File S2

Functional annotations for probe sets in Figure 6, showing both *Inb* and *Dep* effects

For each pattern we give the list of probe sets and their functional information as provided by the *Functional annotation table* tool in the DAVID web page.

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+D

C

-D

Probe sets:

1624717_s_at
1625430_at
1625840_at
1631385_at
1631527_at
1632623_at
1635581_at
1636896_a_at
1637193_at
1637940_s_at
1641126_at
1641381_s_at

Functional annotation table:

ID	Gene Name	Species	GOTERM_BP_FAT	GOTERM_CC_FAT	GOTERM_MF_FAT	INTERPRO	KEGG_PATHWAY	PIR_SUPERFAMILY	SMART	SP_PIR_KEYWORDS	UP_SEQ_FEATURE
1632623_at	Cytochrome b5-related	Drosophila melanogaster	GO:0006631~fatty acid metabolic process,GO:0006633~fatty acid biosynthetic process,GO:0008610~lipid biosynthetic process,GO:0016053~organic acid biosynthetic process,GO:0046394~carboxylic acid biosynthetic process,GO:0055114~oxidation reduction,	GO:0005739~mitochondrion,GO:0005811~lipid particle,	GO:0005506~iron ion binding,GO:0009055~electron carrier activity,GO:0016717~oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water,GO:0020037~heme binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046906~tetrapyrrole binding,GO:0046914~transition metal ion binding,	IPR001199:Cytochrome b5,IPR005804:Fatty acid desaturase, type 1,IPR012171:Fatty acid/sphingolipid desaturase,IPR018506:Cytochrome b5, heme-binding site,		PIRSF015921:fatty acid desaturase/sphingolipid desaturase,PIRSF015921:FA_sphinglp_des,		complete proteome, heme,iron,metal-binding,metalloprotein,	chain:Cytochrome b5-related protein,domain:Cytochrome b5 heme-binding,metal ion-binding site:Iron (heme axial ligand),sequence conflict,sequence variant,
1636896_a_at	Dmel_CG12576	Drosophila melanogaster								complete proteome,	
1641381_s_at	Dmel_CG13213	Drosophila melanogaster				IPR001810:Cyclin-like F-box,IPR018483:Carbohydrate kinase, FGGY, conserved site,		PIRSF036853:conserved protein with F-box/LRR-repeat, AtFBL11 type,	SM00256:FBOX,	complete proteome,	
1625430_at	Dmel_CG14022	Drosophila melanogaster			GO:0003998~acylphosphatase activity,	IPR001792:Acylphosphatase,IPR001792:Acylphosphatase-like,	dme00620:Pyruvate metabolism,	PIRSF001266:acylphosphatase,		complete proteome,hydrolase,	
1631385_at	Dmel_CG2889	Drosophila melanogaster			GO:0008270~zinc ion binding,GO:0043167~ion						

binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR007087:Zinc finger, C2H2-type,IPR012934:Zinc finger, AD-type,IPR015880:Zinc finger, C2H2-like, SM00355:ZnF_C2H2, complete proteome,

1624717_s_at Dmel_CG32647 Drosophila melanogaster IPR001007:von Willebrand factor, type C,IPR002052:N-6 adenine-specific DNA methylase, conserved site, SM00214:VWC, complete proteome,methyltransferase,transferase,

1635581_at Dmel_CG8300 Drosophila melanogaster complete proteome,

1637193_at Eukaryotic translation initiation factor 3 subunit C Drosophila melanogaster GO:0006412~translation,GO:0006413~translational initiation, GO:0005829~cytosol,GO:0005852~eukaryotic translation initiation factor 3 complex, GO:0003743~translation initiation factor activity,GO:0008135~translation factor activity, nucleic acid binding, IPR000717:Proteasome component region PCI,IPR008905:Eukaryotic translation initiation factor 3 subunit 8, N-terminal,IPR011991:Winged helix repressor DNA-binding, PIRSF017001:eukaryotic translation initiation factor 3, subunit 8, SM00088:PINT, complete proteome,cytoplasm,Initiation factor,phosphoprotein,protein biosynthesis, chain:Eukaryotic translation initiation factor 3 subunit C,domain:PCI,modified residue,sequence conflict,

1631527_at Eukaryotic translation initiation factor 3 subunit L Drosophila melanogaster GO:0006412~translation, GO:0003743~translation initiation factor activity,GO:0008135~translation factor activity, nucleic acid binding, IPR019382:RNA polymerase I-associated factor PAF67, complete proteome,cytoplasm,Initiation factor,protein biosynthesis, chain:Eukaryotic translation initiation factor 3 subunit L,

1641126_at Protein LSM12 homolog A Drosophila melanogaster IPR019181:RNA-processing, Lsm domain, complete proteome, chain:Protein LSM12 homolog A,

1625840_at Uncharacterized protein CG12001 Drosophila melanogaster complete proteome,rna editing, chain:Uncharacterized protein CG12001,sequence variant,

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C

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Probe sets:

1624185_at
1628296_at
1628598_s_at
1628938_at
1633463_s_at
1636337_s_at
1636762_a_at
1637778_a_at
1638335_at
1640241_at
1640332_at

