3DSA:1.20.920.10	SSF47370									
aly9138.1	Unknown		n/a																				
aly9138.2	Unknown		n/a																				
aly91453.1	Unknown		n/a										G3DSA:3.30.40.10										
aly91453.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9151.1	Unknown		n/a				SM00355,SM00355,SM00355,SM00355,SM00355,SM00614,SM00614,SM00614,SM00614		PF02892,PF02892	PS50808				SSF57667,SSF57667	69~89									
aly9151.2	Unknown		CG30428-PA						PF13873														
aly9151.3	Unknown	GO:0005575,GO:0003674,GO:0008150	CG10139-PA																				
aly916.1	Putative trypsin-6	GO:0043542,GO:0004252,GO:0007616,GO:0005044,GO:0007614,GO:0016020,GO:0005576,GO:0008061,GO:0006030,GO:0006508,GO:0046872	CG4821-PG				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly916.2	Unknown		n/a																				
aly917.1	EF-hand calcium-binding domain-containing protein 1	GO:0005509	CG2256-PC				SM00054,SM00054		PF13499	PS50222,PS50222		PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly917.2	Epidermal retinol dehydrogenase 2	GO:0043616,GO:0004745,GO:0016021,GO:0005789,GO:0008152,GO:0042572,GO:0042574,GO:0016491	CG14946-PD						PF00106		PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080	PS00061	G3DSA:3.40.50.720	SSF51735									
aly917.3	Epidermal retinol dehydrogenase 2	GO:0043616,GO:0004745,GO:0016021,GO:0005789,GO:0008152,GO:0050908,GO:0042574,GO:0042572,GO:0016491	CG14946-PD						PF00106		PR00080,PR00080,PR00080,PR00081,PR00081,PR00081,PR00081	PS00061	G3DSA:3.40.50.720	SSF51735									
aly917.4	Oxysterol-binding protein-related protein 1	GO:0005737,GO:0005543,GO:0070062,GO:0019886,GO:0006869,GO:0008142,GO:0005634,GO:0005770,GO:0005622,GO:0005654,GO:0005765,GO:0008203,GO:0016192,GO:0015485	CG3860-PB						PF01237			PS01013		SSF144000,SSF144000	372~392								
aly9170.1	Unknown		n/a																				
aly9171.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9181.1	Segmentation polarity homeobox protein engrailed	GO:0035224,GO:0007485,GO:0001158,GO:0035288,GO:0035289,GO:0010629,GO:0048100,GO:0007386,GO:0007411,GO:0001078,GO:0007417,GO:0007388,GO:0043565,GO:0007367,GO:0000122,GO:0005634,GO:0008406,GO:0007474,GO:0035290,GO:0010468,GO:0000980,GO:0007487,GO:0007486,GO:0035215,GO:0048099,GO:0045892,GO:0035277,GO:0007400,GO:0007418,GO:0007447,GO:0003700,GO:0007448,GO:0021960,GO:0006355	CG9015-PB				SM00389		PF10525,PF00046	PS50071	PR00031,PR00031,PR00026,PR00026,PR00024,PR00024,PR00024	PS00033,PS00027	G3DSA:1.10.10.60	SSF46689									
aly91821.1	Unknown	GO:0042127,GO:0005737,GO:0042048,GO:0007560,GO:0046331,GO:0003674,GO:0001738	CG32315-PA																				
aly921.1	Alpha-(1,3)-fucosyltransferase C	GO:0036065,GO:0006486,GO:0016021,GO:0016020,GO:0008417,GO:0005886,GO:0032580,GO:0046920	CG40305-PB						PF17039,PF00852					SSF53756					UPA00378				
aly921.2	Gonadotropin-releasing hormone II receptor	GO:0004930,GO:0070328,GO:0097004,GO:0016500,GO:0016021,GO:0005886,GO:0033500,GO:0016042,GO:0055088,GO:0097003,GO:0005887,GO:0008188,GO:0007186	CG11325-PC						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00896,PR00896,PR00896,PR00896	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly921.3	AP-3 complex subunit beta-2	GO:0008021,GO:0006901,GO:0007040,GO:0030123,GO:0030135,GO:0030137,GO:0008565,GO:0016183,GO:0006886,GO:0006887,GO:0008089,GO:0005654,GO:0031396,GO:0005794,GO:0005215,GO:0006727,GO:0006726,GO:0060967,GO:0048490,GO:0008057,GO:0008340,GO:0030665,GO:0006892,GO:0007220,GO:0006897,GO:0016192,GO:0046907,GO:0005737,GO:0010883	CG11427-PA						PF14796,PF01602,PF01602				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly92109.1	PX domain-containing protein kinase-like protein	GO:0005737,GO:0006468,GO:0043271,GO:0035091,GO:0016772,GO:0005634,GO:0005886,GO:0008022,GO:0005815,GO:0003779,GO:0032780,GO:0006954,GO:0004672,GO:0050804,GO:0005524	CG8726-PB											SSF56112	118~145								
aly92224.1	Unknown		n/a						PF14227														
aly923.1	Dolichyl-phosphate beta-glucosyltransferase	GO:0040003,GO:0007030,GO:0006493,GO:0009880,GO:0006487,GO:0007379,GO:0016021,GO:0019991,GO:0005789,GO:0007029,GO:0007009,GO:0010004,GO:0009953,GO:0007509,GO:0004581,GO:0005783	CG7870-PA						PF00535				G3DSA:3.90.550.10	SSF53448									
aly923.10	Protein kinase C-binding protein NELL1	GO:0005201,GO:0030154,GO:0031012,GO:0030501,GO:0005737,GO:0040005,GO:0005635,GO:0007475,GO:0005509,GO:0048471,GO:2000599,GO:0045669,GO:0010468,GO:0008362,GO:0046331,GO:0007424,GO:0051539,GO:0007399,GO:0033689,GO:0005576,GO:0005515,GO:0005578	CG33196-PQ				SM00179,SM00179,SM00179,SM00282,SM00215,SM00215,SM00214,SM00214,SM00210,SM00181,SM00181,SM00181		PF00093,PF00093,PF12947,PF12947,PF07645	PS50026,PS50184,PS50184,PS50026,PS50026		PS01186,PS00010,PS01186,PS01208,PS00010,PS01187,PS00010,PS01187,PS01186	G3DSA:2.10.25.10,G3DSA:2.60.120.200,G3DSA:2.40.155.10,G3DSA:2.10.70.10,G3DSA:2.10.70.10,G3DSA:2.10.25.10	SSF57603,SSF57184,SSF49899,SSF57603									
aly923.11	Tetraspanin-9	GO:0016021	n/a						PF00335					SSF48652									
aly923.12	Peptidyl-prolyl cis-trans isomerase A	GO:0000413,GO:0006457,GO:0005634,GO:0045069,GO:0005576,GO:0003755,GO:0042277,GO:0005829	CG7768-PA						PF00160,PF13879	PS50072	PR00153,PR00153,PR00153,PR00153		G3DSA:2.40.100.10	SSF50891									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly923.13	CD63 antigen	GO:0042470,GO:2001046,GO:0016021,GO:0048757,GO:0007160,GO:0005765,GO:0008150,GO:0002092,GO:0035646,GO:0097487,GO:0015031,GO:0003674,GO:0016477,GO:0031226,GO:0031902,GO:1900746	CG5492-PA			PIRSF002419			PF00335		PR00259,PR00259,PR00259,PR00259	PS00421		SSF48652									
aly923.14	Tudor domain-containing protein 3	GO:0005737,GO:0035064,GO:0005634,GO:0003713,GO:0003506,GO:0046331,GO:0003723,GO:0003682,GO:0016568,GO:0006397	CG13472-PA				SM00165,SM00333		PF00627,PF06003,PF08585	PS50304,PS50030			G3DSA:1.10.8.10,G3DSA:2.30.30.140	SSF63748,SSF46934	431~451,404~424								
aly923.15	Copper transport protein ATOX1	GO:0006878,GO:0005623,GO:0055070,GO:0030001,GO:0006825,GO:0016531,GO:0046872	CG32446-PB						PF00403	PS50846		PS01047	G3DSA:3.30.70.100	SSF55008									
aly923.16	POC1 centriolar protein homolog A	GO:0030030,GO:0051297,GO:0005515	CG10191-PB				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF00400,PF00400,PF00400,PF00400,PF00400	PS50082,PS50082,PS50082,PS50082,PS50082,PS50294,PS50082	PR00320,PR00320,PR00320	PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978									
aly923.17	Exportin-5	GO:0005737,GO:0008565,GO:0044822,GO:0000049,GO:0006611,GO:0006886,GO:0008536,GO:0070883,GO:1900370,GO:0005654,GO:0010467,GO:0003723,GO:0035281,GO:0042565,GO:0005634,GO:0005829,GO:0003729	CG12234-PA						PF03810,PF08389				G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371,SSF48371									
aly923.18	Leucine--tRNA ligase, cytoplasmic	GO:0005737,GO:0004823,GO:0005829,GO:0042060,GO:0006429,GO:0010467,GO:0002161,GO:0006418,GO:0022008,GO:0005634,GO:0005875,GO:0005524	CG33123-PA					TIGR00395	PF08264,PF00133,PF00133			PS00178	G3DSA:3.90.740.10,G3DSA:3.40.50.620,G3DSA:3.40.50.620,G3DSA:3.40.50.620,G3DSA:1.10.730.10	SSF52374,SSF52374,SSF52374,SSF47323,SSF50677	443~463	00970+6.1.1.4	REACT_71						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly923.19	Recombination repair protein 1	GO:0003906,GO:0008408,GO:0006281,GO:0004518,GO:0005634,GO:0008311,GO:0006284,GO:0005622,GO:0006974,GO:0090305,GO:0003677,GO:0046872	CG3178-PB					TIGR00633,TIGR00195	PF03372	PS51435		PS00727,PS00726	G3DSA:3.60.10.10	SSF56219									
aly923.2	Programmed cell death protein 6	GO:0005783,GO:0048306,GO:0034605,GO:0005789,GO:0051898,GO:0001525,GO:0005737,GO:0036324,GO:0070062,GO:0031410,GO:0006886,GO:0045766,GO:0005509,GO:0043280,GO:0042802,GO:0042803,GO:0070971,GO:0006919,GO:0006915,GO:0031965,GO:0051592,GO:0046330,GO:0060090,GO:0010595,GO:0030948,GO:0005768,GO:0043495,GO:0005575,GO:0001938,GO:0032007,GO:0046983,GO:0004198,GO:0005634	CG40410-PC				SM00054,SM00054,SM00054,SM00054,SM00054		PF13499,PF13499,PF13202	PS50222,PS50222,PS50222,PS50222		PS00018,PS00018	G3DSA:1.10.238.10	SSF47473									
aly923.20	UPF0609 protein CG1218	GO:0005575,GO:0072572,GO:0008150,GO:0008270	CG1218-PA						PF10228,PF10283														
aly923.21	Unknown		CG15431-PA												83~107								
aly923.22	Rab proteins geranylgeranyl transferase component A	GO:0005737,GO:0008021,GO:0005818,GO:0018344,GO:0016192,GO:0005968,GO:0016020,GO:0005096,GO:0017137,GO:0000922,GO:0004663,GO:0007269,GO:0048471,GO:0006886,GO:0007049	CG8432-PA			PIRSF016550			PF00996,PF00996		PR00891,PR00891,PR00891,PR00891,PR00891,PR00891,PR00891		G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.30.519.10,G3DSA:3.30.519.10,G3DSA:1.10.405.10	SSF54373,SSF51905									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly923.23	Inosine-5'-monophosphate dehydrogenase	GO:0005737,GO:0046872,GO:0006909,GO:0003938,GO:0030554,GO:0000166,GO:0006164,GO:0007411,GO:0006177,GO:0048477,GO:0055114	CG1799-PC	MF_01964		PIRSF000130	SM00116,SM00116	TIGR01302	PF00571,PF00478	PS51371,PS51371		PS00487	G3DSA:3.20.20.70	SSF51412,SSF51412		00983+1.1.1.205,00230+1.1.1.205	REACT_1698	PWY-7221,PWY-5695,PWY-6596	UPA00601				
aly923.24	CD151 antigen	GO:0008150,GO:0016021,GO:0003674	CG5492-PA			PIRSF002419			PF00335		PR00259,PR00259,PR00259,PR00259			SSF48652									
aly923.25	Sorting nexin-33	GO:0016197,GO:0007032,GO:0036089,GO:0019898,GO:0006897,GO:0090389,GO:0016023,GO:0006886,GO:0005886,GO:0000281,GO:0005547,GO:0030659,GO:0045335,GO:0044351,GO:0035091,GO:0071456,GO:0007067,GO:0000045,GO:0097320,GO:0005829	CG6757-PA			PIRSF027744	SM00326,SM00312		PF00787,PF14604,PF10456	PS50195,PS50002	PR00452,PR00452,PR00452,PR00452		G3DSA:2.30.30.40,G3DSA:3.30.1520.10	SSF50044,SSF64268	484~504								
aly923.26	Unknown	GO:0007030,GO:0000287,GO:0016021,GO:0006812,GO:0015914,GO:0004012,GO:0019829,GO:0006886,GO:0005524	CG33298-PB																				
aly923.27	Unknown		n/a						PF07645			PS00010	G3DSA:2.10.25.10	SSF57196									
aly923.3	60S ribosomal protein L27a	GO:0015934,GO:0005840,GO:0022625,GO:0006412,GO:0003735,GO:0007052,GO:0005762,GO:0000022,GO:0032543,GO:0051298	CG15442-PD	MF_01341					PF00828			PS00475	G3DSA:3.100.10.10	SSF52080									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly923.4	Unknown		n/a																				
aly923.5	Protein SPT2 homolog	GO:0035091,GO:0005575,GO:0003824,GO:0003674,GO:0008152,GO:0008150	CG5815-PA				SM00784		PF08243						38~71,260~280,674~694,347~410								
aly923.6	7-methylguanosine phosphate-specific 5'-nucleotidase	GO:0009158,GO:0016311,GO:0005829,GO:0000287,GO:0008253,GO:0008252,GO:0000166,GO:1901069,GO:0009117	CG3362-PA					TIGR01544	PF05822				G3DSA:3.40.50.1000,G3DSA:3.40.50.1000	SSF56784		00230+3.1.3.5,00760+3.1.3.5,00240+3.1.3.5		PWY-5381,PWY-7185,PWY-6596,PWY-6607,PWY-6606,PWY-6608,PWY-5695					
aly923.7	Phospholipid-transporting ATPase 1	GO:0016020,GO:0007030,GO:0000287,GO:0005783,GO:0006812,GO:0016021,GO:0004012,GO:0019829,GO:0045332,GO:0005886,GO:0006886,GO:0015914,GO:0005524	CG33298-PB					TIGR01494,TIGR01652,TIGR01652	PF16209,PF16212,PF12710		PR00119,PR00119,PR00119	PS00154	G3DSA:3.40.50.1000,G3DSA:3.40.50.1000,G3DSA:3.40.1110.10,G3DSA:2.70.150.10,G3DSA:2.70.150.10	SSF56784,SSF56784,SSF81660,SSF81665,SSF81665,SSF81665,SSF81653,SSF81653										
aly923.8	Rab GDP dissociation inhibitor alpha	GO:0008021,GO:0050771,GO:0016192,GO:0005794,GO:0005092,GO:0005093,GO:0005829,GO:0050790,GO:0005096,GO:0090315,GO:0032482,GO:0007269,GO:0043209,GO:0015031,GO:0030496,GO:0005875	CG4422-PB						PF00996		PR00891,PR00891,PR00891,PR00891,PR00891,PR00891,PR00892,PR00892,PR00892,PR00892,PR00892,PR00892,PR00892,PR00892,PR00892,PR00892		G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:1.10.405.10,G3DSA:3.30.519.10,G3DSA:3.30.519.10	SSF51905,SSF51905			REACT_11044						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly923.9	Acyl-CoA synthetase family member 4 homolog	GO:0005575,GO:0003824,GO:0006631,GO:0016878,GO:0005524	CG13401-PA				SM00564,SM00564,SM00564		PF00501,PF13360,PF13193			PS00455	G3DSA:2.140.10.10,G3DSA:3.40.50.980,G3DSA:3.40.50.980,G3DSA:3.30.300.30	SSF56801,SSF50998										
aly9245.1	Unknown		n/a										G3DSA:2.10.25.10	SSF57567									
aly9245.2	Unknown		n/a						PF01826				G3DSA:2.10.25.10	SSF57567									
aly9245.3	Unknown		n/a						PF00079				G3DSA:3.30.497.10	SSF56574									
aly9245.4	Unknown		n/a						PF01826				G3DSA:2.10.25.10	SSF57567									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly925.1	Protein tramtrack, beta isoform	GO:0035147,GO:0035151,GO:0048750,GO:0035041,GO:0045467,GO:0035001,GO:0031208,GO:0003676,GO:0003677,GO:0043388,GO:0007298,GO:0001078,GO:0007143,GO:0007276,GO:0005737,GO:0040003,GO:0000122,GO:0005634,GO:0001709,GO:0007476,GO:0030707,GO:0001964,GO:0060446,GO:0042682,GO:0016476,GO:0046872,GO:0000980,GO:0048666,GO:0031987,GO:0017053,GO:0042803,GO:0042675,GO:0008360,GO:0045892,GO:0048053,GO:0002121,GO:0007426,GO:0007422,GO:0003700,GO:0048854,GO:0005700,GO:0048813,GO:0045944,GO:0006351,GO:0000978,GO:0003682,GO:0046843	CG44132-PH				SM00355,SM00355,SM00355,SM00355,SM00355,SM00225		PF00651	PS50157,PS50157,PS50097,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.710.10	SSF57667,SSF54695,SSF57667,SSF57667										
aly925.10	NEDD8-activating enzyme E1 catalytic subunit	GO:0043234,GO:0045116,GO:0019781,GO:0005829,GO:0045879,GO:0016881,GO:0005634,GO:0005524	CG13343-PA						PF08825,PF00899			PS00865	G3DSA:3.10.20.260,G3DSA:1.10.10.520,G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF69572					UPA00885				
aly925.11	Zinc finger protein 800	GO:0005634,GO:0006355,GO:0006351,GO:0003677,GO:0022008,GO:0046872	CG10979-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157		PS00028,PS00028,PS00028		SSF57667	128~148								