Functional annotation table:

ID Gene Name Species COG_ONTOLOGY GOTERM_BP_FAT GOTERM_CC_FAT GOTERM_MF_FAT INTERPRO KEGG_PATHWAY PIR_SUPERFAMILY SMART SP_PIR_KEYWORDS UP_SEQ_FEATURE

1624185_at Dmel_CG1041 Drosophila melanogaster GO:0005739~mitochondrion,GO:0005777~peroxisome,GO:0042579~microbody, GO:0004092~carnitine O-acetyltransferase activity,GO:0008374~O-acyltransferase activity,GO:0016406~carnitine O-acyltransferase activity,GO:0016407~acetyltransferase activity,GO:0016413~O-acetyltransferase activity, IPR000542:Acyltransferase ChoActase/COT/CPT, PIRSF000430:carnitine O-acetyltransferase, Acyltransferase,complete proteome,transferase,

1628938_at Dmel_CG10882 Drosophila melanogaster GO:0006886~intracellular protein transport,GO:0006888~ER to Golgi vesicle-mediated transport,GO:0008104~protein localization,GO:0015031~protein transport,GO:0016192~vesicle-mediated transport,GO:0034613~cellular protein localization,GO:0045184~establishment of protein localization,GO:0046907~intracellular transport,GO:0048193~Golgi vesicle transport,GO:0070727~cellular macromolecule localization, GO:0005794~Golgi apparatus,GO:0005811~lipid particle,GO:0012505~endomembrane system,GO:0012506~vesicle membrane,GO:0012507~ER to Golgi transport vesicle membrane,GO:0016023~cytoplasmic membrane-bounded vesicle,GO:0030117~membrane coat,GO:0030120~vesicle coat,GO:0030127~COPII vesicle coat,GO:0030133~transport vesicle,GO:0030134~ER to Golgi transport vesicle,GO:0030135~coated vesicle,GO:0030658~transport vesicle membrane,GO:0030659~cytoplasmic vesicle membrane,GO:0030662~coated vesicle membrane,GO:0031090~organelle membrane,GO:0031410~cytoplasmic vesicle,GO:0031982~vesicle,GO:0031988~membrane-bounded vesicle,GO:0044431~Golgi apparatus part,GO:0044433~cytoplasmic vesicle part,GO:0048475~coated membrane,

GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0008270~zinc ion binding,GO:0017171~serine hydrolase activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR000183:Orn/DAP/Arg decarboxylase 2,IPR000276:7TM GPCR, rhodopsin-like,IPR006031:XYPPX repeat,IPR006895:Zinc finger, Sec23/Sec24-type,IPR006896:Sec23/Sec24 trunk region,IPR006900:Sec23/Sec24 helical region,IPR007123:Gelsolin region,IPR012990:Sec23/Sec24 beta-sandwich, complete proteome,hydrolase,protein transport,transport,

1628598_s_at Dmel_CG1250 Drosophila melanogaster Intracellular trafficking and secretion, GO:0002164~larval development,GO:0002165~instar larval or pupal development,GO:0002168~instar larval development,GO:0003002~regionalization,GO:0006886~intracellular protein transport,GO:0006888~ER to Golgi vesicle-mediated transport,GO:0007030~Golgi organization,GO:0007389~pattern specification process,GO:0007591~molting cycle, chitin-based cuticle,GO:0007592~protein-based cuticle development,GO:0008104~protein localization,GO:0008363~larval chitin-based cuticle development,GO:0009791~post-embryonic development,GO:0010721~negative regulation of cell development,GO:0010769~regulation of cell morphogenesis involved in differentiation,GO:0010975~regulation of neuron projection development,GO:0015031~protein transport,GO:0016192~vesicle-mediated transport,GO:0018988~molting cycle, protein-based cuticle,GO:0022404~molting cycle process,GO:0022604~regulation of cell morphogenesis,GO:0031344~regulation of cell projection organization,GO:0031345~negative regulation of cell projection organization,GO:0034613~cellular protein localization,GO:0035017~cuticle pattern formation,GO:0035293~chitin-based larval cuticle pattern formation,GO:0040003~chitin-based cuticle development,GO:0042303~molting cycle,GO:0042335~cuticle development,GO:0042336~protein-based cuticle development during molting,GO:0042337~chitin-based cuticle development during molting,GO:0045184~establishment of protein localization,GO:0045596~negative regulation of cell differentiation,GO:0045664~regulation of neuron differentiation,GO:0046907~intracellular transport,GO:0048193~Golgi vesicle transport,GO:0048814~regulation of dendrite morphogenesis,GO:0050767~regulation of neurogenesis,GO:0050768~negative regulation of neurogenesis,GO:0050773~regulation of dendrite development,GO:0050774~negative regulation of dendrite morphogenesis,GO:0051129~negative regulation of cellular component organization,GO:0051960~regulation of nervous system development,GO:0060284~regulation of cell development,GO:0070727~cellular macromolecule localization, GO:0005783~endoplasmic reticulum,GO:0005794~Golgi apparatus,GO:0005795~Golgi stack,GO:0012505~endomembrane system,GO:0012506~vesicle membrane,GO:0012507~ER to Golgi transport vesicle membrane,GO:0016023~cytoplasmic membrane-bounded vesicle,GO:0030117~membrane coat,GO:0030120~vesicle coat,GO:0030127~COPII vesicle coat,GO:0030133~transport vesicle,GO:0030134~ER to Golgi transport vesicle,GO:0030135~coated vesicle,GO:0030658~transport vesicle membrane,GO:0030659~cytoplasmic vesicle membrane,GO:0030662~coated vesicle membrane,GO:0031090~organelle membrane,GO:0031410~cytoplasmic vesicle,GO:0031982~vesicle,GO:0031988~membrane-bounded vesicle,GO:0044431~Golgi apparatus part,GO:0044433~cytoplasmic vesicle part,GO:0048475~coated membrane, GO:0005096~GTPase activator activity,GO:0008047~enzyme activator activity,GO:0008270~zinc ion binding,GO:0030695~GTPase regulator activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding ,GO:0046914~transition metal ion binding,GO:0060589~nucleoside-triphosphatase regulator activity, IPR006895:Zinc finger, Sec23/Sec24-type,IPR006896:Sec23/Sec24 trunk region,IPR006900:Sec23/Sec24 helical region,IPR007123:Gelsolin region,IPR012990:Sec23/Sec24 beta-sandwich, PIRSF003206:SEC23 protein, protein transport,transport,