aly925.12	ATP synthase subunit beta, mitochondrial	GO:0045261,GO:0015986,GO:0015992,GO:0015991,GO:0000275,GO:0005811,GO:0005739,GO:0005743,GO:0046933,GO:0046331,GO:0008553,GO:0005524	CG11154-PD	MF_01347		PIRSF039072	SM00382	TIGR01039	PF00306,PF02874,PF00006			PS00152	G3DSA:3.40.50.300,G3DSA:1.10.1140.10,G3DSA:2.40.10.170	SSF50615,SSF47917,SSF52540		00195+3.6.3.14,00190+3.6.3.14		PWY-7219					
aly925.13	Ubiquinol-cytochrome-c reductase complex assembly factor 1	GO:0005743,GO:0007030,GO:0070131,GO:0034551	CG10075-PA						PF03981														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly925.14	Sphingomyelin phosphodiesterase 1	GO:0016787,GO:0016798,GO:0005764,GO:0005576,GO:0004767,GO:0006684,GO:0006685,GO:0046513	CG15533-PA						PF00149	PS50015			G3DSA:3.60.21.10,G3DSA:3.60.21.10	SSF56300,SSF56300	642~651								
aly925.15	60S ribosomal export protein NMD3	GO:0005737,GO:0030674,GO:0005730,GO:0005634,GO:0016020,GO:0000055,GO:0005654,GO:0043023,GO:0015031,GO:0022008,GO:0044822,GO:0003729	CG3460-PA						PF04981														
aly925.16	ATP synthase subunit beta, mitochondrial	GO:0045261,GO:0015986,GO:0015992,GO:0015991,GO:0000275,GO:0005811,GO:0005739,GO:0005743,GO:0046933,GO:0046331,GO:0008553,GO:0005524	CG11154-PD	MF_01347		PIRSF039072	SM00382	TIGR01039	PF00006,PF02874,PF00306			PS00152	G3DSA:1.10.1140.10,G3DSA:3.40.50.300,G3DSA:2.40.10.170	SSF50615,SSF52540,SSF47917	470~480	00195+3.6.3.14,00190+3.6.3.14		PWY-7219					
aly925.17	60S ribosomal protein L24	GO:0005840,GO:0022625,GO:0003735,GO:0007052,GO:0000022,GO:0006412,GO:0051298	CG9282-PB				SM00746		PF01246				G3DSA:2.30.170.20	SSF57716	102~122								
aly925.18	Coiled-coil domain-containing protein 58	GO:0005739	CG15881-PA						PF09774						88~108								
aly925.19	Importin subunit alpha-7	GO:0005737,GO:0008565,GO:0005643,GO:0005634,GO:0016020,GO:0006606,GO:0008320,GO:0007283,GO:0045944,GO:0060135	CG8548-PA			PIRSF005673	SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185,SM00185		PF01749,PF16186,PF00514,PF00514,PF00514,PF00514,PF00514,PF00514,PF00514,PF00514	PS50176,PS51214,PS50176,PS50176,PS50176			G3DSA:1.25.10.10	SSF48371	16~36								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly925.2	Acetylcholinesterase	GO:0005737,GO:0004104,GO:0042331,GO:0006581,GO:0016020,GO:0052689,GO:0003990,GO:0031225,GO:0043083,GO:0045202,GO:0007268,GO:0001507,GO:0042426,GO:0007271,GO:0005886,GO:0042803,GO:0046683,GO:0030054,GO:0046681	CG17907-PA						PF00135		PR00878,PR00878,PR00878,PR00878,PR00878,PR00878,PR00880,PR00880,PR00880,PR00880,PR00880,PR00880,PR00880,PR00880	PS00122,PS00941	G3DSA:3.40.50.1820	SSF53474		00564+3.1.1.7							
aly925.20	Cholinesterase	GO:0051384,GO:0005783,GO:0007612,GO:0050805,GO:0014016,GO:0016020,GO:0072562,GO:0042802,GO:0008285,GO:0004104,GO:0052689,GO:0051593,GO:0008150,GO:0005788,GO:0008152,GO:0043279,GO:0019695,GO:0005641,GO:0042493,GO:0005575,GO:0033265,GO:0003990	CG10175-PD						PF00135			PS00122	G3DSA:3.40.50.1820	SSF53474									
aly925.21	Leucine-rich repeat-containing protein let-4	GO:0035150,GO:0045177,GO:0016324,GO:0007614,GO:0002119,GO:0005575,GO:0009792,GO:0003674,GO:0016021,GO:0002064	CG42573-PB				SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00369,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365		PF13855,PF13855,PF00560	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	PR00019,PR00019		G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52058									
aly925.22	Unknown		n/a																				
aly925.23	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly925.24	Unknown		n/a																				
aly925.25	Protein timeless homolog	GO:0005730,GO:0006974,GO:0009582,GO:0015630,GO:0000077,GO:0002009,GO:0005634,GO:0000122,GO:0042752,GO:0048754,GO:0044770,GO:0000790,GO:0045892,GO:0006351,GO:0009649,GO:0007623,GO:0030324,GO:0009628,GO:0007067,GO:0051301	CG7855-PA						PF04821														
aly925.26	Protein timeless homolog	GO:0002009,GO:0000077,GO:0005634,GO:0001822,GO:0006974,GO:0042752,GO:0042753,GO:0045892,GO:0006351,GO:0009649,GO:0001658,GO:0007623,GO:0007067,GO:0051301	CG7855-PA						PF05029						474~494								
aly925.27	Methyl-CpG-binding domain protein 5	GO:0070062,GO:0007399,GO:0044708,GO:0005634,GO:0040014,GO:0010369,GO:0098779,GO:0042593,GO:0002230,GO:0003677,GO:0003682,GO:0060399	CG13598-PH				SM00391		PF00855	PS50812,PS50982			G3DSA:2.30.30.160	SSF63748,SSF54171										
aly925.28	U3 small nucleolar RNA-associated protein 18 homolog	GO:0034388,GO:0032040,GO:0030532,GO:0005634,GO:0005730,GO:0042585,GO:0006364,GO:0005515,GO:0048132,GO:0003674,GO:0007405,GO:0022008	CG7989-PA				SM00320,SM00320,SM00320,SM00320			PS50082,PS50294			G3DSA:2.130.10.10	SSF50978										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly925.29	DnaJ homolog subfamily A member 1	GO:0051087,GO:0006457,GO:0005783,GO:0031072,GO:0005739,GO:0043508,GO:0051223,GO:1901998,GO:0070062,GO:0030521,GO:0030544,GO:0005634,GO:0016020,GO:0051082,GO:0043065,GO:0043066,GO:0031397,GO:0048471,GO:0046872,GO:0005524,GO:0030317,GO:0007283,GO:0009408,GO:0022008,GO:0070585,GO:0005829,GO:0000151	CG8863-PA				SM00271		PF00684,PF01556,PF00226	PS51188,PS50076	PR00625,PR00625,PR00625	PS00636	G3DSA:2.60.260.20,G3DSA:1.10.287.110,G3DSA:2.10.230.10,G3DSA:2.60.260.20,G3DSA:2.60.260.20	SSF57938,SSF49493,SSF49493,SSF49493,SSF46565	307~312								
aly925.3	Corticotropin-releasing factor-binding protein	GO:0042445,GO:0051424,GO:0005576,GO:0005615,GO:0042562	CG15537-PB						PF05428														
aly925.30	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	GO:0004367,GO:0005737,GO:0031430,GO:0005975,GO:0006650,GO:0009331,GO:0046168,GO:0006127,GO:0051287,GO:0006641,GO:0005811,GO:0007629,GO:0030018,GO:0006072,GO:0055114,GO:0042803	CG9042-PF			PIRSF000114		TIGR03376	PF07479,PF01210		PR00077,PR00077,PR00077,PR00077,PR00077,PR00077	PS00957	G3DSA:3.40.50.720,G3DSA:1.10.1040.10	SSF51735,SSF48179		00564+1.1.1.94,00564+1.1.1.8		PWY-6118,PWY-7385,PWY-5981,PWY-7411,PWY-5667	UPA00940				
aly925.31	Methionyl-tRNA formyltransferase, mitochondrial	GO:0006996,GO:0070124,GO:0004479,GO:0005739,GO:0016742,GO:0071951,GO:0009058,GO:0032543	CG1750-PA					TIGR00460	PF00551,PF02911				G3DSA:3.40.50.170,G3DSA:3.10.25.10	SSF53328,SSF50486		00670+2.1.2.9,00970+2.1.2.9							
aly925.32	Opsin Rh3	GO:0008020,GO:0004930,GO:0009584,GO:0009589,GO:0016021,GO:0007601,GO:0018298,GO:0007602,GO:0007604,GO:0007186,GO:0016039	CG5638-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237,PR00577,PR00577,PR00577,PR00577,PR00577,PR00238,PR00238,PR00238	PS00237,PS00238	G3DSA:1.20.1070.10	SSF81321			REACT_14797						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly925.33	Unknown	GO:0008020,GO:0007186,GO:0016021,GO:0007601	CG5638-PA																				
aly925.34	Acetylcholine receptor subunit alpha-like	GO:0006810,GO:0016021,GO:0005230,GO:0016020,GO:0015464,GO:0005892,GO:0045211,GO:0004889,GO:0006811,GO:0030054	CG12414-PC					TIGR00860	PF02931,PF02932		PR00252,PR00252,PR00252,PR00252,PR00254,PR00254,PR00254,PR00254	PS00236	G3DSA:2.70.170.10,G3DSA:1.20.120.370,G3DSA:1.20.120.370	SSF90112,SSF90112,SSF63712			REACT_13685						
aly925.35	Unknown		n/a												128~152								
aly925.36	Multiple epidermal growth factor-like domains protein 11	GO:0006909,GO:0035212,GO:0035071,GO:0043652,GO:0008345,GO:0016021,GO:0016322,GO:0016323,GO:0010842,GO:0034109,GO:0042742,GO:0005515,GO:0043277,GO:0007155,GO:0048190,GO:0001786,GO:0031224	CG2086-PE				SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00180,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181,SM00181		PF00053,PF00053,PF00053,PF00053,PF00053,PF00053	PS50027,PS50026,PS50026,PS50027,PS50027,PS50027,PS50026,PS50026,PS50026,PS51041,PS50026,PS50026,PS50027,PS50027,PS50026,PS50027	PR00011,PR00011,PR00011	PS00022,PS00022,PS00022,PS00022,PS00022,PS00022,PS00022,PS00022,PS00022,PS00022,PS00022,PS00022,PS00022,PS00022	G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.170.300.10,G3DSA:2.10.25.10									
aly925.37	Unknown	GO:0016325,GO:0008569,GO:0051493,GO:0008407,GO:0007309	CG12114-PB												210~244,161~181								
aly925.38	39S ribosomal protein L32, mitochondrial	GO:0003735,GO:0006412,GO:0005762	CG12220-PA											SSF57829									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly925.39	Decaprenyl-diphosphate synthase subunit 1	GO:0046982,GO:0000010,GO:0006744,GO:1990234,GO:0014019,GO:0051290,GO:0008299,GO:0043066,GO:0044281,GO:0033554,GO:0050347,GO:0005759,GO:0046872	CG31005-PA						PF00348			PS00444,PS00723	G3DSA:1.10.600.10	SSF48576									
aly925.4	Unknown	GO:0003674,GO:0008150,GO:0005887	CG15538-PB						PF07898														
aly925.40	Unknown		n/a																				
aly925.41	Unknown		n/a																				
aly925.42	Unknown		n/a																				
aly925.43	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly925.44	Zinc finger protein 554	GO:0000122,GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG5683-PD				SM00355,SM00355,SM00355,SM00355		PF12171,PF13894	PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly925.5	Serine protease nudel	GO:0004252,GO:0007306,GO:0007343,GO:0009950,GO:0016485,GO:0005576,GO:0007313,GO:0005515,GO:0007310,GO:0008063,GO:0006508,GO:0008233,GO:0005578,GO:0008236	CG10129-PA				SM00020,SM00192,SM00192,SM00192,SM00192,SM00192,SM00192		PF00089,PF09342,PF00057	PS50068,PS50068,PS50068,PS50068,PS50068,PS50287,PS50240,PS50068,PS50068,PS50287	PR00261,PR00261,PR00261,PR00261,PR00261,PR00261	PS00134,PS01209,PS01209,PS00135,PS01209,PS01209	G3DSA:4.10.400.10,G3DSA:2.40.10.10,G3DSA:4.10.400.10,G3DSA:2.40.10.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.40.10.10	SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF50494,SSF57424,SSF50494,SSF57424										
aly925.6	Venom allergen 3	GO:0008150,GO:0005576,GO:0003674	CG8483-PA				SM00198		PF00188		PR00838,PR00838,PR00838,PR00838,PR00837,PR00837,PR00837,PR00837	PS01009,PS01010	G3DSA:3.40.33.10	SSF55797									
aly925.7	Unknown		n/a												35~55								
aly925.8	Lachesin	GO:0004714,GO:0005515,GO:0005886,GO:0007155,GO:0007169,GO:0031225	CG14010-PD				SM00408,SM00408,SM00408,SM00409,SM00409,SM00409		PF07679,PF07686,PF13927	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly925.9	Signal peptidase complex catalytic subunit SEC11C	GO:0005787,GO:0016021,GO:0016020,GO:0006465,GO:0008233,GO:0005789,GO:0008236	CG2358-PA					TIGR02228	PF00717		PR00728,PR00728	PS00501,PS00761	G3DSA:2.10.109.10	SSF51306			REACT_15380						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9265.1	Chorion class A protein Ld19	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a																				
aly9265.2	Chorion class CB protein PC404 (Fragment)	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														
aly9265.3	Chorion class CB protein PC404 (Fragment)	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														
aly9265.4	Chorion class B protein Ld34	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														
aly9265.5	Chorion class CB protein M5H4	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														
aly9265.6	Chorion class CB protein PC404 (Fragment)	GO:0042600,GO:0007304,GO:0007275,GO:0005213	n/a						PF01723														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly927.1	DE-cadherin	GO:0035147,GO:0016318,GO:0008105,GO:0007507,GO:0016337,GO:0042078,GO:0008258,GO:0030031,GO:0016339,GO:0035160,GO:0017022,GO:0048103,GO:0035019,GO:0007163,GO:0004872,GO:0001748,GO:0005887,GO:0007411,GO:0007298,GO:0001745,GO:0071907,GO:0008354,GO:0003151,GO:0002009,GO:0030708,GO:0045176,GO:0000902,GO:0008356,GO:0016021,GO:0016020,GO:0030720,GO:0050839,GO:0005509,GO:0098730,GO:0048477,GO:0042803,GO:0007506,GO:0016342,GO:0035212,GO:0007424,GO:0007314,GO:0042060,GO:0007281,GO:0007280,GO:0005915,GO:0005914,GO:0005913,GO:0005938,GO:0007409,GO:0005886,GO:0007155,GO:0044331,GO:0007156,GO:0036099,GO:0001738,GO:0007297,GO:0035099,GO:0007370,GO:0008406,GO:0007420,GO:0007399,GO:0008013,GO:0050832,GO:0030175,GO:0045186,GO:0007379,GO:0035262,GO:0010004,GO:0007435,GO:0005515,GO:0043296,GO:0005912	CG3722-PA				SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00282		PF00028,PF00028,PF00028,PF00028,PF00028,PF00028,PF02210,PF01049	PS50268,PS50268,PS50268,PS50268,PS50268,PS50025,PS50268,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00232,PS00232,PS00022,PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.120.200,G3DSA:2.60.40.60,G3DSA:4.10.900.10	SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49899,SSF49313,SSF49313,SSF49313,SSF49313									
aly927.2	Spondin-1	GO:0007155,GO:0005578,GO:0005576,GO:0005615,GO:0004867	CG17739-PA						PF06468,PF02014	PS51020,PS51019													
aly927.3	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly92756.1	Potassium voltage-gated channel protein Shaw	GO:0071805,GO:0006813,GO:0016021,GO:0051260,GO:0008076,GO:0022843,GO:0005249,GO:0005886,GO:0005251,GO:0055085,GO:0030431	CG34366-PC						PF02214				G3DSA:3.30.710.10	SSF54695									
aly9292.1	Protein diaphanous	GO:0008104,GO:0030589,GO:0090303,GO:0017048,GO:0007349,GO:0007279,GO:0045448,GO:0003383,GO:0005912,GO:0051225,GO:0005737,GO:0045177,GO:0045010,GO:0030838,GO:0000281,GO:0005546,GO:0003779,GO:0009306,GO:0016476,GO:0043234,GO:0032507,GO:0030029,GO:0007424,GO:0007605,GO:0032154,GO:0035011,GO:0007283,GO:0051489,GO:0005938,GO:0012506,GO:0022008,GO:0005826,GO:0007111,GO:0007110,GO:0007015,GO:0000915,GO:0005856,GO:0031532,GO:0097320,GO:0005515,GO:0000910,GO:0005884	CG1768-PD				SM00498		PF02181	PS51444				SSF101447	156~176									
aly93.1	Unknown		n/a																				
aly93.10	Homeobox protein Hox-A1 (Fragment)	GO:0043565,GO:0030154,GO:0007494,GO:0007420,GO:0006355,GO:0003700,GO:0005634,GO:0001709,GO:0003705,GO:0009790,GO:0006357,GO:0045944,GO:0006351,GO:0003677,GO:0046982,GO:0035284,GO:0007275	CG1264-PA				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly93.11	Cuticle protein 7	GO:0005214,GO:0040003,GO:0031012,GO:0042302,GO:0008010	CG15007-PA						PF00379	PS51155	PR00947,PR00947,PR00947	PS00233											
aly93.12	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	GO:0045254,GO:0004739,GO:0006086,GO:0005811,GO:0005739,GO:0031122,GO:0005759,GO:0006096,GO:0006090,GO:0005875	CG11876-PD				SM00861		PF02779,PF02780				G3DSA:3.40.50.970,G3DSA:3.40.50.920	SSF52518,SSF52922									
aly93.13	Neuropeptide FF receptor 1	GO:0008528,GO:0004930,GO:0042277,GO:0016021,GO:0007268,GO:0007218,GO:0004983,GO:0032870,GO:1901652,GO:0005887,GO:0008188,GO:0008340,GO:0007186	CG10823-PA						PF00001	PS50262	PR00237,PR00237		G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly93.14	Neuropeptide FF receptor 2	GO:0009582,GO:0008528,GO:0004930,GO:0042277,GO:0015629,GO:2000479,GO:0045761,GO:0016021,GO:0005886,GO:0007218,GO:0004983,GO:0032870,GO:0007268,GO:1901652,GO:0005887,GO:0008188,GO:0008340,GO:0007186,GO:0043408	CG10823-PA						PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR01012,PR01012,PR01012	PS00237	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly93.15	Cadherin-89D	GO:0016339,GO:0016020,GO:0005509,GO:0005887,GO:0005886,GO:0007155,GO:0044331,GO:0007156,GO:0016021	CG14900-PB				SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112,SM00112		PF00028,PF00028,PF00028,PF00028,PF00028,PF00028	PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268,PS50268	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00232,PS00232,PS00232,PS00232,PS00232,PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60	SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly93.16	Unknown	GO:0008445,GO:0005777,GO:0055114	CG12338-PA										G3DSA:3.40.50.720										
aly93.17	Facilitated trehalose transporter Tret1-2 homolog	GO:0005355,GO:0022891,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083					SSF103473,SSF103473	69~89								
aly93.18	Protein transport protein sft2	GO:0005794,GO:0016192,GO:0006895,GO:0016021,GO:0000329,GO:0000139,GO:0006886,GO:0042802	CG33635-PA						PF04178														
aly93.19	Unknown		n/a																				
aly93.2	D-aspartate oxidase	GO:0008445,GO:0005777,GO:0055114	CG12338-PA			PIRSF000189			PF01266				G3DSA:3.40.50.720,G3DSA:3.40.50.720,G3DSA:3.40.50.720	SSF51971,SSF51971,SSF54373									
aly93.20	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly93.21	Unknown		n/a																				
aly93.22	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG4797-PB						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473									
aly93.23	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0005886,GO:0055085	CG4797-PB						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473	236~256								
aly93.3	Unknown	GO:0022008,GO:0046872	CG11317-PB				SM00355,SM00355		PF12874	PS50157		PS00028,PS00028		SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly93.4	Fragile X mental retardation syndrome-related protein 1 homolog A	GO:0016319,GO:0050808,GO:0007269,GO:0035068,GO:0008582,GO:0007614,GO:0007268,GO:0050807,GO:0007279,GO:0045886,GO:0045448,GO:0007294,GO:0007411,GO:0051028,GO:0007413,GO:0007416,GO:0008355,GO:0005737,GO:0007517,GO:0008049,GO:0042331,GO:0005634,GO:0005811,GO:0007349,GO:0007616,GO:0043621,GO:0050802,GO:0003723,GO:0042127,GO:0050976,GO:0030154,GO:0007623,GO:0006935,GO:0050774,GO:0017148,GO:0007528,GO:0003729,GO:0045475,GO:0007409,GO:0007310,GO:0007288,GO:0008345,GO:0048134,GO:0040011,GO:0007281,GO:0031507,GO:0007420,GO:0048813,GO:0048812,GO:0048814,GO:0005515,GO:0051964,GO:0006417,GO:0051823,GO:0016442,GO:0009794	CG6203-PG				SM00322,SM00322		PF05641,PF00013,PF00013,PF12235	PS50084,PS51641,PS51641,PS50084			G3DSA:3.30.1370.10,G3DSA:3.30.1370.10	SSF54791,SSF54791	544~564,193~213,358~378								
aly93.5	Probable GDP-L-fucose synthase	GO:0050662,GO:0033227,GO:0016853,GO:0042356,GO:0042350,GO:0042351,GO:0005575,GO:0050577	CG3495-PA						PF01370				G3DSA:3.40.50.720	SSF51735									
aly93.6	Phenylalanine-tRNA ligase alpha subunit B	GO:0005737,GO:0004826,GO:0000049,GO:0006432,GO:0009328,GO:0005524	CG2263-PA						PF01409,PF01409	PS50862			G3DSA:3.30.930.10,G3DSA:3.30.930.10	SSF55681		00970+6.1.1.20	REACT_71						
aly93.7	Saccharopine dehydrogenase like oxidoreductase	GO:0005811,GO:0005634,GO:0016020,GO:0030496,GO:0035220,GO:0022416,GO:0005739,GO:0055114,GO:0016491	CG2604-PA						PF03435				G3DSA:3.40.50.720	SSF51735									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly93.8	Saccharopine dehydrogenase like oxidoreductase	GO:0022416,GO:0055114,GO:0005811,GO:0035220,GO:0016491	CG2604-PA																				
aly93.9	Saccharopine dehydrogenase like oxidoreductase	GO:0005811,GO:0005634,GO:0016020,GO:0030496,GO:0035220,GO:0022416,GO:0005739,GO:0055114,GO:0016491	CG2604-PA						PF03435				G3DSA:3.40.50.720	SSF51735									
aly93061.1	Unknown		n/a																				
aly93081.1	Histone acetyltransferase KAT2A	GO:0021537,GO:1990090,GO:0031647,GO:0035066,GO:0003713,GO:0022037,GO:0031667,GO:0035264,GO:0007412,GO:0010485,GO:0010484,GO:0044154,GO:0000124,GO:0007517,GO:0001701,GO:0005615,GO:0000123,GO:0071929,GO:0005634,GO:0055007,GO:0004402,GO:0048813,GO:0043997,GO:0030914,GO:0033276,GO:0005671,GO:1903955,GO:0014070,GO:0016573,GO:0001843,GO:0031346,GO:0042826,GO:0016578,GO:0006351,GO:0048312,GO:1903146,GO:0043966,GO:0043967,GO:0008134,GO:0000790,GO:0072686,GO:0001756,GO:0008283,GO:0008080,GO:0006338,GO:0035948,GO:0043983,GO:0071356,GO:0005703,GO:0005700,GO:0006355,GO:0016407,GO:0030901,GO:0007399,GO:0003682,GO:2000679	CG4107-PA						PF13508	PS51186			G3DSA:3.40.630.30	SSF55729									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly93091.1	Unknown		n/a																				
aly9313.1	Unknown	GO:0016198,GO:0005576,GO:0003674,GO:0005887,GO:0007155,GO:0007157,GO:0007415	CG7644-PA																				
aly93177.1	Unknown		n/a																				
aly9336.1	Unknown		n/a																				
aly93434.1	Unknown	GO:0003676	n/a											SSF53098									
aly9349.1	Transcriptional repressor scratch 2	GO:0000122,GO:0005634,GO:0006351,GO:0003676,GO:0003677,GO:2001222,GO:0046872	CG7691-PA				SM00355,SM00355,SM00355			PS50157,PS50157,PS50157		PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9349.2	TLD domain-containing protein 1	GO:0005923,GO:0005198	CG5149-PA				SM00584		PF07534				G3DSA:1.10.238.10										
aly9349.3	26S protease regulatory subunit 8	GO:0005737,GO:0016787,GO:0004175,GO:0005838,GO:0043161,GO:0005634,GO:0017111,GO:0006974,GO:0006511,GO:0030163,GO:0016887,GO:0000502,GO:0006508,GO:0005875,GO:0005524,GO:0008540	CG1489-PA				SM00382	TIGR01242	PF00004			PS00674	G3DSA:1.10.8.60,G3DSA:3.40.50.300	SSF52540	24~65		REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045						
aly9349.4	Putative vitellogenin receptor	GO:0006898,GO:0048477,GO:0016021,GO:0005886,GO:0007296,GO:0005509,GO:0005515,GO:0031410,GO:0030135,GO:0008196	CG1372-PB				SM00179,SM00179,SM00192,SM00192,SM00192,SM00192,SM00181,SM00181,SM00181,SM00181,SM00135,SM00135,SM00135		PF07645,PF00057,PF00057	PS50026,PS50068,PS50068,PS50068,PS50068,PS50068	PR00261,PR00261,PR00261,PR00261,PR00261	PS01187,PS00010,PS01209,PS01209,PS01186,PS01209,PS01209	G3DSA:2.120.10.30,G3DSA:4.10.400.10,G3DSA:2.120.10.30,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:4.10.400.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57424,SSF57196,SSF63825										
aly9349.5	Putative vitellogenin receptor	GO:0006898,GO:0048477,GO:0016021,GO:0005886,GO:0007296,GO:0005509,GO:0031410,GO:0030135,GO:0008196	CG1372-PB				SM00181,SM00181,SM00181,SM00135,SM00135,SM00135,SM00135,SM00135,SM00135,SM00179		PF00058	PS51120,PS51120,PS51120,PS51120,PS51120		PS01187	G3DSA:2.120.10.30,G3DSA:2.120.10.30,G3DSA:2.10.25.10,G3DSA:2.10.25.10	SSF63825,SSF63825,SSF57196									
aly9349.6	Trifunctional enzyme subunit beta, mitochondrial	GO:0042645,GO:0003988,GO:0006635,GO:0070062,GO:0044822,GO:0005811,GO:0005739,GO:0005743,GO:0005741,GO:0016747,GO:0008152,GO:0008340,GO:0016507,GO:0005783,GO:0005875,GO:0016509	CG4581-PA						PF00108			PS00098	G3DSA:3.40.47.10,G3DSA:3.40.47.10	SSF53901			REACT_22258						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly935.1	Unknown		n/a												158~178								
aly935.2	Talin-1	GO:0005200,GO:0006909,GO:0015629,GO:0060439,GO:0035160,GO:0007044,GO:0007298,GO:0005925,GO:0005737,GO:0001726,GO:0070062,GO:0007430,GO:0007475,GO:0003779,GO:0016203,GO:0005178,GO:0009986,GO:0005158,GO:0008360,GO:0045892,GO:0030274,GO:0005886,GO:0007155,GO:0032587,GO:0007526,GO:0007016,GO:0005815,GO:0030866,GO:0017166,GO:0005515,GO:0070527	CG6831-PB										G3DSA:1.20.1440.10		578~601								
aly935.3	Vinculin	GO:0005737,GO:0007160,GO:0007016,GO:0006909,GO:0015629,GO:0051015,GO:0005198,GO:0003779,GO:0048812,GO:0005886,GO:0007155,GO:0005925	CG3299-PA						PF01044,PF01044		PR00806,PR00806,PR00806,PR00806		G3DSA:1.20.120.230,G3DSA:1.20.120.230	SSF47220,SSF47220,SSF47220									
aly935.4	Apolipophorins	GO:0005319,GO:0005501,GO:0005811,GO:0005615,GO:0020037,GO:0006869,GO:0008017,GO:0016055,GO:0019841,GO:0008289,GO:0007224,GO:0030139,GO:0005576,GO:0045178,GO:0006810,GO:0005504,GO:0005102,GO:0005198,GO:0005875	CG11064-PA				SM00638,SM00216		PF00094,PF09172,PF01347,PF06448	PS51233,PS51211			G3DSA:2.20.80.10,G3DSA:2.20.50.20,G3DSA:2.20.50.20,G3DSA:1.25.10.20,G3DSA:2.30.230.10	SSF56968,SSF58113,SSF58113,SSF56968,SSF48431	2630~2650,2377~2397		REACT_22258							
aly935.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly935.6	Talin-2	GO:0005200,GO:0006909,GO:0015629,GO:0060439,GO:0035160,GO:0045202,GO:0007298,GO:0005925,GO:0005737,GO:0001726,GO:0007430,GO:0007475,GO:0003779,GO:0016203,GO:0005178,GO:0005158,GO:0005916,GO:0008360,GO:0045892,GO:0005886,GO:0007155,GO:0007526,GO:0007016,GO:0005856,GO:0005515	CG6831-PB						PF09379															
aly935.7	Unknown	GO:0001726,GO:0005200,GO:0005925,GO:0007016	n/a						PF09141				G3DSA:1.20.1420.10	SSF109880									
aly935.8	Unknown		n/a										G3DSA:1.20.1440.10		119~139								
aly935.9	Unknown		n/a						PF16511														
aly93711.1	Fructose-bisphosphate aldolase	GO:0031430,GO:0007498,GO:0005829,GO:0003824,GO:0004332,GO:0007095,GO:0006096,GO:0030018	CG6058-PE						PF00274			PS00158	G3DSA:3.20.20.70	SSF51569		00030+4.1.2.13,00710+4.1.2.13,00010+4.1.2.13,00051+4.1.2.13,00680+4.1.2.13	REACT_474	PWY-1042,PWY-6142,PWY-5484,PWY-1861,PWY-7385	UPA00109				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly939.1	Trans-Golgi network integral membrane protein 2	GO:0005794,GO:0016021,GO:0005802,GO:0005654,GO:0005886,GO:0030133	n/a																				
aly939.10	Probable ATP-dependent RNA helicase pitchoune	GO:0016049,GO:0008152,GO:0005730,GO:0005634,GO:0008283,GO:0004004,GO:0003724,GO:0003723,GO:0003676,GO:0005524	CG6375-PB				SM00487		PF00270	PS51192,PS51195		PS00039	G3DSA:3.40.50.300	SSF52540									
aly939.11	Modifier of mdg4	GO:0016311,GO:0000785,GO:0003677,GO:0007060,GO:0008354,GO:0007141,GO:0005730,GO:0006325,GO:0010032,GO:0005634,GO:0046872,GO:0048477,GO:0042803,GO:0006915,GO:0000794,GO:0005886,GO:0001672,GO:0008195,GO:0005704,GO:0005700,GO:0006355,GO:0006351,GO:0005515,GO:0031208,GO:0003682,GO:0016568	CG32491-PT				SM00225		PF00651,PF13842	PS50097			G3DSA:3.30.710.10	SSF54695									
aly939.12	Lachesin	GO:0007424,GO:0016331,GO:0035151,GO:0043005,GO:0005767,GO:0009986,GO:0019991,GO:0035160,GO:0042803,GO:0005918,GO:0061343,GO:0005515,GO:0005886,GO:0016337,GO:0007156,GO:0043025,GO:0031225	CG40378-PB				SM00408,SM00408,SM00408,SM00406,SM00406,SM00409,SM00409,SM00409		PF07679,PF07679,PF07679	PS50835,PS50835,PS50835		PS00290	G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly939.13	Lachesin	GO:0007424,GO:0016331,GO:0035151,GO:0050767,GO:0009986,GO:0019991,GO:0035160,GO:0042803,GO:0005918,GO:0061343,GO:0043005,GO:0005886,GO:0016337,GO:0007156,GO:0043025,GO:0031225	CG40378-PB				SM00408,SM00408,SM00409,SM00409,SM00409		PF07679,PF07679	PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly939.2	Unknown		n/a																				
aly939.3	Unknown		n/a																				
aly939.4	Lachesin	GO:0007424,GO:0016331,GO:0035151,GO:0043005,GO:0050767,GO:0009986,GO:0019991,GO:0035160,GO:0042803,GO:0005918,GO:0061343,GO:0005515,GO:0005886,GO:0016337,GO:0007156,GO:0043025,GO:0031225	CG31646-PA			PIRSF000615	SM00409,SM00409,SM00409,SM00408,SM00408,SM00408		PF07679,PF07679,PF07679	PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726									
aly939.5	WD repeat-containing protein 36	GO:0034388,GO:0032040,GO:0005730,GO:0044822,GO:0007601,GO:0006364,GO:0005515,GO:0030516,GO:0001895,GO:0050896	CG9799-PA				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF04192	PS50294,PS50082		PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10	SSF50978,SSF50978,SSF50978	883~889								
aly939.6	Splicing factor 3A subunit 3	GO:0051726,GO:0071011,GO:0071013,GO:0009566,GO:0000398,GO:0051533,GO:0005654,GO:0007052,GO:0008270,GO:0003676,GO:0005686,GO:0007067,GO:0006397,GO:0044822,GO:0005681,GO:0003723	CG2925-PA						PF16837,PF12108,PF13297														
aly939.7	Glucosidase 2 subunit beta	GO:0017177,GO:0001701,GO:0005783,GO:0006491,GO:0051291,GO:0051219,GO:0006807,GO:0046331,GO:0001889,GO:0005509,GO:0005515,GO:0005080,GO:0010977,GO:0044325,GO:0004558,GO:0072001,GO:0003723	CG6453-PA						PF13015,PF13202,PF13202,PF12999	PS50222,PS50222		PS00018,PS00018	G3DSA:4.10.400.10,G3DSA:2.70.130.10,G3DSA:4.10.400.10,G3DSA:1.10.238.10	SSF50911,SSF47473,SSF57424	183~255								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly939.8	ATP-dependent RNA helicase DDX18	GO:0016020,GO:0016049,GO:0005730,GO:0005634,GO:0008283,GO:0004004,GO:0003724,GO:0003676,GO:0010501,GO:0044822,GO:0005524	CG6375-PB				SM00487,SM00490		PF00270,PF00271	PS51194,PS51195,PS51192		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540										