1638335_at Dmel_CG18493 Drosophila melanogaster GO:0006508~proteolysis, GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR008758:Peptidase S28, PIRSF016539:Lysosomal Pro-X carboxypeptidase / Dipeptidyl-peptidase 2, complete proteome,

1640332_at Dmel_CG6972 Drosophila melanogaster complete proteome,

1640241_at Dmel_CG7008 Drosophila melanogaster GO:0010605~negative regulation of macromolecule metabolic process,GO:0010608~posttranscriptional regulation of gene expression,GO:0010629~negative regulation of gene expression,GO:0016246~RNA interference,GO:0016441~posttranscriptional gene silencing,GO:0016458~gene silencing,GO:0031047~gene silencing by RNA,GO:0035194~posttranscriptional gene silencing by RNA,GO:0040029~regulation of gene expression, epigenetic, GO:0005811~lipid particle,GO:0016442~RNA-induced silencing complex,GO:0030529~ribonucleoprotein complex,GO:0031332~RNAi effector complex, GO:0003712~transcription cofactor activity,GO:0003713~transcription coactivator activity,GO:0008134~transcription factor binding,GO:0016563~transcription activator activity,GO:0030528~transcription regulator activity, IPR002999:Tudor domain,IPR006021:Staphylococcal nuclease (SNase-like),IPR008191:Maternal tudor protein,IPR016685:RNA-induced silencing complex, nuclease component Tudor-SN,IPR018351:Tudor subgroup, PIRS F017179:RISC-Tudor-SN, SM00318:SNc,SM00333:TUDOR, complete proteome,hydrolase, 1637778_a_at Probable glucosamine 6-phosphate N-acetyltransferase Drosophila melanogaster GO:0004343~glucosamine 6-phosphate N-acetyltransferase activity,GO:0008080~N-acetyltransferase activity,GO:0016407~acetyltransferase activity,GO:0016410~N-acyltransferase activity,GO:0042802~identical protein binding, IPR000182:GCN5-related N-acetyltransferase,IPR016181:Acyl-CoA N-acyltransferase, dme00520:Amino sugar and nucleotide sugar metabolism, Acyltransferase,complete proteome,transferase, binding site:Substrate,chain:Probable glucosamine 6-phosphate N- acetyltransferase,domain:N-acetyltransferase,region of interest:Acetyl-CoA binding,region of interest:Substrate binding,

1633463_s_at Putative polypeptide N-acetylgalactosaminyltransferase 9 Drosophila melanogaster GO:0005794~Golgi apparatus,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity,GO:0005509~calcium ion binding,GO:0005529~sugar binding,GO:0008376~acetylgalactosaminyltransferase activity,GO:0030145~manganese ion binding,GO:0030246~carbohydrate binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR000772:Ricin B lectin,IPR001173:Glycosyl transferase, family 2, dme00512:O-Glycan biosynthesis, SM00458:RICIN, alternative splicing,calcium,complete proteome,disulfide bond,glycoprotein,glycosyltransferase,golgi apparatus,Lectin,manganese,membrane,Signal-anchor,transferase,transmembrane, chain:Putative polypeptide N- acetylgalactosaminyltransferase 9,compositionally biased region:Gly-rich,disulfide bond,domain:Ricin B-type lectin,glycosylation site:N-linked (GlcNAc...) ,region of interest:Catalytic subdomain A,region of interest:Catalytic subdomain B,sequence conflict,splice variant,topological domain:Cytoplasmic,topological domain:Lumenal,transmembrane region,