aly939.9	Probable ATP-dependent RNA helicase pitchoune	GO:0016049,GO:0008152,GO:0005730,GO:0005634,GO:0008283,GO:0004004,GO:0003724,GO:0003723,GO:0003676,GO:0005524	CG6375-PB				SM00490,SM00487		PF13959,PF00270,PF00271	PS51195,PS51192,PS51194		PS00039	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540	81~101								
aly9435.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0015771,GO:0016021,GO:0022857,GO:0005886,GO:0055085	CG4797-PB						PF00083	PS50850			G3DSA:1.20.1250.20	SSF103473									
aly94414.1	Contactin-associated protein-like 2	GO:0019226,GO:0042297,GO:0031175,GO:0007612,GO:0030425,GO:0030424,GO:0021761,GO:0043204,GO:0016021,GO:0016020,GO:0044224,GO:0043025,GO:0071625,GO:0005794,GO:0035176,GO:0009986,GO:0008076,GO:0008038,GO:0019899,GO:0004867,GO:0007155,GO:0045163,GO:0030534,GO:0030673,GO:0071205,GO:0005576,GO:0005769	CG43225-PG											SSF56496									
aly9443.1	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG4302-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9443.2	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152,GO:0050488	CG8652-PA						PF00201				G3DSA:3.40.50.2000	SSF53756									
aly9443.3	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG15661-PA						PF00201			PS00375	G3DSA:3.40.50.2000	SSF53756,SSF53756									
aly9443.4	Ecdysteroid UDP-glucosyltransferase	GO:0016758,GO:0015020,GO:0008152	CG6475-PD						PF00201,PF00201				G3DSA:3.40.50.2000	SSF53756									
aly945.1	Membrane-associated transporter protein	GO:0045177,GO:0008506,GO:0015770,GO:0031410,GO:0016021,GO:0007601,GO:0048066,GO:0050896,GO:0042438,GO:0008515,GO:0033162	CG4484-PA										G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473									
aly945.10	Exosome complex exonuclease RRP44	GO:0071027,GO:0005085,GO:0090305,GO:0000288,GO:0043547,GO:0005634,GO:0016020,GO:0005654,GO:0010467,GO:0006364,GO:0005652,GO:0006402,GO:0010468,GO:0071034,GO:0022008,GO:0043928,GO:0090503,GO:0000178,GO:0016075,GO:0004519,GO:0005829,GO:0000176,GO:0000177,GO:0000175,GO:0003723,GO:0006397	CG6413-PA				SM00955		PF00773			PS01175		SSF50249,SSF50249									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly945.2	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0030672,GO:0016021,GO:0007268,GO:0022857,GO:0001669,GO:0006836,GO:0055085,GO:0030054	CG3168-PC						PF07690	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473,SSF103473,SSF103473									
aly945.3	Charged multivesicular body protein 5	GO:0032509,GO:0046426,GO:0007034,GO:0000815,GO:0030713,GO:0060429,GO:0050680,GO:0007293,GO:0003674,GO:0015031,GO:0045807	CG6259-PA						PF03357						65~92,21~55,125~148								
aly945.4	Thiamin pyrophosphokinase 1	GO:0006772,GO:0030975,GO:0005829,GO:0016301,GO:0004788,GO:0009229,GO:0005524	CG14721-PA				SM00983	TIGR01378	PF04263,PF04265				G3DSA:2.60.120.320,G3DSA:3.40.50.10240	SSF63862,SSF63999		00730+2.7.6.2		PWY-6907,PWY-6898,PWY-6908	UPA00060				
aly945.5	V-type proton ATPase 116 kDa subunit a isoform 1	GO:0005737,GO:0005794,GO:0070072,GO:0015986,GO:0070062,GO:0015991,GO:0051117,GO:0016021,GO:0005654,GO:1901998,GO:0033181,GO:0030659,GO:0000220,GO:0007035,GO:0046961,GO:0005886,GO:0016471,GO:0042470,GO:0043231	CG18617-PB			PIRSF001293			PF01496						828~836,94~121								
aly945.6	Tetratricopeptide repeat protein 21B	GO:0005737,GO:0005856,GO:0030991,GO:0072372,GO:0021591,GO:0035721,GO:0060271,GO:0006357,GO:0006996,GO:0061512,GO:0008589,GO:0007224,GO:0097542,GO:0000790,GO:0021798,GO:0035735,GO:0005515,GO:0005929	n/a				SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028,SM00028		PF14559,PF07719,PF00515,PF00515	PS50293,PS50005,PS50293,PS50293,PS50293,PS50005,PS50293,PS50005,PS50293,PS50005,PS50005,PS50005,PS50005,PS50005			G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10,G3DSA:1.25.40.10	SSF48452,SSF48452,SSF48452,SSF48452,SSF48452,SSF48452	770~790,994~1017								
aly945.7	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly945.8	Unknown	GO:0007476	CG42268-PI																				
aly945.9	Unknown	GO:0004144	CG33120-PA						PF06974							00561+2.3.1.20,00073+2.3.1.20			UPA00282				
aly94873.1	LINE-1 type transposase domain-containing protein 1		n/a																				
aly95020.1	Unknown		n/a																				
aly95029.1	Unknown		n/a																				
aly95180.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly954.1	Unknown	GO:0035075,GO:0046872,GO:0003700,GO:0005634,GO:0007552,GO:0006355,GO:0010977,GO:0003676,GO:0045316	CG45074-PB				SM00384,SM00384,SM00384,SM00355,SM00355		PF02178,PF02178,PF02178	PS50157	PR00929,PR00929,PR00929	PS00028	G3DSA:3.30.160.60	SSF57667										
aly954.2	Nucleolysin TIA-1 isoform p40	GO:0005737,GO:0010494,GO:0097165,GO:0044822,GO:0006915,GO:0000166,GO:0017091,GO:0008143,GO:0017148,GO:0003676,GO:0042036,GO:0048024,GO:0005654,GO:0003729	CG34354-PF				SM00360,SM00360,SM00360,SM00361,SM00361		PF00076,PF00076	PS50102,PS50102			G3DSA:3.30.70.330,G3DSA:3.30.70.330	SSF54928,SSF54928									
aly954.3	Unknown		n/a																				
aly95415.1	Unknown		n/a						PF14680														
aly95430.1	Unknown		n/a																				
aly95447.1	Unknown	GO:0016021,GO:0006810,GO:0000062	CG14232-PA																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly956.1	Unknown		n/a										G3DSA:3.40.50.720,G3DSA:3.90.180.10	SSF51735,SSF50129									
aly956.2	Protein EFR3 homolog cmp44E	GO:0016079,GO:0016021,GO:0005886,GO:0000281,GO:0005623,GO:0007602,GO:0045202,GO:0007268,GO:0030100,GO:0048488	CG8739-PC										G3DSA:1.25.10.10,G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371									
aly956.3	Unknown		CG8740-PD												1370~1370								
aly956.4	Cyclin-L2	GO:0016607,GO:0016538,GO:0005634,GO:0005730,GO:0019901,GO:0006355,GO:0030054,GO:0022008,GO:0000079,GO:0006396,GO:0006351	CG16903-PA			PIRSF036580	SM00385,SM00385		PF00134				G3DSA:1.10.472.10,G3DSA:1.10.472.10	SSF47954,SSF47954	294~314								
aly957.1	Protein toll	GO:0009897,GO:0007416,GO:0019732,GO:0019730,GO:0006963,GO:0019955,GO:0006967,GO:0007165,GO:0008063,GO:0006955,GO:0005737,GO:0070976,GO:0016021,GO:0009617,GO:0000281,GO:0010508,GO:0002229,GO:0042802,GO:0016201,GO:0009880,GO:0008329,GO:0007507,GO:0045087,GO:0035172,GO:0050832,GO:0050830,GO:0005886,GO:0007155,GO:0007352,GO:0043234,GO:0006952,GO:0051607,GO:0002752,GO:0009950,GO:0009620,GO:0046790,GO:0004888,GO:0045944,GO:0005515,GO:0030097,GO:0045610,GO:0005769,GO:0035007	CG8595-PA				SM00364,SM00364,SM00364,SM00364,SM00364,SM00364,SM00013,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00365,SM00255,SM00369		PF13855,PF13855,PF13855,PF13855,PF13306,PF01582	PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS50104,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450,PS51450	G3DSA:3.40.50.10140,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.80.10.10	SSF52058,SSF52058,SSF52058,SSF52058,SSF52200,SSF52058								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly957.2	Unknown		n/a																				
aly957.3	Circadian clock-controlled protein	GO:0007623,GO:0005615,GO:0032504	CG10407-PA				SM00700		PF06585														
aly957.4	Unknown	GO:0005615,GO:0032504	CG10407-PA						PF06585														
aly957.5	Protein takeout	GO:0007631,GO:0007623,GO:0005615,GO:0032504,GO:0007617,GO:0005576,GO:0042594,GO:0042595,GO:0008343,GO:0008049,GO:0007622	CG10407-PA						PF06585														
aly9588.1	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6467-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9588.10	TFIIH basal transcription factor complex helicase XPD subunit	GO:0008022,GO:0001113,GO:0001111,GO:0000439,GO:0009411,GO:1901990,GO:0003677,GO:0006283,GO:0035315,GO:0005737,GO:0005819,GO:0005634,GO:0033683,GO:0006367,GO:0043141,GO:0007059,GO:0007088,GO:0005524,GO:0006468,GO:0006915,GO:0047485,GO:0004003,GO:0032508,GO:0006366,GO:0006289,GO:0006974,GO:0010972,GO:0045893,GO:0005675,GO:0004386,GO:0006979,GO:0051983,GO:0046872,GO:0051539,GO:0071817,GO:0005705,GO:0005703,GO:0005700,GO:0045944,GO:0000990,GO:0043139	CG9433-PA				SM00488,SM00491	TIGR00604	PF06777,PF06733,PF13307	PS51193	PR00852,PR00852,PR00852,PR00852,PR00852,PR00852,PR00852	PS00690	G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540	80~100,256~276								
aly9588.11	Probable ATP-dependent RNA helicase YTHDC2	GO:0005737,GO:0030718,GO:0070063,GO:0005783,GO:0000900,GO:0034612,GO:0006396,GO:0044822,GO:0044829,GO:0004004,GO:0004386,GO:0007281,GO:0007283,GO:0007282,GO:0007284,GO:0005524,GO:0045478,GO:0008186,GO:0048477,GO:0070555,GO:0007140	CG30170-PA				SM00393,SM00490,SM00847,SM00487,SM00248,SM00248		PF00271,PF07717,PF01424,PF04408	PS51192,PS51194,PS51061,PS50297,PS50088			G3DSA:3.30.1370.50,G3DSA:3.40.50.300,G3DSA:1.25.40.20,G3DSA:3.40.50.300	SSF48403,SSF52540,SSF52540,SSF82708	1366~1386								
aly9588.12	RNA-binding protein NOB1	GO:0022008,GO:0046872,GO:0005634	CG2972-PA			PIRSF037125			PF08772					SSF144206	182~202								
aly9588.13	UPF0528 protein CG10038	GO:0005575,GO:0003674,GO:0008150	CG10038-PA						PF09757				G3DSA:3.40.50.1820	SSF53474									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9588.14	Syntaxin-18	GO:0007269,GO:1903358,GO:0005789,GO:0031594,GO:0005484,GO:0007274,GO:0031201,GO:0005783,GO:0016021,GO:1902117,GO:0006886,GO:1902953,GO:0007528,GO:0005938,GO:0061025,GO:0005886,GO:0090158,GO:0006890,GO:0016192,GO:0000139,GO:0000149,GO:0019904	CG13626-PA						PF10496						219~246									
aly9588.15	m7GpppN-mRNA hydrolase	GO:0005737,GO:0016787,GO:0010603,GO:0000184,GO:0071044,GO:0035195,GO:0005634,GO:0000932,GO:0030145,GO:0000956,GO:0000290,GO:0050072,GO:0003723,GO:0005515,GO:0006402	CG6169-PE						PF00293,PF05026	PS51462		PS00893	G3DSA:3.90.79.10	SSF140586,SSF55811										
aly9588.16	Glycosylated lysosomal membrane protein A	GO:0005764,GO:0005765,GO:0016021	n/a						PF15065														
aly9588.17	Probable tRNA (guanine(26)-N(2))-dimethyltransferase	GO:0000049,GO:0005634,GO:0004809,GO:0005739,GO:0003723,GO:0006400,GO:0002940	CG6388-PA					TIGR00308	PF02005	PS51626			G3DSA:3.40.50.150	SSF53335,SSF53335,SSF53335				PWY-6829					
aly9588.18	Lon protease homolog, mitochondrial	GO:0004176,GO:0004252,GO:0042645,GO:0045732,GO:0051131,GO:0051260,GO:0005777,GO:0090296,GO:0005739,GO:0005737,GO:0003727,GO:0070407,GO:0007005,GO:0006515,GO:0005759,GO:0070361,GO:0034599,GO:0001666,GO:0003697,GO:0005524,GO:0043565	CG8798-PA	MF_03120			SM00464,SM00382	TIGR00763	PF05362,PF00004,PF02190		PR00830,PR00830,PR00830,PR00830	PS01046	G3DSA:1.10.8.60,G3DSA:3.40.50.300,G3DSA:3.30.230.10	SSF54211,SSF52540,SSF88697	272~292									
aly9588.19	Conserved oligomeric Golgi complex subunit 5	GO:0007111,GO:0005794,GO:0006891,GO:0007112,GO:0017119,GO:0000916,GO:0061024,GO:0005829,GO:0016020,GO:0000139,GO:0005654,GO:0043147,GO:0007290,GO:0015031,GO:0048219,GO:0007110	CG6549-PC						PF10392						77~97									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9588.2	Unknown		n/a																				
aly9588.20	Ras-like protein 1	GO:2001234,GO:0048749,GO:0016020,GO:0030307,GO:0000082,GO:0008586,GO:0046673,GO:0007165,GO:0006184,GO:0007309,GO:0007298,GO:0005622,GO:0042981,GO:0038202,GO:0002168,GO:0035088,GO:0048863,GO:0016049,GO:0048865,GO:0030381,GO:0045500,GO:0007455,GO:0040008,GO:0007369,GO:0007476,GO:0030707,GO:0043066,GO:0007552,GO:0060438,GO:0016242,GO:0005525,GO:0008284,GO:0035099,GO:0008283,GO:0042066,GO:0003924,GO:0006606,GO:0008594,GO:0008595,GO:0008361,GO:0001558,GO:0009267,GO:0005886,GO:0046664,GO:0072002,GO:0007264,GO:0036335,GO:0043410,GO:0007507,GO:0007426,GO:0040014,GO:0007422,GO:0007428,GO:0007391,GO:0010507,GO:0007472,GO:0019003,GO:0046534,GO:0005515,GO:0008293,GO:0001709,GO:0072089,GO:0045610,GO:0001708	CG9375-PA				SM00174,SM00173,SM00175	TIGR00231	PF00071	PS51421	PR00449,PR00449,PR00449,PR00449,PR00449		G3DSA:3.40.50.300	SSF52540			REACT_11044						
aly9588.21	Unknown		n/a						PF15104														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9588.22	Cytochrome P450 4C1	GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0005789,GO:0070330,GO:0005506,GO:0055114,GO:0009055	CG1438-PA						PF00067		PR00385,PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						
aly9588.23	Alpha-(1,3)-fucosyltransferase C	GO:0036065,GO:0006486,GO:0016021,GO:0016020,GO:0008417,GO:0005886,GO:0032580,GO:0046920	CG40305-PB						PF17039,PF00852					SSF53756					UPA00378				
aly9588.24	Alpha-(1,3)-fucosyltransferase C	GO:0036065,GO:0006486,GO:0016021,GO:0016020,GO:0008417,GO:0005886,GO:0032580,GO:0046920	CG40305-PB						PF17039,PF00852					SSF53756					UPA00378				
aly9588.25	Unknown		n/a																				
aly9588.3	Cytochrome P450 6k1	GO:0004497,GO:0016705,GO:0043231,GO:0020037,GO:0016020,GO:0031000,GO:0005789,GO:0017085,GO:0005506,GO:0055114,GO:0009055	CG9438-PA						PF00067		PR00385,PR00385,PR00385,PR00463,PR00463,PR00463,PR00463	PS00086	G3DSA:1.10.630.10	SSF48264			REACT_13433						

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9588.4	Unknown		n/a																				
aly9588.5	A-kinase anchor protein 17A	GO:0005737,GO:0016607,GO:0051018,GO:0005634,GO:0005654,GO:0044822,GO:0042113,GO:0000166,GO:0005575,GO:0006355,GO:0043484,GO:0046331,GO:0003674,GO:0007165,GO:0007411,GO:0008380,GO:0005681,GO:0006397	CG2179-PA												286~334,406~426									
aly9588.6	Unknown	GO:0007476	CG43736-PI																				
aly9588.7	Zinc finger protein 846	GO:0045931,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00868,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF12171	PS50157,PS50157,PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667,SSF57667,SSF57716,SSF57667									
aly9588.8	Omega-amidase NIT2	GO:0000257,GO:0005737,GO:0016810,GO:0006807,GO:0050152	CG8132-PA						PF00795	PS50263		PS01227	G3DSA:3.60.110.10	SSF56317									
aly9588.9	D-aspartate oxidase	GO:0008445,GO:0005777,GO:0055114	CG11236-PA			PIRSF000189			PF01266				G3DSA:3.30.9.10,G3DSA:3.30.9.10,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51971,SSF51971,SSF54373									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly96.1	Unknown		CG31998-PA											SSF81321									
aly96.2	Acidic repeat-containing protein	GO:0005634	CG14814-PB				SM00731		PF10263						232~259								
aly96.3	Solute carrier family 41 member 2	GO:0006812,GO:0016021,GO:0008324,GO:0005886	CG33181-PC						PF01769,PF01769				G3DSA:1.10.357.20,G3DSA:1.10.357.20	SSF161093,SSF161093									
aly96.4	Unknown		n/a																				
aly96.5	Plasma membrane calcium-transporting ATPase 2 (Fragment)	GO:0006874,GO:0016021,GO:0070588,GO:0005886,GO:0005388,GO:0046872,GO:0005524	CG42314-PS				SM00831		PF00690				G3DSA:2.70.150.10	SSF81665									
aly96.6	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly96267.1	Unknown		n/a										G3DSA:3.30.40.10	SSF57903	166~200								
aly963.1	Titin	GO:0030241,GO:0007596,GO:0019899,GO:0006941,GO:0051592,GO:0060048,GO:0030018,GO:0097493,GO:0031433,GO:0035995,GO:0031430,GO:0070062,GO:0030240,GO:0043621,GO:0002576,GO:0003300,GO:0031674,GO:0004674,GO:0005509,GO:0002020,GO:0042805,GO:0042802,GO:0005516,GO:0055003,GO:0006936,GO:0055008,GO:0048769,GO:0050790,GO:0051015,GO:0030049,GO:0045859,GO:0045214,GO:0018108,GO:0000794,GO:0007076,GO:0005865,GO:0030168,GO:0019901,GO:0005829,GO:0051371,GO:0008307,GO:0048739,GO:0005576,GO:0005524,GO:0004713	CG14372-PD				SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408		PF08205,PF08205,PF07679,PF07686,PF13927	PS50835,PS50835,PS50835,PS50835,PS50835,PS50853			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726									
aly963.2	Unknown		n/a																				
aly963.3	Unknown	GO:0008270,GO:0005515	n/a				SM00249		PF00628	PS50016,PS50089		PS01359	G3DSA:3.30.40.10	SSF57903	132~201								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly963.4	Unknown		n/a																				
aly963.5	Unknown		n/a																				
aly963.6	Unknown		n/a																				
aly9645.1	Gelsolin	GO:0006909,GO:0045010,GO:0005829,GO:0051016,GO:0051014,GO:0003779,GO:0005576,GO:0005884,GO:0030041,GO:0005509	CG1106-PB										G3DSA:3.40.20.10	SSF55753									
aly9645.2	Gelsolin	GO:0006909,GO:0045010,GO:0005829,GO:0051016,GO:0051014,GO:0003779,GO:0005576,GO:0005884,GO:0030041,GO:0005509	CG1106-PB				SM00262,SM00262,SM00262		PF00626,PF00626,PF00626		PR00597,PR00597,PR00597,PR00597,PR00597		G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10	SSF55753,SSF55753,SSF55753									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly96528.1	Fat-like cadherin-related tumor suppressor homolog	GO:0016339,GO:0007293,GO:0004872,GO:0007295,GO:0050829,GO:0005925,GO:0007156,GO:0030950,GO:0005509,GO:0009925,GO:0048477,GO:0045089,GO:0007442,GO:0060429,GO:0005887,GO:0005886,GO:0044331,GO:0050839,GO:0007424,GO:0007440,GO:0007431,GO:0042247,GO:0045571	CG7749-PD				SM00112,SM00112,SM00112,SM00112,SM00182,SM00181,SM00181,SM00181,SM00181,SM00179,SM00179		PF00008,PF00008,PF00028,PF00028,PF00028,PF02210	PS50025,PS50268,PS50026,PS50268,PS50268,PS50268,PS50268,PS50268,PS50026,PS50026	PR00205,PR00205,PR00205,PR00205,PR00205,PR00205	PS00022,PS00022,PS01187,PS00232,PS00010,PS00022,PS00232,PS00232,PS00232	G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.60.40.60,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.10.25.10,G3DSA:2.60.120.200	SSF57196,SSF49313,SSF57196,SSF49899,SSF49899,SSF49313,SSF49313,SSF49313,SSF49313,SSF49313										
aly96537.1	Unknown		n/a																				
aly967.1	OTU domain-containing protein 7B	GO:0005737,GO:1900181,GO:0000122,GO:1990380,GO:0071108,GO:0035871,GO:0004843,GO:0032717,GO:0030177,GO:0008270,GO:0003677,GO:0043124,GO:0005634,GO:0008234,GO:0002385,GO:0070536	CG9448-PA						PF02338,PF01754	PS50802,PS51036													
aly967.10	Unknown		CG31068-PC																				
aly967.11	Steroid receptor seven-up, isoforms B/C	GO:0061331,GO:0021782,GO:0007419,GO:0004872,GO:0043401,GO:0007270,GO:0001078,GO:0004879,GO:0007417,GO:0005737,GO:0043565,GO:0001700,GO:0030522,GO:0007510,GO:0042331,GO:0005634,GO:0014019,GO:0042803,GO:0048749,GO:0007601,GO:0001752,GO:0007507,GO:0000122,GO:0007503,GO:0003700,GO:0007462,GO:0007465,GO:0007464,GO:0003707,GO:0046530,GO:0006355,GO:0006351,GO:0005515,GO:0046982,GO:0008270	CG11502-PA				SM00399,SM00430		PF00105,PF00104	PS51030	PR01282,PR01282,PR01282,PR01282,PR01282,PR01282,PR01282,PR01282,PR01282,PR00398,PR00398,PR00398,PR00398,PR00398,PR00047,PR00047,PR00047,PR00047	PS00031	G3DSA:1.10.565.10,G3DSA:3.30.50.10	SSF57716,SSF48508			REACT_71							

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly967.12	Tumor suppressor p53-binding protein 1	GO:0005737,GO:0006974,GO:0035064,GO:0006281,GO:0042162,GO:0005634,GO:0005654,GO:0008134,GO:0043565,GO:0001104,GO:0006355,GO:0005657,GO:0045944,GO:0000784,GO:0001102,GO:0006366,GO:0002039,GO:0003684,GO:0000776,GO:0000777	n/a						PF15057	PS50172,PS50172			G3DSA:3.40.50.10190,G3DSA:3.40.50.10190,G3DSA:3.40.50.10190	SSF52113,SSF52113,SSF63748	1240~1244								
aly967.13	Unknown	GO:0005515	n/a						PF12937	PS50181			G3DSA:1.20.1280.50	SSF81383									
aly967.14	Unknown		n/a						PF15868														
aly967.15	Unknown		n/a																				
aly967.16	Unknown		n/a																				
aly967.2	UPF0469 protein KIAA0907 homolog	GO:0003723	n/a										G3DSA:3.30.1370.10	SSF54791									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly967.3	V-type proton ATPase subunit D 1	GO:0042626,GO:0015992,GO:0015991,GO:0033181,GO:0000221,GO:0046961,GO:0005886	CG8186-PA					TIGR00309	PF01813														
aly967.4	Unknown		n/a																				
aly967.5	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 13	GO:0005737,GO:0030308,GO:0008137,GO:0016021,GO:0097190,GO:0005739,GO:0006120,GO:0005654,GO:0005746,GO:0005747,GO:0045892,GO:0003954	CG3446-PA						PF06212														
aly967.6	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase	GO:0018812,GO:0005783,GO:0016021,GO:0030497,GO:0005789,GO:0042761	CG9267-PA						PF04387,PF04969	PS51203			G3DSA:2.60.40.790	SSF49764		00062+4.2.1.134		PWY-7053,PWY-5353,PWY-7592,PWY-6433,PWY-7602,PWY-7049,PWY-7601,PWY-7606,PWY-6598,PWY-7036,PWY-	UPA00094					
aly967.7	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha	GO:0005737,GO:0007015,GO:0016308,GO:0016309,GO:0030307,GO:0005634,GO:0046854,GO:0016310,GO:0007155,GO:0008360,GO:0005886,GO:0040018,GO:0032006,GO:0005524	CG17471-PA				SM00330		PF01504	PS51455			G3DSA:3.30.810.10,G3DSA:3.30.800.10	SSF56104									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly967.8	Beta-ureidopropionase	GO:0005737,GO:0070062,GO:0006208,GO:0006207,GO:0016810,GO:0019483,GO:0003837,GO:0006807,GO:0046872	CG3027-PA						PF00795,PF00227	PS51476,PS50263		PS00854	G3DSA:3.60.20.10,G3DSA:3.60.110.10	SSF56317,SSF56235			REACT_6185,REACT_13,REACT_152,REACT_6850,REACT_13635,REACT_1538,REACT_578,REACT_383,REACT_11045						
aly967.9	Beta-ureidopropionase	GO:0005737,GO:0006208,GO:0006207,GO:0016810,GO:0019483,GO:0003837,GO:0006807,GO:0046872	CG3027-PA						PF00795	PS50263			G3DSA:3.60.110.10	SSF56317									
aly9673.1	PiggyBac transposable element-derived protein 4		n/a						PF13843,PF13843						346~366								
aly9673.10	Unknown		n/a																				
aly9673.11	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment)	GO:0003964,GO:0004519,GO:0046872	n/a						PF00078	PS50878				SSF56672									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9673.12	Unknown		n/a						PF09631					SSF53032				PWY-6689					
aly9673.13	Unknown		CG15080-PA												1867~1871								
aly9673.2	Ribosomal protein S6 kinase-like 1	GO:0005737,GO:0006468,GO:0043231,GO:0035091,GO:0004674,GO:0048812,GO:0007165,GO:0004672,GO:0005524,GO:0005840	CG7156-PA				SM00745,SM00220		PF04212,PF00787,PF00069	PS50011,PS50195			G3DSA:1.10.510.10,G3DSA:3.30.200.20,G3DSA:1.20.58.280,G3DSA:3.30.1520.10	SSF116846,SSF56112,SSF56112,SSF64268										
aly9673.3	Lipoma HMGIC fusion partner-like 3 protein	GO:0007605,GO:0016021	CG12026-PB						PF10242														
aly9673.4	Tektin-4	GO:0005737,GO:0007017,GO:0030030,GO:0008017,GO:0031514,GO:0000226,GO:0005874,GO:0005875	CG4767-PA						PF03148				G3DSA:1.20.5.50		235~255,169~196,444~471,370~411,30~50								
aly9673.5	Tektin-4	GO:0005737,GO:0007017,GO:0030030,GO:0008017,GO:0031514,GO:0000226,GO:0005874,GO:0005875	CG4767-PA						PF03148						441~461,173~200,360~394								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9673.6	Lipoma HMGIC fusion partner-like 3 protein	GO:0007605,GO:0016021	CG12026-PB						PF10242														
aly9673.7	Protein N-lysine methyltransferase METTL20	GO:0005759,GO:0008168	n/a						PF06325				G3DSA:3.40.50.150	SSF53335									
aly9673.8	Growth arrest and DNA damage-inducible protein GADD45 gamma	GO:0005737,GO:0000186,GO:0000185,GO:0030154,GO:0051726,GO:0006950,GO:0005634,GO:0006915,GO:0007254,GO:0043065,GO:0046330,GO:0006469,GO:1900745,GO:0007275,GO:0046662	CG11086-PA						PF01248														
aly9673.9	Glucose dehydrogenase [FAD, qui]	GO:0050660,GO:0016614,GO:0008812,GO:0006066,GO:0046331,GO:0005576,GO:0045455,GO:0055114,GO:0016491	CG9518-PA			PIRSF000137			PF00732,PF05199			PS00624	G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF54373,SSF51905,SSF51905		00260+1.2.1.8+1.1.99.1		PWY-7494,PWY-3722	UPA00529				
aly96803.1	Unknown		n/a																				
aly9687.1	Signal transducer and activator of transcription 5A	GO:0005737,GO:0043565,GO:0048609,GO:0060056,GO:0045471,GO:0003700,GO:0005829,GO:0007595,GO:0007259,GO:0006355,GO:0007165,GO:0004871,GO:0006366,GO:0003690,GO:0038161,GO:0005634,GO:0031667	n/a				SM00964		PF02865				G3DSA:1.10.532.10	SSF48092									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9687.2	Zinc finger protein 771	GO:0031935,GO:0003700,GO:0005634,GO:0006355,GO:0048813,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG11352-PF				SM00355,SM00355,SM00355,SM00355,SM00355		PF00096	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667	124~144								
aly9687.3	Dynein light chain 1, axonemal	GO:0005515	CG8800-PA				SM00365,SM00365,SM00365,SM00365			PS51450,PS51450,PS51450,PS51450,PS51450			G3DSA:3.80.10.10	SSF52058									
aly9687.4	E3 ubiquitin-protein ligase Rnf220	GO:0005737,GO:0090263,GO:0061630,GO:0016567,GO:0051865,GO:0004842,GO:0008270,GO:0016874	CG4813-PA				SM00184		PF15926,PF13923	PS50089			G3DSA:3.30.40.10	SSF57850	207~234								
aly9687.5	Zinc finger protein 569	GO:0045931,GO:0031935,GO:0006357,GO:0005634,GO:0007476,GO:0006355,GO:0046331,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0007155,GO:0046872,GO:0030178	CG14938-PA				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355,SM00355			PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57667,SSF57667									
aly971.1	G-protein coupled receptor moody	GO:0008502,GO:0004930,GO:0048149,GO:0048148,GO:0016021,GO:0019991,GO:0035095,GO:0030866,GO:0007419,GO:0060857,GO:0008366,GO:0005886,GO:0007186,GO:0005919	CG4322-PA						PF00001,PF00001	PS50262	PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237	G3DSA:1.20.1070.10,G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly971.10	Unknown	GO:0016021,GO:0003674,GO:0003382	CG15335-PB				SM00241		PF00100	PS51034													

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly971.11	Unknown		n/a						PF13873						209~248								
aly971.12	Zinc finger protein 28	GO:0003700,GO:0005634,GO:0006355,GO:0006351,GO:0003676,GO:0003677,GO:0046872	CG1832-PB				SM00355,SM00355,SM00355,SM00355,SM00355,SM00355		PF07776	PS50157,PS50157,PS50157,PS50157,PS50157		PS00028,PS00028,PS00028,PS00028,PS00028,PS00028	G3DSA:3.30.160.60,G3DSA:3.30.160.60,G3DSA:3.30.160.60	SSF57667,SSF57716,SSF57667,SSF57667									
aly971.13	V-type proton ATPase subunit D 1	GO:0042626,GO:0015992,GO:0015991,GO:0033181,GO:0000221,GO:0046961,GO:0005886	CG8186-PA					TIGR00309	PF01813						177~197,202~222								
aly971.14	Unknown		n/a																				
aly971.15	Unknown	GO:0051726	CG2865-PA						PF06031	PS51053					98~118								
aly971.16	Beta-amyloid-like protein	GO:0016319,GO:0051602,GO:0007614,GO:0050808,GO:0007399,GO:0046914,GO:0007422,GO:0007616,GO:0016021,GO:0048678,GO:0007611,GO:0048812,GO:0005515,GO:0005886,GO:1901215,GO:0008201,GO:0005576	CG7727-PB				SM00006		PF02177,PF12925,PF12924			PS00319	G3DSA:3.90.570.10,G3DSA:3.30.1490.140	SSF109843,SSF89811,SSF56491	651~671,520~559,465~485,373~393								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly971.17	Persulfide dioxygenase ETHE1, mitochondrial	GO:0005737,GO:0016787,GO:0070813,GO:0050313,GO:0005739,GO:0005654,GO:0006749,GO:0005759,GO:0005506	CG30022-PB				SM00849		PF00753				G3DSA:3.60.15.10	SSF56281									
aly971.18	Tubulin-specific chaperone cofactor E-like protein	GO:0005737,GO:0005856,GO:0031117,GO:0007291,GO:0003674,GO:0007286,GO:0005930	CG12214-PB						PF14560	PS50053			G3DSA:3.80.10.10,G3DSA:3.80.10.10,G3DSA:3.10.20.90	SSF54236,SSF52058	70~90								
aly971.19	DNA repair protein REV1	GO:0010569,GO:0042276,GO:0006281,GO:0019985,GO:0005634,GO:0000287,GO:0017125,GO:0003887,GO:0009411,GO:0003684	CG12189-PA				SM00292		PF00817,PF16589,PF11799,PF16727	PS50172,PS50173			G3DSA:3.40.50.10190,G3DSA:3.30.1490.100,G3DSA:3.30.70.270,G3DSA:1.10.150.20	SSF100879,SSF56672,SSF56672,SSF52113		00240+2.7.7.7,00230+2.7.7.7							
aly971.2	Zinc finger CCCH domain containing protein 14	GO:0005737,GO:0016607,GO:0006909,GO:0043488,GO:0008143,GO:1900364,GO:0005634,GO:0046872,GO:0044822	CG5720-PA				SM00356,SM00356			PS50103,PS50103					120~140,245~272,424~444								
aly971.20	Unknown		n/a						PF11111														