1628296_at polypeptide GalNAc transferase 4 Drosophila melanogaster GO:0009311~oligosaccharide metabolic process,GO:0009312~oligosaccharide biosynthetic process,GO:0016051~carbohydrate biosynthetic process, GO:0005794~Golgi apparatus,GO:0005795~Golgi stack,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0044431~Golgi apparatus part, GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity,GO:0005509~calcium ion binding,GO:0005529~sugar binding,GO:0008376~acetylgalactosaminyltransferase activity,GO:0030145~manganese ion binding,GO:0030246~carbohydrate binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR000772:Ricin B lectin,IPR001173:Glycosyl transferase, family 2, dme00512:O-Glycan biosynthesis, SM00458:RICIN, calcium,complete proteome,disulfide bond,glycoprotein,glycosyltransferase,golgi apparatus,Lectin,manganese,membrane,Signal-anchor,transferase,transmembrane, chain:N-acetylgalactosaminyltransferase 4,disulfide bond,domain:Ricin B-type lectin,glycosylation site:N-linked (GlcNAc...),region of interest:Catalytic subdomain A,region of interest:Catalytic subdomain B,topological domain:Cytoplasmic,topological domain:Lumenal,transmembrane region,

1636337_s_at polypeptide GalNAc transferase 6 Drosophila melanogaster GO:0009311~oligosaccharide metabolic process,GO:0009312~oligosaccharide biosynthetic process,GO:0016051~carbohydrate biosynthetic process, GO:0005794~Golgi apparatus,GO:0005795~Golgi stack,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0044431~Golgi apparatus part, GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity,GO:0005509~calcium ion binding,GO:0005529~sugar binding,GO:0008376~acetylgalactosaminyltransferase activity,GO:0030145~manganese ion binding,GO:0030246~carbohydrate binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR000772:Ricin B lectin,IPR001173:Glycosyl transferase, family 2, dme00512:O-Glycan biosynthesis, SM00458:RICIN, calcium,complete proteome,disulfide bond,glycoprotein,glycosyltransferase,golgi apparatus,Lectin,manganese,membrane,Signal-anchor,transferase,transmembrane, chain:N-acetylgalactosaminyltransfer ase 6,disulfide bond,domain:Ricin B-type lectin,glycosylation site:N-linked (GlcNAc...),region of interest:Catalytic subdomain A,region of interest:Catalytic subdomain B,sequence conflict,topological domain:Cytoplasmic,topological domain:Lumenal,transmembrane region,

1636762_a_at supercoiling factor Drosophila melanogaster Signal transduction mechanisms / Cytoskeleton / Cell division and chromosome partitioning / General function prediction only, GO:0006325~chromatin organization,GO:0007549~dosage compensation,GO:0009047~dosage compensation, by hyperactivation of X chromosome,GO:0040029~regulation of gene expression, epigenetic,GO:0051276~chromosome organization, GO:0005694~chromosome,GO:0005700~polytene chromosome,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0003677~DNA binding,GO:0003916~DNA topoisomerase activity,GO:0005509~calcium ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding, IPR002048:Calcium-binding EF-hand,IPR011992:EF-Hand type,IPR018247:EF-HAND 1,IPR018248:EF hand,IPR018249:EF-HAND 2, SM00054:EFh, calcium,

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+D

C

Probe sets:

1622935_at
1623032_at
1623766_at
1623783_at
1623928_at
1624158_at
1624699_s_at
1624840_at
1624888_at
1624984_at
1625027_a_at
1625375_at
1625814_at
1626075_at
1626222_at
1626503_at
1626811_at
1627078_at
1627459_at
1627888_at
1628376_x_at
1628634_at
1629391_at
1629476_at
1629718_at
1629955_at
1630131_at
1631200_at
1631627_at
1631648_at
1631877_a_at
1631909_at
1631998_at
1632318_at
1632374_at
1632583_at
1633810_at
1634575_at
1634697_at
1635305_s_at
1635821_at
1635983_a_at
1635987_at
1636014_at
1636131_at
1636711_at
1636829_at
1636921_at
1637124_at
1637547_at
1638217_at
1638224_at
1638272_at
1638350_at
1638970_at
1639071_a_at
1639152_at
1639341_at
1639993_at
1640824_at
1640826_at
1641201_at
1641568_a_at

Functional annotation table:

ID	Gene Name	Species	COG_ONTOLOGY	GOTERM_BP_FAT	GOTERM_CC_FAT	GOTERM_MF_FAT	INTERPRO	KEGG_PATHWAY	PIR_SUPERFAMILY	SMART	SP_PIR_KEYWORDS	UP_SEQ_FEATURE

1624840_at Accessory gland-specific peptide 29AB Drosophila melanogaster GO:0007320~insemination,GO:0007321~sperm displacement,GO:0007610~behavior,GO:0007618~mating,GO:0007620~copulation,GO:0019098~reproductive behavior,GO:0032504~multicellular organism reproduction,GO:0045297~post-mating behavior,GO:0046692~sperm competition,GO:0046693~sperm storage,GO:0048609~reproductive process in a multicellular organism, GO:0005576~extracellular region, GO:0005179~hormone activity,GO:0005529~sugar binding,GO:0005534~galactose binding,GO:0030246~carbohydrate binding,GO:0048029~monosaccharide binding, IPR001304:C-type lectin,IPR016186:C-type lectin-like,IPR018378:C-type lectin, conserved site, SM00034:CLECT, behavior,complete proteome,disulfide bond,glycoprotein,Lectin,polymorphism,Secreted,signal, chain:Accessory gland protein Acp29AB,disulfide bond,domain:C-type lectin,glycosylation site:N-linked (GlcNAc...),sequence variant,signal peptide,