aly971.21	Transcriptional regulator ATRX homolog	GO:0005722,GO:0051276,GO:0007399,GO:0006281,GO:0006336,GO:0005524,GO:0005634,GO:0003677,GO:0007411,GO:0005700,GO:0004386,GO:0042585,GO:0006351,GO:0016887,GO:0070868,GO:0003678,GO:0046328,GO:0097193,GO:0000775,GO:0008347	CG4548-PA				SM00490,SM00487		PF00176,PF00271	PS51192,PS51194			G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	1383~1403,751~785,907~934,2262~2264								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly971.22	Unknown	GO:0005747	CG11752-PA						PF15880														
aly971.23	Prohibitin-2	GO:0043234,GO:0033147,GO:0005811,GO:0070062,GO:0033600,GO:0009986,GO:0016020,GO:0005739,GO:0005743,GO:0045892,GO:0006351,GO:0060762,GO:0060744,GO:0060749,GO:0016363	CG15081-PF				SM00244		PF01145		PR00679,PR00679,PR00679,PR00679,PR00679,PR00679,PR00679			SSF117892	219~239								
aly971.24	Protein RMD5 homolog A		CG3295-PA				SM00667		PF13445	PS50896			G3DSA:3.30.40.10	SSF57850	22~42								
aly971.25	Forkhead box protein N3	GO:0006909,GO:0009790,GO:0051302,GO:0007049,GO:0007389,GO:0031571,GO:0005634,GO:0071456,GO:0003690,GO:0043565,GO:0008134,GO:0009888,GO:0035050,GO:0008301,GO:0051090,GO:0003700,GO:0000122,GO:0003705,GO:0006355,GO:0000976,GO:0006351,GO:0005667	CG12690-PA				SM00339		PF00250	PS50039	PR00053,PR00053,PR00053	PS00658	G3DSA:1.10.10.10	SSF46785									
aly971.26	Unknown		n/a												136~156,59~98								
aly971.27	Hypoxia up-regulated protein 1	GO:0006457,GO:0005615,GO:0032504,GO:0005811,GO:0005788,GO:0003674,GO:0005524	CG2918-PA						PF00012,PF00012		PR00301,PR00301,PR00301,PR00301,PR00301		G3DSA:3.90.640.10,G3DSA:3.30.420.40,G3DSA:3.30.420.40,G3DSA:1.20.120.10,G3DSA:2.60.34.10,G3DSA:2.60.34.10	SSF53067,SSF100934,SSF53067									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly971.28	Interference hedgehog	GO:0048749,GO:0008284,GO:0008589,GO:0007219,GO:0016021,GO:0035017,GO:0007224,GO:0035222,GO:0009986,GO:0007476,GO:0005515,GO:0007155,GO:0001751,GO:0008201,GO:0042803	CG32796-PG				SM00060,SM00060,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408		PF13895,PF00041,PF00047	PS50853,PS50853,PS50835,PS50835,PS50835,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF49265,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726										
aly971.29	Unknown		n/a																				
aly971.3	Dopamine N-acetyltransferase	GO:0005737,GO:0030187,GO:0008080,GO:0004059,GO:0006584,GO:0048066,GO:0045187,GO:0030431,GO:0046334,GO:0042429,GO:0004060,GO:0042420	CG3318-PB										G3DSA:3.40.630.30,G3DSA:3.40.630.30	SSF55729,SSF55729										
aly971.4	Dopamine N-acetyltransferase	GO:0005737,GO:0030187,GO:0008080,GO:0004059,GO:0006584,GO:0048066,GO:0045187,GO:0030431,GO:0046334,GO:0042429,GO:0004060,GO:0042420	CG13759-PA										G3DSA:3.40.630.30,G3DSA:3.40.630.30	SSF55729,SSF55729										
aly971.5	DnaJ-like protein 60	GO:0016020,GO:0006457,GO:0016021,GO:0030154,GO:0051082,GO:0007283,GO:0007275	CG42567-PC				SM00271		PF00226	PS50076	PR00625,PR00625,PR00625		G3DSA:1.10.287.110	SSF46565										
aly971.6	Fasciculation and elongation protein zeta-2	GO:0019894,GO:0006909,GO:0007399,GO:0008088,GO:0007165,GO:0007411,GO:0022008	CG3981-PB						PF07763						94~114								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly971.7	Collagenase	GO:0006508,GO:0005576,GO:0030574,GO:0004252	CG6592-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly971.8	Collagenase	GO:0004252,GO:0005576,GO:0030574,GO:0006508	CG6298-PA				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly971.9	Spectrin beta chain	GO:0005200,GO:0050807,GO:0030424,GO:0031594,GO:0007009,GO:0016199,GO:0007411,GO:0007274,GO:0030506,GO:0045170,GO:0007026,GO:0005811,GO:0030721,GO:0005546,GO:0003779,GO:0051693,GO:0016328,GO:0072499,GO:0008017,GO:0016327,GO:0042062,GO:0051015,GO:0007409,GO:0005886,GO:0045478,GO:0008091,GO:0007399,GO:0008092,GO:0048790,GO:0045169,GO:0005516	CG5870-PB				SM00033,SM00033,SM00020,SM00233,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150,SM00150		PF15410,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00435,PF00089,PF00307,PF00307	PS50003,PS50021,PS50021,PS50240	PR00683,PR00683,PR00683,PR00683	PS00020,PS00019,PS00134	G3DSA:1.10.418.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:2.40.10.10,G3DSA:1.10.418.10,G3DSA:2.40.10.10,G3DSA:2.30.29.30,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:2.40.10.10,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60,G3DSA:1.20.58.60	SSF47576,SSF46966,SSF50494,SSF46966,SSF46966,SSF50729,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966,SSF46966	1094~1114,1567~1587,610~630,988~1022,1171~1191,1243~1281,1985~2005,1946~1966,397~417,2734~2735,109~129,1454~1474,2052~2072,1201~1221,783~803,2087~2117,1627~1647								
aly97122.1	E3 ubiquitin-protein ligase HECTD1	GO:0005737,GO:0005838,GO:0060708,GO:0060707,GO:0001892,GO:0005634,GO:1903077,GO:0016874,GO:0051865,GO:0042787,GO:0061630,GO:0001843,GO:0046872,GO:0004842,GO:0070534,GO:0001779	CG5604-PA											SSF56204					UPA00143				
aly9735.1	Unknown	GO:0005737,GO:0006468,GO:0005819,GO:0004674,GO:0004672,GO:0005524	CG11533-PD																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9735.2	Unknown		n/a																				
aly974.1	Unknown		n/a												167~187								
aly974.10	Transcription factor AP-1	GO:0051124,GO:0006909,GO:0034138,GO:0034134,GO:0034154,GO:0035419,GO:0005737,GO:0043565,GO:0007254,GO:0010259,GO:0005634,GO:0000165,GO:0035681,GO:0002224,GO:0045944,GO:0045087,GO:0046529,GO:0006351,GO:0005515,GO:0008134,GO:0042060,GO:0008348,GO:0034146,GO:0034142,GO:0001736,GO:0035682,GO:0002755,GO:0003700,GO:0007465,GO:0007464,GO:0007391,GO:0006355,GO:0006357,GO:0045823,GO:0000981,GO:0005667,GO:0046844,GO:0046982,GO:0046843	CG2275-PC				SM00338		PF00170,PF03957	PS50217	PR00043,PR00043,PR00043,PR00043,PR00043	PS00036	G3DSA:1.10.880.10,G3DSA:1.20.5.170	SSF57959	184~225								
aly974.11	WD repeat-containing protein CG11141	GO:0005575,GO:0008150,GO:0003674	CG11141-PB																				
aly974.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly974.3	Unknown		n/a				SM00233			PS50003			G3DSA:2.30.29.30	SSF50729									
aly974.4	Beta-hexosaminidase subunit beta	GO:0016020,GO:0030203,GO:0005783,GO:0007626,GO:0016231,GO:0009313,GO:0007040,GO:0001501,GO:0001669,GO:0019915,GO:0008049,GO:0044267,GO:0043615,GO:0042552,GO:0070062,GO:0050885,GO:0005770,GO:0004563,GO:0006874,GO:0006032,GO:0048477,GO:0005794,GO:0007605,GO:0032428,GO:0008360,GO:0005886,GO:0007341,GO:0006689,GO:0007420,GO:0006491,GO:0008654,GO:0005764,GO:0045944	CG8824-PB			PIRSF001093			PF14845,PF00728		PR00738,PR00738,PR00738,PR00738,PR00738,PR00738,PR00738		G3DSA:3.20.20.80,G3DSA:3.30.379.10	SSF51445,SSF55545		00604+3.2.1.52,00520+3.2.1.52,00511+3.2.1.52,00603+3.2.1.52,00513+3.2.1.52,00531+3.2.1.52		PWY-6902					
aly974.5	ER membrane protein complex subunit 7	GO:0003779,GO:0016021,GO:0072546,GO:0030246	CG8397-PA						PF09430				G3DSA:2.60.40.1120	SSF49452									
aly974.6	CD109 antigen	GO:0046331,GO:0005615,GO:0061045,GO:0019731,GO:0009986,GO:0004867,GO:0045616,GO:0006910,GO:0030512,GO:0050832,GO:0072675,GO:0005576,GO:0005515,GO:0004866,GO:0005886,GO:0001933,GO:0010839,GO:0050431,GO:0001942,GO:0031225	CG7586-PA						PF07678,PF07677				G3DSA:2.60.40.690,G3DSA:1.50.10.20	SSF49410,SSF48239									
aly974.7	CD109 antigen	GO:0050431,GO:0005615,GO:0061045,GO:0019731,GO:0009986,GO:0004867,GO:0045616,GO:0006910,GO:0030512,GO:0050832,GO:0072675,GO:0046331,GO:0005515,GO:0004866,GO:0005886,GO:0001933,GO:0010839,GO:0001942,GO:0031225	CG7586-PA				SM00192		PF07678,PF10569,PF00207,PF07703,PF01835	PS50068			G3DSA:1.50.10.20,G3DSA:4.10.400.10	SSF57424,SSF48239,SSF48239	1347~1349								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly974.8	CCHC-type zinc finger protein CG3800	GO:0005575,GO:0008150,GO:0008270,GO:0003676	CG3800-PA				SM00343,SM00343,SM00343,SM00343,SM00343,SM00343		PF00098,PF00098,PF00098,PF00098,PF00098,PF00098	PS50158,PS50158,PS50158,PS50158,PS50158,PS50158			G3DSA:4.10.60.10,G3DSA:4.10.60.10,G3DSA:4.10.60.10,G3DSA:4.10.60.10	SSF57756,SSF57756,SSF57756,SSF57756										
aly974.9	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	GO:0000413,GO:0006457,GO:0071013,GO:0000398,GO:0005654,GO:0003755,GO:0005634	CG3511-PA				SM00320,SM00320,SM00320,SM00320		PF00160,PF00400,PF00400	PS50072,PS50294	PR00153,PR00153,PR00153,PR00153,PR00153		G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:2.40.100.10	SSF50978,SSF50978,SSF50891										
aly97548.1	Unknown		n/a																				
aly977.1	Intersectin-1	GO:0005089,GO:0008021,GO:0008104,GO:0019209,GO:0097190,GO:0030139,GO:0051124,GO:0043524,GO:0005905,GO:0045202,GO:0007411,GO:0051897,GO:0030054,GO:0005737,GO:0043065,GO:0070064,GO:0043547,GO:0045179,GO:0045746,GO:0005509,GO:0043005,GO:0051056,GO:0030027,GO:0005085,GO:0007269,GO:0005886,GO:0048011,GO:0048013,GO:0007264,GO:0042734,GO:0005829,GO:0002052,GO:0005515,GO:0045860,GO:0048488,GO:0032947	CG1099-PD				SM00027,SM00027		PF12763,PF12763	PS50031,PS50031,PS50222,PS50222		PS00018,PS00018	G3DSA:1.10.238.10,G3DSA:1.10.238.10	SSF47473,SSF47473										
aly977.2	MIP18 family protein CG7949	GO:0005737,GO:0016226,GO:0005575,GO:0003674,GO:0007059,GO:0008150	CG7949-PA						PF01883					SSF117916	122~142								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly977.3	Gelsolin	GO:0006909,GO:0045010,GO:0005829,GO:0051016,GO:0051014,GO:0003779,GO:0005576,GO:0005884,GO:0030041,GO:0005509	CG1106-PB				SM00262,SM00262,SM00262,SM00262,SM00262,SM00262		PF00626,PF00626,PF00626		PR00597,PR00597,PR00597,PR00597,PR00597,PR00597,PR00597		G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10,G3DSA:3.40.20.10	SSF55753,SSF55753,SSF55753,SSF55753,SSF55753,SSF55753	736~749								
aly977.4	PDZ and LIM domain protein 7	GO:0005737,GO:0001725,GO:0001726,GO:0015629,GO:0030239,GO:0005634,GO:0030154,GO:0030036,GO:0001503,GO:0008270,GO:0005925,GO:0045669,GO:0007275	CG14168-PG				SM00228		PF00595	PS50106			G3DSA:2.30.42.10	SSF50156	235~255,883~903,1838~1858,208~228,355~392,548~596								
aly977.5	Copper chaperone for superoxide dismutase	GO:0005737,GO:0016532,GO:0005743,GO:0005829,GO:0005777,GO:0006979,GO:0050821,GO:0019430,GO:0015680,GO:0030001,GO:0006801,GO:0008340,GO:0004784,GO:0046872,GO:0005634,GO:0055114,GO:0008270	CG17753-PB						PF00080		PR00068,PR00068		G3DSA:2.60.40.200	SSF49329				PWY-6854					
aly977.6	Polyadenylate-binding protein-interacting protein 2B	GO:0000900,GO:0008143,GO:0017148,GO:0005575,GO:0001558,GO:0005515,GO:0045947	CG12358-PA						PF07145														
aly97824.1	Unknown		n/a																				
aly981.1	Dorsal-ventral patterning protein tolloid	GO:0007362,GO:0004222,GO:0009880,GO:0007378,GO:0007313,GO:0008586,GO:0005575,GO:0008293,GO:0010629,GO:0005576,GO:0003674,GO:0005509,GO:0006508,GO:0016485,GO:0008150,GO:0030513,GO:0017015,GO:0008270	CG34370-PG				SM00042,SM00042		PF00431,PF00431	PS01180,PS01180,PS01180			G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290,G3DSA:2.60.120.290	SSF49854,SSF49854,SSF49854										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly981.2	3-hydroxyisobutyrate dehydrogenase, mitochondrial	GO:0006573,GO:0008442,GO:0051287,GO:0006520,GO:0005811,GO:0005739,GO:0006098,GO:0004616,GO:0006574,GO:0055114	CG15093-PB			PIRSF000103		TIGR01692	PF03446,PF14833			PS00895	G3DSA:1.10.1040.10,G3DSA:3.40.50.720	SSF48179,SSF51735		00280+1.1.1.31			UPA00362				
aly981.3	Unknown		n/a																				
aly98314.1	Transposable element P transposase	GO:0004803,GO:0006313,GO:0015074,GO:0016740,GO:0003693,GO:0046872	n/a																				
aly98514.1	Solute carrier organic anion transporter family member 4A1	GO:0015349,GO:0008514,GO:0005215,GO:0016021,GO:0015711,GO:0042403,GO:0005886,GO:0043252,GO:0055085	CG3811-PA						PF03137				G3DSA:1.20.1250.20	SSF103473									
aly9855.1	Unknown		n/a																				
aly9855.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9855.3	Ribosomal RNA processing protein 1 homolog	GO:0005634,GO:0016072,GO:0030688,GO:0006364,GO:0000022	CG12396-PA						PF05997						525~555								
aly986.1	Homeotic protein distal-less	GO:0016319,GO:0008587,GO:0007485,GO:0010629,GO:0003677,GO:0048264,GO:0043565,GO:0007479,GO:0005634,GO:0048728,GO:0007487,GO:0035215,GO:0007480,GO:0042048,GO:0035114,GO:0045893,GO:0007469,GO:0003700,GO:0010092,GO:0021553,GO:0000976,GO:0006351,GO:0007449	CG3629-PC							PS50071			G3DSA:1.10.10.60	SSF46689									
aly9863.1	Ceropsin	GO:0008020,GO:0004930,GO:0016028,GO:0009881,GO:0000122,GO:0007605,GO:0016021,GO:0007601,GO:0018298,GO:0007602,GO:0007186	CG5192-PB						PF00001	PS50262	PR00238,PR00238,PR00238,PR00578,PR00578,PR00578,PR00578,PR00578,PR00237,PR00237,PR00237,PR00237,PR00237,PR00237	PS00237,PS00238	G3DSA:1.20.1070.10	SSF81321			REACT_14797						
aly9863.10	Translin	GO:0005737,GO:0043565,GO:0004519,GO:0005634,GO:0004521,GO:0050821,GO:0003723,GO:0003677,GO:0016246,GO:0007630	CG11761-PA						PF01997				G3DSA:1.20.58.190,G3DSA:1.20.58.200	SSF74784									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9863.11	Unknown		n/a																				
aly9863.12	NADH dehydrogenase [ubiqui] 1 alpha subcomplex subunit 8	GO:0008137,GO:0006120,GO:0005747,GO:0005758,GO:0003954,GO:0055114	CG3683-PA			PIRSF017016																	
aly9863.13	Synaptic vesicle glycoprotein 2B	GO:0008021,GO:0030672,GO:0016021,GO:0016020,GO:0022857,GO:0001669,GO:0005886,GO:0006836,GO:0030054	n/a											SSF103473,SSF103473									
aly9863.2	BarH-like 1 homeobox protein	GO:0043565,GO:0003700,GO:0005634,GO:0060361,GO:0006355,GO:0001077,GO:0043524,GO:0030901,GO:0003677,GO:0007605,GO:0001764,GO:0007526	CG13424-PB				SM00389		PF00046	PS50071	PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689	1~21								
aly9863.3	Alpha-1,3-mannosyl-glycoprotein 2 beta-N-acetylglucosaminyltransferase	GO:0016319,GO:0006049,GO:0005797,GO:0001701,GO:0005975,GO:0070062,GO:0006486,GO:0006487,GO:0046872,GO:0018279,GO:0016021,GO:0016020,GO:0000139,GO:0043687,GO:0035010,GO:0003827,GO:0008375,GO:0008340,GO:1903561,GO:0044267,GO:0008344	CG13431-PA						PF03071,PF03071				G3DSA:3.90.550.10,G3DSA:3.90.550.10,G3DSA:3.90.550.10,G3DSA:3.10.180.20	SSF53448	33~89				UPA00378				