1631200_at Accessory gland-specific peptide 32CD Drosophila melanogaster GO:0007610~behavior,GO:0007617~mating behavior,GO:0007618~mating,GO:0007621~negative regulation of female receptivity,GO:0019098~reproductive behavior,GO:0032504~multicellular organism reproduction,GO:0033057~reproductive behavior in a multicellular organism,GO:0045297~post-mating behavior,GO:0045434~negative regulation of female receptivity, post-mating,GO:0045924~regulation of female receptivity,GO:0046008~regulation of female receptivity, post-mating,GO:0048609~reproductive process in a multicellular organism,GO:0051705~behavioral interaction between organisms,GO:0060180~female mating behavior, GO:0005576~extracellular region, GO:0005179~hormone activity, alternative initiation,behavior,complete proteome,polymorphism,Secreted,signal, chain:Accessory gland protein Acp32CD,compositionally biased region:Arg-rich,compositionally biased region:Gly-rich,sequence variant,signal peptide,splice variant,

1628634_at Adenosine 3'-phospho 5'-phosphosulfate transporter 2 Drosophila melanogaster GO:0015858~nucleoside transport,GO:0015860~purine nucleoside transport,GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport,GO:0046963~3'-phosphoadenosine 5'-phosphosulfate transport, GO:0005794~Golgi apparatus,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane, GO:0005337~nucleoside transmembrane transporter activity,GO:0015211~purine nucleoside transmembrane transporter activity,GO:0015932~nucleobase, nucleoside, nucleotide and nucleic acid transmembrane transporter activity,GO:0046964~3'-phosphoadenosine 5'-phosphosulfate transmembrane transporter activity, IPR013657:UAA transporter, PIRSF017416:solute carrier family 35, member B type,PIRSF500839:solute carrier family 35, member B3, complete proteome,developmental protein,glycoprotein,golgi apparatus,membrane,phosphoprotein,transmembrane,transport, chain:Adenosine 3'-phospho 5'-phosphosulfate transporter 2,glycosylation site:N-linked (GlcNAc...),modified residue,transmembrane region,

1624699_s_at	Beadex	Drosophila melanogaster	GO:0002165~instar larval or pupal development,GO:0003002~regionalization,GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0007389~pattern specification process,GO:0007444~imaginal disc development,GO:0007472~wing disc morphogenesis,GO:0007476~imaginal disc-derived wing morphogenesis,GO:0007552~metamorphosis,GO:0007560~imaginal disc morphogenesis,GO:0007610~behavior,GO:0007622~rhythmic behavior,GO:0007623~circadian rhythm,GO:0007626~locomotory behavior,GO:0009791~post-embryonic development,GO:0009886~post-embryonic morphogenesis,GO:0010033~response to organic substance,GO:0010324~membrane invagination,GO:0014070~response to organic cyclic substance,GO:0014073~response to tropane,GO:0016044~membrane organization,GO:0016192~vesicle-mediated transport,GO:0035107~appendage morphogenesis,GO:0035108~limb morphogenesis,GO:0035110~leg morphogenesis,GO:0035114~imaginal disc-derived appendage morphogenesis,GO:0035120~post-embryonic appendage morphogenesis,GO:0035218~leg disc development,GO:0035220~wing disc development,GO:0035282~segmentation,GO:0035285~appendage segmentation,GO:0035286~leg segmentation,GO:0042220~response to cocaine,GO:0043279~response to alkaloid,GO:0045475~locomotor rhythm,GO:0048511~rhythmic process,GO:0048512~circadian behavior,GO:0048563~post-embryonic organ morphogenesis,GO:0048569~post-embryonic organ development,GO:0048707~instar larval or pupal morphogenesis,GO:0048736~appendage development,GO:0048737~imaginal disc-derived appendage development,GO:0060173~limb development,	GO:0008270~zinc ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,	IPR001781:Zinc finger, LIM-type,	SM00132:LIM,	complete proteome,LIM domain,metal-binding,zinc,
1636131_at	DNA ligase III	Drosophila melanogaster	GO:0006259~DNA metabolic process,GO:0006260~DNA replication,GO:0006281~DNA repair,GO:0006310~DNA recombination,GO:0006974~response to DNA damage stimulus,GO:0033554~cellular response to stress,	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0003677~DNA binding,GO:0003909~DNA ligase activity,GO:0003910~DNA ligase (ATP) activity,GO:0005524~ATP binding,GO:0016886~ligase activity, forming phosphoric ester bonds,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding,	IPR000977:ATP-dependent DNA ligase,IPR001357:BRCT,IPR012308:DNA ligase, N-terminal,IPR012309:ATP dependent DNA ligase, C-terminal,IPR012310:ATP dependent DNA ligase, central,IPR012340:Nucleic acid-binding, OB-fold,IPR016059:ATP-dependent DNA		

ligase, conserved site, dme03410:Base excision repair, SM00292:BRCT, atp-binding,complete proteome,DNA damage,dna recombination,dna repair,dna replication,ligase,nucleotide-binding,