aly9863.4	Histidine triad nucleotide-binding protein 1	GO:0005737,GO:0016787,GO:0070062,GO:0009154,GO:0008252,GO:0000166,GO:0000118,GO:0006355,GO:0050850,GO:0006351,GO:0005886,GO:0072332	CG2862-PC						PF01230	PS51084			G3DSA:3.30.428.10	SSF54197									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9863.5	Histidine triad nucleotide-binding protein 1	GO:0005737,GO:0016787,GO:0070062,GO:0006355,GO:0009154,GO:0008252,GO:0000166,GO:0000118,GO:0003824,GO:0050850,GO:0006351,GO:0005886,GO:0072332	CG2862-PC						PF01230	PS51084	PR00332,PR00332,PR00332	PS00892	G3DSA:3.30.428.10	SSF54197									
aly9863.6	NF-kappa-B-repressing factor	GO:0005783,GO:0005730,GO:0005634,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0044822	CG31301-PA						PF01424				G3DSA:3.30.1370.50	SSF82708									
aly9863.7	Unknown	GO:0003676	CG31301-PA						PF11952														
aly9863.8	NF-kappa-B-repressing factor	GO:0005783,GO:0005730,GO:0005634,GO:0045892,GO:0006351,GO:0003676,GO:0003677,GO:0044822	CG31301-PA				SM00443		PF01585,PF11952	PS50174			G3DSA:3.30.1370.50										
aly9863.9	Unknown		n/a																				
aly9865.1	Unknown		n/a										G3DSA:3.90.640.10										

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9867.1	Facilitated trehalose transporter Tret1	GO:0005355,GO:0015574,GO:0005353,GO:0015771,GO:0016021,GO:0016020,GO:0005886,GO:0055085	CG8234-PA						PF00083	PS50850			G3DSA:1.20.1250.20,G3DSA:1.20.1250.20	SSF103473									
aly9867.2	Unknown		n/a																				
aly9867.3	Juvenile hormone epoxide hydrolase	GO:0008096,GO:0006719,GO:0033961,GO:0016021,GO:0005789,GO:0004301,GO:0019439	CG15101-PA			PIRSF001112			PF06441		PR00412,PR00412,PR00412,PR00412,PR00412		G3DSA:3.40.50.1820	SSF53474		00980+3.3.2.9							
aly9867.4	Serpin A3-7	GO:0005615,GO:0031410,GO:0042583,GO:0004867,GO:0010951,GO:0045861,GO:0035009	CG6680-PA				SM00093		PF00079				G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:2.30.39.10,G3DSA:2.30.39.10	SSF56574									
aly9867.5	Alpha-1-antiproteinase F (Fragment)	GO:0006953,GO:0045861,GO:0035009,GO:0005615,GO:0004867	CG6680-PA				SM00093		PF00079				G3DSA:3.30.497.10,G3DSA:3.30.497.10,G3DSA:2.30.39.10,G3DSA:2.30.39.10	SSF56574	117~137								
aly9867.6	Unknown		CG31886-PB						PF16040,PF16041														

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9867.7	T-cell acute lymphocytic leukemia protein 2	GO:0006351,GO:0003700,GO:0005634,GO:0009791,GO:0006357,GO:0000977,GO:0035264,GO:0003677,GO:0046983,GO:0021794,GO:0000981,GO:0030901	CG2655-PA				SM00353		PF00010	PS50888			G3DSA:4.10.280.10	SSF47459									
aly9867.8	Juvenile hormone epoxide hydrolase	GO:0008096,GO:0043231,GO:0033961,GO:0016021,GO:0005789,GO:0004301,GO:0019439,GO:0006719	CG15102-PA						PF06441				G3DSA:3.40.50.1820,G3DSA:3.40.50.1820	SSF53474		00980+3.3.2.9							
aly987.1	Homeotic protein distal-less	GO:0016319,GO:0008587,GO:0007485,GO:0010629,GO:0048264,GO:0043565,GO:0007479,GO:0005634,GO:0048728,GO:0007487,GO:0035215,GO:0007480,GO:0042048,GO:0035114,GO:0045893,GO:0007469,GO:0003700,GO:0010092,GO:0021553,GO:0006355,GO:0000976,GO:0006351,GO:0007449	CG3629-PC				SM00389		PF00046	PS50071	PR00031,PR00031,PR00024,PR00024,PR00024	PS00027	G3DSA:1.10.10.60	SSF46689									
aly987.2	Isochorismatase domain-containing protein 1	GO:0003824,GO:0008152	CG3663-PA						PF00857				G3DSA:3.40.50.850	SSF52499									
aly987.3	Unknown		n/a																				
aly9884.1	Unknown		n/a										G3DSA:2.40.128.20	SSF50814									
aly9884.2	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly98851.1	Unknown	GO:0007016,GO:0006909,GO:0015629,GO:0005198,GO:0003779,GO:0048812,GO:0007155,GO:0005925	CG3299-PA								PR00806,PR00806												
aly9889.1	S-adenosylmethionine mitochondrial carrier protein homolog	GO:1901962,GO:0005743,GO:0000095,GO:0016021,GO:0022857,GO:0015805,GO:0005740,GO:0055085	CG4743-PA						PF00153	PS50920			G3DSA:1.50.40.10	SSF103506									
aly99.1	Protein fem-1 homolog CG6966	GO:0005575,GO:0004842,GO:0051438	CG6966-PB				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF00023,PF13606,PF12796,PF13637	PS50088,PS50088,PS50297,PS50088,PS50297,PS50088,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403,SSF48403									
aly99.2	Protein groucho	GO:0007541,GO:0003677,GO:0071906,GO:0070491,GO:0000122,GO:0005634,GO:0003714,GO:0030178,GO:0005654,GO:0090090,GO:0008134,GO:0045879,GO:0001106,GO:0046331,GO:0045892,GO:0071837,GO:0043234,GO:0007015,GO:0007399,GO:0016055,GO:0006355,GO:0048813,GO:0006351,GO:0005515	CG8384-PE				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00320		PF00400,PF03920	PS50294,PS50294,PS50082,PS50082,PS50082	PR01850,PR01850,PR01850,PR01850,PR01850,PR01850	PS00678,PS00678	G3DSA:2.130.10.10	SSF50978	29~56								
aly99.3	Conserved oligomeric Golgi complex subunit 1	GO:0015031,GO:0000139	CG4848-PA						PF08700														
aly99.4	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly99.5	Unknown		n/a												329~329								
aly99.6	Epsin-1	GO:0007015,GO:0000147,GO:0043547,GO:0030479,GO:0016020,GO:0005546,GO:0043130,GO:0030276,GO:0006897	n/a																				
aly990.1	Down syndrome cell adhesion molecule-like protein Dscam2	GO:0005515,GO:0048812,GO:0005887,GO:0005886,GO:0007155,GO:0007156,GO:0042802	CG31190-PE				SM00409,SM00409,SM00409,SM00409,SM00409,SM00409,SM00408,SM00408,SM00408,SM00408,SM00408,SM00408,SM00060,SM00060,SM00060,SM00060,SM00060,SM00060		PF07679,PF07679,PF07679,PF07679,PF07686,PF13895,PF00041,PF00041,PF00041,PF00041,PF00041,PF00041,PF13927	PS50853,PS50853,PS50835,PS50835,PS50835,PS50835,PS50853,PS50853,PS50853,PS50853,PS50835,PS50853,PS50835			G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10,G3DSA:2.60.40.10	SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF48726,SSF49265,SSF48726,SSF49265,SSF49265									
aly990.2	Attacin-B	GO:0019731,GO:0045087,GO:0050830,GO:0005576,GO:0042742,GO:0031201	CG7629-PA						PF03769					SSF56935,SSF56935									
aly99001.1	Unknown		n/a																				
aly991.1	Unknown	GO:0015271,GO:0005267,GO:0016021,GO:0071805	CG10864-PA						PF07885				G3DSA:1.10.287.70	SSF81324									
aly991.10	AT-rich interactive domain-containing protein 2	GO:0035060,GO:0031936,GO:0046872,GO:0006909,GO:0006351,GO:0007480,GO:0003713,GO:0005654,GO:0008587,GO:0008586,GO:0005700,GO:0050821,GO:0006355,GO:0005886,GO:0045893,GO:0005515,GO:0003677,GO:0090544,GO:0042059,GO:0016568,GO:0006337	CG3274-PA				SM00501,SM00355,SM00355,SM01014		PF01388,PF02257	PS50157,PS51011,PS51526		PS00028	G3DSA:3.30.160.60,G3DSA:1.10.10.10,G3DSA:1.10.150.60	SSF46774,SSF48371	1621~1624,411~431								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly991.11	Pogo transposable element with KRAB domain	GO:0006355,GO:0005634,GO:0007275,GO:0003676,GO:0003677	n/a						PF03184				G3DSA:1.10.10.60										
aly991.12	Glutamate-gated chloride channel	GO:0045211,GO:0048812,GO:1902476,GO:0006811,GO:0008068,GO:0034707,GO:0006821,GO:0005886,GO:0016935,GO:0016934,GO:0022008,GO:0005254,GO:0016021,GO:0030054	CG44099-PN						PF02932,PF02931		PR00253,PR00253,PR00253,PR00253		G3DSA:1.20.58.390,G3DSA:1.20.58.390,G3DSA:2.70.170.10	SSF63712,SSF90112									
aly991.13	ELMO domain-containing protein 2	GO:0005856,GO:0006909,GO:0051607,GO:0090175,GO:0016020,GO:0005096,GO:0000281,GO:0050688	CG10068-PA						PF04727	PS51335													
aly991.14	Thioredoxin domain-containing protein	GO:0045454,GO:0016021,GO:0005789	CG11790-PA						PF00085,PF00085				G3DSA:3.40.30.10,G3DSA:3.40.30.10	SSF52833,SSF52833									
aly991.15	Unknown	GO:0003824,GO:0046331,GO:0009116	CG12065-PA																				
aly991.16	Unknown		n/a																				
aly991.2	Protein tumorous imaginal discs, mitochondrial	GO:0006457,GO:0007224,GO:0031072,GO:0005829,GO:0005739,GO:0005741,GO:0051082,GO:0009408,GO:0046872,GO:0005113,GO:0007275,GO:0005524	CG5504-PB	MF_01152			SM00271		PF00684,PF00226,PF01556	PS51188,PS50076	PR00625,PR00625,PR00625,PR00625	PS00636	G3DSA:2.10.230.10,G3DSA:2.60.260.20,G3DSA:2.60.260.20,G3DSA:2.60.260.20,G3DSA:1.10.287.110	SSF57938,SSF46565,SSF49493									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly991.3	Protein king tubby	GO:0005737,GO:0009744,GO:0016028,GO:0006897,GO:0007608,GO:0016059,GO:0035091,GO:0005634,GO:0042593,GO:0061512,GO:0003674,GO:0005929,GO:0070328	CG9398-PC						PF01167		PR01573,PR01573,PR01573,PR01573,PR01573,PR01573,PR01573	PS01200,PS01201	G3DSA:3.20.90.10	SSF54518									
aly991.4	60S ribosomal protein L28	GO:0051298,GO:0022625,GO:0006412,GO:0003735,GO:0007052,GO:0022008,GO:0000022,GO:0005840	CG12740-PB						PF01778														
aly991.5	Unknown		n/a																				
aly991.6	Unknown		n/a																				
aly991.7	Unknown		n/a																				
aly991.8	AF4/FMR2 family member 4	GO:0008283,GO:0016049,GO:0032368,GO:0042051,GO:0007365,GO:0003700,GO:0006355,GO:0005634,GO:0032783,GO:0051493,GO:0007611,GO:0042048,GO:0007379,GO:0008361,GO:0006351,GO:0003677,GO:0007366,GO:0048190,GO:0000915	CG8817-PC						PF05110,PF05110														
aly991.9	Polycomb protein l(1)G0020	GO:0008080,GO:0005634,GO:0006355,GO:0006351,GO:0009267,GO:0022008,GO:0005524	CG1994-PA						PF13718,PF08351,PF05127,PF13725				G3DSA:3.40.630.30,G3DSA:3.40.630.30,G3DSA:3.40.630.30	SSF55729	965~985,894~918								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly9924.1	Cyclic nucleotide-gated cation channel subunit A	GO:0030553,GO:0042391,GO:0005249,GO:0071805,GO:0005221,GO:0006812,GO:0005223,GO:0005222,GO:0005622,GO:0019934,GO:0005887,GO:0001666,GO:0055085,GO:0017071	CG42701-PB				SM00100		PF00027,PF16526,PF00520	PS50042		PS00888,PS00889	G3DSA:1.20.58.60,G3DSA:1.10.287.630,G3DSA:1.10.287.70,G3DSA:2.60.120.10	SSF51206,SSF81324	566~586,534~561								
aly9924.2	Unknown		n/a																				
aly9924.3	cGMP-gated cation channel alpha-1	GO:0030553,GO:0042391,GO:0050896,GO:1902495,GO:0005249,GO:0042622,GO:0071805,GO:0005221,GO:0006812,GO:0005223,GO:0005222,GO:0007601,GO:0001750,GO:0019934,GO:0005887,GO:0001666,GO:0055085,GO:0017071	CG42701-PB						PF16526						8~35								
aly994.1	Leucine-rich repeat-containing protein 71		n/a										G3DSA:3.80.10.10	SSF52047									
aly994.10	Gamma-aminobutyric acid type B receptor subunit 2	GO:0005737,GO:0031631,GO:0043005,GO:0042048,GO:0038039,GO:0016021,GO:0007268,GO:0007214,GO:0045211,GO:0046676,GO:0005887,GO:0005886,GO:0004965,GO:0046982,GO:0007186,GO:0007194,GO:0030054	CG6706-PC						PF01094,PF00003	PS50259	PR01177,PR01177,PR01177,PR01177,PR01177,PR01177,PR01177,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176,PR01176		G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300,G3DSA:3.40.50.2300	SSF53822	753~773								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly994.11	Unknown	GO:0031631,GO:0042048,GO:0038039,GO:0016021,GO:0007214,GO:0046676,GO:0005887,GO:0004965,GO:0046982,GO:0007186,GO:0007194	CG6706-PC																				
aly994.12	Unknown		n/a																				
aly994.13	Vinculin	GO:0005737,GO:0007160,GO:0007016,GO:0006909,GO:0015629,GO:0005198,GO:0003779,GO:0048812,GO:0005886,GO:0007155,GO:0005925	CG3299-PA						PF01044,PF01044,PF01044,PF01044		PR00806,PR00806,PR00806,PR00806,PR00806		G3DSA:1.20.1490.10,G3DSA:1.20.120.230,G3DSA:1.20.120.230,G3DSA:1.20.120.230,G3DSA:1.20.120.230,G3DSA:1.20.120.230,G3DSA:1.20.120.230	SSF47220,SSF47220,SSF47220,SSF47220										
aly994.14	Transcription factor Adf-1	GO:0040011,GO:0006366,GO:0050773,GO:0007616,GO:0005634,GO:0005705,GO:0007613,GO:0007611,GO:0001077,GO:0048813,GO:0006357,GO:0045944,GO:0045893,GO:0005667,GO:0003677,GO:0008345,GO:0003712,GO:0007416,GO:0008355	CG15845-PE				SM00595		PF10545,PF02944	PS51029														
aly994.15	Transcription factor Adf-1	GO:0040011,GO:0006366,GO:0050773,GO:0007616,GO:0005634,GO:0005705,GO:0007613,GO:0007611,GO:0005575,GO:0048813,GO:0046331,GO:0003674,GO:0045893,GO:0005667,GO:0003677,GO:0001077,GO:0045944,GO:0008345,GO:0003712,GO:0007416,GO:0008355	CG8765-PA				SM00595		PF10545	PS51029														
aly994.16	Unknown		n/a																				
aly994.17	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly994.18	Protein transport protein Sec24C	GO:0048208,GO:0048081,GO:0035149,GO:0005789,GO:0061024,GO:0008270,GO:0030011,GO:0022409,GO:0070971,GO:0040003,GO:0006888,GO:0000902,GO:0007029,GO:0006886,GO:0005811,GO:0034394,GO:0035158,GO:0044267,GO:0048471,GO:0018279,GO:0016203,GO:0035151,GO:0019886,GO:0002474,GO:0009306,GO:0005215,GO:0043687,GO:0008360,GO:0012507,GO:0030127,GO:0090110,GO:0007030,GO:0005048,GO:0003331,GO:0005829,GO:0000139,GO:0071711,GO:0044281	CG10882-PC						PF04810				SSF82919			REACT_11123							
aly994.2	Nuclear hormone receptor HR78	GO:0007424,GO:0006351,GO:0045089,GO:0035071,GO:0043565,GO:0003700,GO:0005634,GO:0048102,GO:0003707,GO:0035002,GO:0006355,GO:0008270,GO:0043401,GO:0003677,GO:0050829,GO:0030522,GO:0022008,GO:0004879,GO:0000977	CG7199-PC				SM00399		PF00104,PF00105	PS51030	PR00398,PR00398,PR00398,PR00047,PR00047,PR00047	PS00031	G3DSA:1.10.565.10,G3DSA:1.10.565.10,G3DSA:3.30.50.10	SSF48508,SSF57716	463~468		REACT_71						
aly994.3	Carbonyl reductase [NADPH] 3	GO:0005737,GO:0000253,GO:0005615,GO:0042376,GO:0005829,GO:0050890,GO:0005654,GO:0004090,GO:0008152,GO:0070402	CG11200-PB						PF00106,PF00106		PR00081,PR00081,PR00081,PR00081,PR00081,PR00080,PR00080,PR00080	PS00061	G3DSA:3.40.50.720	SSF51735									
aly994.4	Adapter molecule Crk	GO:0005070,GO:0006911,GO:0046330,GO:0007165,GO:0005515,GO:0032956,GO:0007520,GO:0007298,GO:0043087,GO:0048013,GO:0046529	CG1587-PC				SM00326,SM00326,SM00252		PF00017,PF00018,PF07653	PS50001,PS50002	PR00452,PR00452,PR00452,PR00452,PR00401,PR00401,PR00401,PR00401,PR00401		G3DSA:2.30.30.40,G3DSA:3.30.505.10,G3DSA:2.30.30.40	SSF50044,SSF50044,SSF55550,SSF55550										