1639071_a_at Death related ced-3/Nedd2-like protein Drosophila melanogaster GO:0002697~regulation of immune effector process,GO:0002700~regulation of production of molecular mediator of immune response,GO:0002759~regulation of antimicrobial humoral response,GO:0002784~regulation of antimicrobial peptide production,GO:0002786~regulation of antibacterial peptide production,GO:0002805~regulation of antimicrobial peptide biosynthetic process,GO:0002807~positive regulation of antimicrobial peptide biosynthetic process,GO:0002808~regulation of antibacterial peptide biosynthetic process,GO:0002831~regulation of response to biotic stimulus,GO:0002920~regulation of humoral immune response,GO:0003006~reproductive developmental process,GO:0006508~proteolysis,GO:0006915~apoptosis,GO:0006952~defense response,GO:0006955~immune response,GO:0006963~positive regulation of antibacterial peptide biosynthetic process,GO:0007276~gamete generation,GO:0007281~germ cell development,GO:0007283~spermatogenesis,GO:0007286~spermatid development,GO:0007291~sperm individualization,GO:0007349~cellularization,GO:0008219~cell death,GO:0009617~response to bacterium,GO:0009891~positive regulation of biosynthetic process,GO:0012501~programmed cell death,GO:0016265~death,GO:0016485~protein processing,GO:0019953~sexual reproduction,GO:0031328~positive regulation of cellular biosynthetic process,GO:0032504~multicellular organism reproduction,GO:0042742~defense response to bacterium,GO:0043900~regulation of multi-organism process,GO:0045087~innate immune response,GO:0048232~male gamete generation,GO:0048515~spermatid differentiation,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process,GO:0050829~defense response to Gram-negative bacterium,GO:0051604~protein maturation,GO:0051605~protein maturation by peptide bond cleavage, GO:0004175~endopeptidase activity,GO:0004197~cysteine-type endopeptidase activity,GO:0008047~enzyme activator activity,GO:0008233~peptidase activity,GO:0008234~cysteine-type peptidase activity,GO:0016504~peptidase activator activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001309:Peptidase C14, ICE, catalytic subunit p20,IPR002138:Peptidase C14, caspase non-catalytic subunit p10,IPR002398:Peptidase C14, caspase precursor p45,IPR011600:Peptidase C14, caspase catalytic,IPR015917:Peptidase C14, caspase precursor p45, core,IPR016129:Peptidase C14, ICE, catalytic subunit p20, active site, SM00115:CASc, alternative splicing,Apoptosis,complete proteome,cytoplasm,hydrolase,immune response,Protease,thiol protease,zymogen, chain:Caspase-8 subunit p10,chain:Caspase-8 subunit p15,sequence conflict,splice variant, 1634575_at Dmel_CG11037 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin,IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site, SM00020:Tryp_SPc, complete proteome,hydrolase,

1640824_at Dmel_CG11306 Drosophila melanogaster GO:0000026~alpha-1,2-mannosyltransferase activity,GO:0000030~mannosyltransferase activity, IPR001296:Glycosyl transferase, group 1, dme00510:N-Glycan biosynthesis, complete proteome,glycosyltransferase,transferase,

1626075_at Dmel_CG11664 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin, PIRSF001135:trypsin, SM00020:Tryp_SPc, complete proteome,hydrolase,

1641568_a_at Dmel_CG11790 Drosophila melanogaster GO:0019725~cellular homeostasis,GO:0042592~homeostatic process,GO:0045454~cell redox homeostasis, IPR012335:Thioredoxin fold,IPR013766:Thioredoxin domain, complete proteome,

1635987_at Dmel_CG12116 Drosophila melanogaster Secondary metabolites biosynthesis, transport, and catabolism / General function prediction only, GO:0055114~oxidation reduction, GO:0004757~sepiapterin reductase activity, IPR002198:Short-chain dehydrogenase/reductase SDR,IPR016040:NAD(P)-binding domain, dme00790:Folate biosynthesis, complete proteome,oxidoreductase,

1632318_at Dmel_CG12773 Drosophila melanogaster GO:0006865~amino acid transport,GO:0015837~amine transport,GO:0015849~organic acid transport,GO:0046942~carboxylic acid transport, GO:0005275~amine transmembrane transporter activity,GO:0008509~anion transmembrane transporter activity,GO:0008511~sodium:potassium:chloride symporter activity,GO:0015171~amino acid transmembrane transporter activity,GO:0015293~symporter activity,GO:0015294~solute:cation symporter activity,GO:0015296~anion:cation symporter activity,GO:0015377~cation:chloride symporter activity, IPR004841:Amino acid permease-associated region, complete proteome,

1622935_at Dmel_CG12828 Drosophila melanogaster complete proteome,

1629955_at	Dmel_CG13309	Drosophila melanogaster	GO:0005976~polysaccharide metabolic process,GO:0006022~aminoglycan metabolic process,GO:0006030~chitin metabolic process, GO:0005576~extracellular region, GO:0001871~pattern binding,GO:0008061~chitin binding,GO:0030246~carbohydrate binding,GO:0030247~polysaccharide binding, IPR002557:Chitin binding protein, peritrophin-A, SM00494:ChtBD2, complete proteome,
1632583_at	Dmel_CG13539	Drosophila melanogaster	IPR009961:Protein of unknown function DUF1487, complete proteome,
1628376_x_at	Dmel_CG13947	Drosophila melanogaster	complete proteome,
1623766_at	Dmel_CG14054	Drosophila melanogaster	complete proteome,
1624158_at	Dmel_CG14481	Drosophila melanogaster	complete proteome,
1638970_at	Dmel_CG14543	Drosophila melanogaster	IPR019398:Pre-rRNA-processing protein TSR2, conserved region, complete proteome,
1639341_at	Dmel_CG14971	Drosophila melanogaster	GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane, IPR004853:Protein of unknown function DUF250, complete proteome,membrane,transmembrane,
1629391_at	Dmel_CG1656	Drosophila melanogaster	GO:0005529~sugar binding,GO:0005534~galactose binding,GO:0030246~carbohydrate binding,GO:0048029~monosaccharide binding, IPR001304:C-type lectin,IPR016186:C-type lectin-like, SM00034:CLECT, complete proteome,
1629718_at	Dmel_CG16727	Drosophila melanogaster	GO:0015101~organic cation transmembrane transporter activity, IPR011701:Major facilitator superfamily MFS-1, complete proteome,transmembrane,
1625027_a_at	Dmel_CG17035	Drosophila melanogaster	GO:0006644~phospholipid metabolic process,GO:0016042~lipid catabolic process,GO:0019637~organophosphate metabolic process, GO:0005576~extracellular region, GO:0004091~carboxylesterase activity,GO:0004620~phospholipase activity,GO:0004623~phospholipase A2 activity,GO:0005509~calcium ion binding,GO:0016298~lipase activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding, IPR010711:Phospholipase A2, group XII secretory,IPR013090:Phospholipase A2, active site, dme00564:Glycerophospholipid

metabolism,dme00565:Ether lipid metabolism,dme00590:Arachidonic acid metabolism,dme00591:Linoleic acid metabolism,dme00592:alpha-Linolenic acid metabolism,
complete proteome,hydrolase,

1639152_at Dmel_CG18243 Drosophila melanogaster GO:0000902~cell morphogenesis,GO:0000904~cell morphogenesis involved in
differentiation,GO:0006470~protein amino acid dephosphorylation,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0006928~cell
motion,GO:0007409~axonogenesis,GO:0007411~axon guidance,GO:0016311~dephosphorylation,GO:0030030~cell projection organization,GO:0030182~neuron
differentiation,GO:0031175~neuron projection development,GO:0032989~cellular component morphogenesis,GO:0032990~cell part morphogenesis,GO:0048666~neuron
development,GO:0048667~cell morphogenesis involved in neuron differentiation,GO:0048812~neuron projection morphogenesis,GO:0048858~cell projection morphogenesis,
GO:0004721~phosphoprotein phosphatase activity,GO:0004725~protein tyrosine phosphatase activity,GO:0016791~phosphatase activity,
IPR000242:Protein-tyrosine phosphatase, receptor/non-receptor type,IPR000387:Dual-specific/protein-tyrosine phosphatase, conserved region,IPR000387:Protein -
tyrosine phosphatase,IPR000572:Oxidoreductase, molybdopterin binding,IPR003961:Fibronectin, type III,IPR008957:Fibronectin, type III-like fold,IPR016130:Protein-tyrosine
phosphatase, active site, SM00060:FN3,SM00194:PTPc, hydrolase,

1626503_at Dmel_CG2254 Drosophila melanogaster GO:0055114~oxidation reduction, GO:0005811~lipid particle, IPR002198:Short-chain
dehydrogenase/reductase SDR,IPR002347:Glucose/ribitol dehydrogenase,IPR016040:NAD(P)-binding domain, PIRSF000126:11beta-hydroxysteroid dehydrogenase,
complete proteome,oxidoreductase,

1623032_at Dmel_CG2336 Drosophila melanogaster GO:0055114~oxidation reduction, IPR009961:Protein of unknown function DUF1487,
complete proteome,oxidoreductase,

1636711_at Dmel_CG31265 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type
endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on
L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin,IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site,
PIRSF001135:trypsin, SM00020:Tryp_SPc, complete proteome,hydrolase,Protease,Serine protease,

1636014_at Dmel_CG31419 Drosophila melanogaster complete proteome, 1636829_at Dmel_CG31902 Drosophila melanogaster GO:0004857~enzyme inhibitor activity,GO:0004866~endopeptidase inhibitor activity,GO:0004867~serine-type endopeptidase inhibitor activity,GO:0030414~peptidase inhibitor activity, IPR000215:Protease inhibitor I4, serpin, SM00093:SERPIN, complete proteome,