aly994.5	Ubiquitin-conjugating enzyme E2 H	GO:0005737,GO:0031625,GO:0070979,GO:0004842,GO:0061630,GO:0046331,GO:0043161,GO:0070936,GO:0016874,GO:0061631,GO:0005524	CG2257-PA				SM00212		PF00179	PS50127		PS00183	G3DSA:3.10.110.10	SSF54495					UPA00143				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly994.6	Mitochondrial import receptor subunit TOM40 homolog 1	GO:0015450,GO:0046930,GO:0006626,GO:0005739,GO:0005742,GO:0005741,GO:0015288,GO:0071456,GO:0006811,GO:0055085	CG12157-PA						PF01459				G3DSA:2.40.160.10,G3DSA:2.40.160.10										
aly994.7	UPF0428 protein CXorf56 homolog	GO:0071013,GO:0016846,GO:0003674,GO:0000398,GO:0008152	CG16865-PA										G3DSA:3.90.1590.10			00680+4.4.1.22		PWY-1801	UPA00562				
aly994.8	Voltage-dependent calcium channel type D subunit alpha-1	GO:0046872,GO:0042045,GO:0006936,GO:0034220,GO:0016324,GO:0008331,GO:0070588,GO:0006816,GO:0016323,GO:0009790,GO:0005891,GO:0070509,GO:0005886,GO:0005245,GO:0086010	CG4894-PC				SM01062		PF16885,PF16905,PF08763,PF00520,PF00520,PF00520		PR00167,PR00167,PR00167,PR00167,PR00167,PR00167,PR01630,PR01630,PR01630,PR01630		G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350,G3DSA:1.20.120.350	SSF81324,SSF81324,SSF81324,SSF81324,SSF81324,SSF81324,SSF81324	1588~1608,1880~1880		REACT_18266						
aly994.9	Protein transport protein Sec24C	GO:0048208,GO:0048081,GO:0035149,GO:0005789,GO:0061024,GO:0008270,GO:0030011,GO:0022409,GO:0070971,GO:0040003,GO:0006888,GO:0000902,GO:0007029,GO:0006886,GO:0005811,GO:0034394,GO:0035158,GO:0044267,GO:0048471,GO:0018279,GO:0016203,GO:0035151,GO:0019886,GO:0002474,GO:0009306,GO:0005215,GO:0043687,GO:0008360,GO:0012507,GO:0030127,GO:0090110,GO:0007030,GO:0005048,GO:0003331,GO:0005829,GO:0000139,GO:0071711,GO:0044281	CG10882-PC						PF00626,PF04811,PF08033,PF04815				G3DSA:3.40.20.10,G3DSA:3.40.50.410	SSF81811,SSF82754,SSF53300,SSF81995,SSF81995			REACT_11123						
aly9944.1	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly995.1	P protein	GO:0005737,GO:0016020,GO:0030318,GO:0008283,GO:0005302,GO:0005215,GO:0016021,GO:0006810,GO:0005789,GO:0005765,GO:0042438,GO:0007286,GO:0033162,GO:0015828,GO:0006726,GO:0055085,GO:0010008	CG12787-PC						PF03600														
aly995.2	Unknown		n/a																				
aly9964.1	Unknown		n/a																				
aly997.1	Dipeptidyl aminopeptidase-like protein 6	GO:0042391,GO:0070062,GO:0016021,GO:0016020,GO:0019228,GO:0008076,GO:0008239,GO:0043266,GO:1901379,GO:0005886,GO:0006508,GO:0072659,GO:0015459,GO:1901381,GO:0008236	CG11319-PB						PF00326,PF00930				G3DSA:3.40.50.1820,G3DSA:2.140.10.30,G3DSA:2.140.10.30	SSF53474,SSF82171,SSF82171										
aly997.10	FUN14 domain-containing protein 1	GO:0031307,GO:0001666,GO:0000422	CG5676-PA						PF04930														
aly997.11	Unknown		n/a												2322~2322,2280~2314								
aly997.12	NF-X1-type zinc finger protein NFXL1	GO:0003700,GO:0005634,GO:0006355,GO:0008270,GO:0005515,GO:0016021	CG15011-PA				SM00438,SM00438,SM00438,SM00438,SM00438,SM00438,SM00438,SM00438,SM00438,SM00438,SM00438		PF01422,PF01422,PF01422,PF01422,PF01422,PF01422,PF01422,PF01422,PF01422,PF01422,PF01422,PF01422	PS50089,PS50016		PS01359			824~824,745~772								
aly997.13	Unknown		n/a										G3DSA:3.30.40.10	SSF57903	173~207								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly997.2	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial (Fragment)	GO:0004129,GO:0007030,GO:0000278,GO:0008283,GO:0005811,GO:0006123,GO:0005739,GO:0005751,GO:0005743	CG10664-PA						PF02936		PR01873,PR01873,PR01873,PR01873		G3DSA:1.10.442.10	SSF81406									
aly997.3	Trypsin-7	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG7829-PA				SM00020		PF00089	PS50240			G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly997.4	Cytochrome c oxidase subunit 4 isoform 2, mitochondrial	GO:0004129,GO:0007030,GO:0000278,GO:0008283,GO:0005811,GO:0006123,GO:0005739,GO:0005751,GO:0005743	CG10664-PA						PF02936		PR01873,PR01873,PR01873,PR01873		G3DSA:1.10.442.10	SSF81406									
aly997.5	Cytochrome c oxidase subunit 4 isoform 2, mitochondrial	GO:0004129,GO:0007030,GO:0000278,GO:0008283,GO:0005811,GO:0006123,GO:0005739,GO:0005751,GO:0005743	CG10664-PA						PF02936		PR01873,PR01873,PR01873,PR01873		G3DSA:1.10.442.10	SSF81406									
aly997.6	Trypsin-7	GO:0007586,GO:0004252,GO:0005576,GO:0006508	CG7829-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly997.7	V-type proton ATPase subunit G	GO:0001700,GO:0016820,GO:0015992,GO:0015991,GO:0016324,GO:0033181,GO:0000221,GO:0046961,GO:0016471	CG6213-PA					TIGR01147	PF03179						8~57								

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly997.8	E3 ubiquitin-protein ligase MYLIP-A	GO:0005856,GO:0005737,GO:0002814,GO:0005829,GO:0007369,GO:0007476,GO:0016567,GO:0008270,GO:0006955,GO:0016874,GO:0030178,GO:0030431	CG12489-PB				SM00295		PF09379,PF13920,PF00373	PS50089,PS50057			G3DSA:2.30.29.30,G3DSA:3.30.40.10,G3DSA:1.20.80.10,G3DSA:3.10.20.90	SSF47031,SSF50729,SSF57850,SSF54236										
aly997.9	Unknown	GO:0005654,GO:0002121,GO:0016363,GO:0008586	CG4444-PA												915~944								
aly998.1	Senecionine N oxygenase	GO:0050661,GO:0050660,GO:0043231,GO:0009820,GO:0005829,GO:0051289,GO:0004499,GO:0004497,GO:0005739,GO:0005576,GO:0033784,GO:0055114	CG3006-PA						PF00743,PF00743		PR00370,PR00370,PR00370,PR00370,PR00370,PR00370,PR00370		G3DSA:3.50.50.60,G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905									
aly998.10	Protein FAM161A	GO:0030030,GO:0005737,GO:0005856,GO:0005929	n/a						PF10595						671~691								
aly998.11	Serine protease easter	GO:0004252,GO:0009950,GO:0050832,GO:0045087,GO:0045752,GO:0031638,GO:0006964,GO:0006952,GO:0050830,GO:0005576,GO:0007311,GO:0008063,GO:0050829,GO:0006508,GO:0008233,GO:0006959,GO:0008236	CG16705-PA				SM00680,SM00020		PF00089,PF12032	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly998.12	Serine protease easter	GO:0004252,GO:0006909,GO:0009950,GO:0031638,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG9737-PA				SM00020		PF00089	PS50240	PR00722,PR00722,PR00722	PS00134,PS00135	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly998.13	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG2045-PA				SM00020,SM00680		PF12032,PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly998.14	Serine protease easter	GO:0004252,GO:0009950,GO:0031638,GO:0006952,GO:0005576,GO:0007311,GO:0008063,GO:0006508,GO:0008233,GO:0008236	CG4920-PA				SM00020		PF12032,PF00089	PS50240	PR00722,PR00722,PR00722	PS00135,PS00134	G3DSA:2.40.10.10,G3DSA:2.40.10.10,G3DSA:2.40.10.10	SSF50494									
aly998.15	Uncharacterized protein C14orf119	GO:0005575,GO:0008150,GO:0003674,GO:0005739	CG12948-PA						PF14969														
aly998.16	Zinc transporter ZIP1	GO:0016324,GO:0016021,GO:0016020,GO:0005385,GO:0030001,GO:0071577,GO:0005886,GO:0046873,GO:0006829,GO:0055085,GO:0008270	CG6898-PA						PF02535														
aly998.17	Unknown	GO:0016324,GO:0046873,GO:0016020,GO:0030001,GO:0055085	CG6898-PA						PF02535														
aly998.18	Synaptosomal-associated protein 25	GO:0006887,GO:0006906,GO:0045202,GO:0005484,GO:0007274,GO:0031201,GO:0030054,GO:0048489,GO:0005737,GO:0000149,GO:0016020,GO:0005886,GO:0016081,GO:0016082,GO:0048172,GO:0007269,GO:0007268,GO:0006893,GO:0043195,GO:0016192,GO:0031629,GO:0005515,GO:0019905	CG40452-PA				SM00397,SM00397		PF00835	PS50192,PS50192			G3DSA:1.20.5.110,G3DSA:1.20.5.110	SSF58038,SSF58038	57~91,172~192								
aly998.19	Zinc transporter ZIP1	GO:0055069,GO:0016021,GO:0016324,GO:0008344,GO:0016020,GO:0005622,GO:0030001,GO:0071577,GO:0005886,GO:0008340,GO:0046873,GO:0016323,GO:0055085	CG9428-PA						PF02535														
aly998.2	Senecionine N oxygenase	GO:0050661,GO:0050660,GO:0043231,GO:0009820,GO:0005829,GO:0051289,GO:0004499,GO:0004497,GO:0005739,GO:0005576,GO:0033784,GO:0055114	CG3006-PA						PF00743,PF00743		PR00370,PR00370,PR00370,PR00370,PR00370,PR00370,PR00370		G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly998.20	Beta-1,3-galactosyltransferase 5 (Fragment)	GO:0006486,GO:0016021,GO:0016020,GO:0000139,GO:0008378,GO:0016757,GO:0008499	CG3038-PA						PF01762										UPA00378				
aly998.21	Unknown		CG13599-PA						PF06581						50~70								
aly998.22	63 kDa chaperonin, mitochondrial	GO:0005811,GO:0006457,GO:0006626,GO:0006458,GO:0051082,GO:0005875,GO:0005743,GO:0042026,GO:0005739,GO:0005524,GO:0005759,GO:0009408,GO:0034605,GO:0007005	CG12101-PA					TIGR02348	PF00118		PR00298,PR00298,PR00298,PR00298,PR00298		G3DSA:1.10.560.10,G3DSA:3.50.7.10,G3DSA:1.10.560.10	SSF52029,SSF54849,SSF48592,SSF48592	362~389,146~166								
aly998.23	Claspin homolog	GO:0033314,GO:0005634,GO:0003674	CG32251-PA												707~744								
aly998.24	Enolase-phosphatase E1	GO:0005737,GO:0043874,GO:0000287,GO:0019509,GO:0005634	CG12173-PA	MF_01681,MF_03117				TIGR01549,TIGR01691	PF13419				G3DSA:3.40.50.1000	SSF56784	687~707,549~569	00270+3.1.3.77			UPA00904				
aly998.25	Helicase SKI2W	GO:0000381,GO:0008152,GO:0008026,GO:0005634,GO:0004004,GO:0004386,GO:0005654,GO:0003723,GO:0003676,GO:0005524,GO:0055087	CG10210-PA																				
aly998.26	Transient receptor potential channel pyrexia	GO:0005261,GO:0005262,GO:0048060,GO:0006812,GO:0016021,GO:0070588,GO:0006816,GO:0051290,GO:0034703,GO:0009408,GO:0098655,GO:0055085	CG17142-PA				SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248,SM00248		PF00023,PF00023,PF00520,PF12796,PF12796	PS50088,PS50088,PS50088,PS50088,PS50088,PS50297,PS50088,PS50088,PS50088	PR01415,PR01415		G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20,G3DSA:1.25.40.20	SSF48403	881~901									

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly998.3	Helicase SKI2W	GO:0000381,GO:0008152,GO:0008026,GO:0005634,GO:0004004,GO:0004386,GO:0005654,GO:0003723,GO:0003676,GO:0005524,GO:0055087	CG10210-PA				SM00487,SM00490		PF08148,PF00270,PF13234,PF00271	PS51192,PS51194			G3DSA:3.40.50.300,G3DSA:3.40.50.300,G3DSA:3.40.50.300	SSF52540,SSF52540,SSF52540	178~198,1033~1053								
aly998.4	Proteasome activator complex subunit 4	GO:0016607,GO:1990111,GO:0006281,GO:0005829,GO:0010499,GO:0006974,GO:0070577,GO:0005488,GO:0016504,GO:0035093,GO:0010952,GO:0005634	n/a						PF16507				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371,SSF48371,SSF48371									
aly998.5	Proteasome activator complex subunit 4	GO:0016607,GO:1990111,GO:0006281,GO:0005829,GO:0010499,GO:0006974,GO:0070577,GO:0016504,GO:0035093,GO:0010952,GO:0005634	n/a						PF11919				G3DSA:1.25.10.10,G3DSA:1.25.10.10	SSF48371									
aly998.6	Transcription initiation factor IIA subunit 2	GO:0051123,GO:0005634,GO:0005672,GO:0006357,GO:0045944,GO:0006367,GO:0001128,GO:0001129,GO:0022008	CG5163-PA			PIRSF009415			PF02751,PF02268				G3DSA:1.10.287.190,G3DSA:2.30.18.10	SSF47396,SSF50784									
aly998.7	Unknown		n/a																				
aly998.8	Unknown	GO:0005575,GO:0003674,GO:0008150	CG33229-PA												46~66								
aly998.9	Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial	GO:0005794,GO:0004497,GO:0006744,GO:0016709,GO:0044550,GO:0005739,GO:0005743,GO:0050660,GO:0042995,GO:0055114	CG7277-PA					TIGR01988,TIGR01988	PF01494,PF01494		PR00420,PR00420	PS01304	G3DSA:3.50.50.60,G3DSA:3.50.50.60	SSF51905,SSF51905					UPA00232				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly999.1	Unknown		n/a																				
aly999.2	Conserved oligomeric Golgi complex subunit 7	GO:0005794,GO:0007030,GO:0007112,GO:0017119,GO:0036063,GO:0006886,GO:0009166,GO:0000139	CG31040-PA						PF10191														
aly999.3	F-box/WD repeat-containing protein 1A	GO:0008589,GO:0008588,GO:0046599,GO:0045849,GO:0006470,GO:0033598,GO:0007611,GO:0007293,GO:0030111,GO:0007304,GO:0007165,GO:0000209,GO:0007298,GO:0061630,GO:0030178,GO:0008355,GO:0016032,GO:0030708,GO:0016874,GO:0030727,GO:0030720,GO:0030707,GO:0043433,GO:0005654,GO:0000086,GO:0060444,GO:0045893,GO:0006508,GO:0007088,GO:0043122,GO:0002223,GO:0007623,GO:0000278,GO:0031146,GO:0061136,GO:0045087,GO:0006623,GO:0045879,GO:0060253,GO:0046627,GO:0042752,GO:0042753,GO:0030162,GO:0045475,GO:0045862,GO:0031648,GO:0004842,GO:0030512,GO:0031145,GO:0071407,GO:0030713,GO:0016055,GO:0051219,GO:0000151,GO:0051439,GO:0016567,GO:0006511,GO:0016322,GO:0019005,GO:0005515,GO:0043161,GO:0032007,GO:0045892,GO:0046983,GO:0005829,GO:0051437,GO:0046843	CG3412-PB				SM00320,SM00320,SM00320,SM00320,SM00320,SM00320,SM00256,SM01028		PF12125,PF00400,PF00400,PF00400,PF00400,PF00400,PF00400,PF12937	PS50082,PS50082,PS50181,PS50082,PS50082,PS50082,PS50082,PS50294	PR00320,PR00320,PR00320	PS00678,PS00678,PS00678,PS00678,PS00678,PS00678	G3DSA:2.130.10.10,G3DSA:2.130.10.10,G3DSA:1.20.1280.50	SSF81383,SSF50978										
aly999.4	Syndetin	GO:0070062,GO:0055037,GO:0016020,GO:0032456,GO:0015031,GO:1990745	CG4996-PA						PF10475,PF10474						116~154								
aly999.5	Unknown		n/a																				

protein ID	Function annotation	Associated GO terms	Flybase ortholog	Protein family or conserved domains							Functional motifs		Homologous structure and Coiled coil prediction			Pathways mapped by interproscan				Transmembrane helices		Signal Peptides	
				Hamap	PANTHER	PIRSF	SMART	TIGRFAM	Pfam	ProSiteProfiles	PRINTS	ProSitePatterns	Gene3D	SUPERFAMILY	Coils	KEGG	Reactome	MetaCyc	UniPathway	Phobius	TMHMM	Phobius	SignalP
aly999.6	THAP domain containing protein 1	GO:0043565,GO:0016605,GO:0007346,GO:0006355,GO:0006351,GO:0003676,GO:0046872,GO:0001935,GO:0007049,GO:0008270	CG10631-PA				SM00980,SM00692		PF05485	PS50950				SSF57716									
aly999.7	Unknown		n/a																				
aly999.8	Protein MAATS1	GO:0005739	CG15144-PB						PF14738						344~371								
aly9991.1	Unknown		n/a												19~39								