1625375_at Dmel_CG32201 Drosophila melanogaster GO:0006575~cellular amino acid derivative metabolic process,GO:0018208~peptidyl-proline modification,GO:0018401~peptidyl-proline hydroxylation to 4-hydroxy-L-proline,GO:0019471~4-hydroxyproline metabolic process,GO:0055114~oxidation reduction, GO:0005783~endoplasmic reticulum,GO:0016222~procollagen-proline 4-dioxygenase complex,GO:0044432~endoplasmic reticulum part, GO:0004656~procollagen-proline 4-dioxygenase activity,GO:0005506~iron ion binding,GO:0016706~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors,GO:0019798~procollagen-proline dioxygenase activity,GO:0019842~vitamin binding,GO:0031406~carboxylic acid binding,GO:0031418~L-ascorbic acid binding,GO:0031543~peptidyl-proline dioxygenase activity,GO:0031545~peptidyl-proline 4-dioxygenase activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR005123:Oxoglutarate and iron-dependent oxygenase,IPR006620:Prolyl 4-hydroxylase, alpha subunit, dme00330:Arginine and proline metabolism, SM00702:P4Hc, oxidoreductase,

1638224_at Dmel_CG32250 Drosophila melanogaster GO:0005739~mitochondrion,GO:0005740~mitochondrial envelope,GO:0005743~mitochondrial inner membrane,GO:0005777~peroxisome,GO:0005778~peroxisomal membrane,GO:0005779~integral to peroxisomal membrane,GO:0016021~integral to membrane,GO:0019866~organelle inner membrane,GO:0031090~organelle membrane,GO:0031224~intrinsic to membrane,GO:0031231~intrinsic to peroxisomal membrane,GO:0031300~intrinsic to organelle membrane,GO:0031301~integral to organelle membrane,GO:0031903~microbody membrane,GO:0031966~mitochondrial membrane,GO:0031967~organelle envelope,GO:0031975~envelope,GO:0042579~microbody,GO:0044429~mitochondrial part,GO:0044438~microbody part,GO:0044439~peroxisomal part, IPR001993:Mitochondrial substrate carrier,IPR002113:Adenine nucleotide translocator 1,IPR018108:Mitochondrial substrate/solute carrier, complete proteome,membrane,repeat,transmembrane,transport,

1634697_at Dmel_CG32667 Drosophila melanogaster IPR001007:von Willebrand factor, type C, SM00214:VWC, complete proteome,

1640826_at	Dmel_CG3947	Drosophila melanogaster	GO:0007031~peroxisome organization,		IPR013919:Peroxisome membrane protein, Pex16,			complete proteome,
1626222_at	Dmel_CG4812	Drosophila melanogaster	GO:0006508~proteolysis,	GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides,	IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin,IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site,	PIRSF001135:trypsin,	SM00020:Tryp_SPc,	complete proteome,hydrolase,Protease,Serine protease,
1641201_at	Dmel_CG5267	Drosophila melanogaster			IPR013032:EGF-like region, conserved site,IPR018453:Protease inhibitor I8, cysteine-rich trypsin inhibitor-like subgroup,			complete proteome,
1631627_at	Dmel_CG5335	Drosophila melanogaster		GO:0005529~sugar binding,GO:0030246~carbohydrate binding,	IPR001079:Galectin, carbohydrate recognition domain,IPR013320:Concanavalin A-like lectin/glucanase, subgroup,		SM00276:GLECT,	complete proteome,Lectin,
1626811_at	Dmel_CG5510	Drosophila melanogaster			IPR005052:Legume-like lectin,IPR013320:Concanavalin A-like lectin/glucanase, subgroup,	PIRSF017635:L-type lectin, animal type,PIRSF500265:vesicular integral-membrane protein VIP36,		complete proteome,
1623928_at	Dmel_CG5910	Drosophila melanogaster						complete proteome,
1630131_at	Dmel_CG6567	Drosophila melanogaster		GO:0004091~carboxylesterase activity,GO:0004620~phospholipase activity,GO:0004622~lysophospholipase activity,GO:0016298~lipase activity,	IPR003140:Phospholipase/carboxylesterase,			complete proteome,hydrolase,
1627888_at	Dmel_CG6672	Drosophila melanogaster	GO:0006811~ion transport,GO:0006812~cation transport,	GO:0005385~zinc ion transmembrane transporter activity,GO:0015082~di-, tri-valent inorganic cation transmembrane transporter activity,GO:0022890~inorganic cation transmembrane transporter activity,GO:0046873~metal ion transmembrane transporter activity,GO:0046915~transition metal ion transmembrane transporter activity,	IPR002524:Cation efflux protein,			complete proteome,

1632374_at Dmel_CG6769 Drosophila melanogaster GO:0008270~zinc ion binding,GO:0043167~ion binding,GO:0043169~cation
binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR003604:Zinc finger, U1-type,IPR007087:Zinc finger, C2H2-type,IPR015880:Zinc finger,
C2H2-like, SM00355:ZnF_C2H2,SM00451:ZnF_U1, complete proteome,

1637124_at Dmel_CG6773 Drosophila melanogaster GO:0002164~larval development,GO:0002165~instar larval or pupal development,GO:0002168~instar larval
development,GO:0003002~regionalization,GO:0006900~membrane budding,GO:0007389~pattern specification process,GO:0007591~molting cycle, chitin-based
cuticle,GO:0007592~protein-based cuticle development,GO:0008363~larval chitin-based cuticle development,GO:0009791~post-embryonic development,GO:0016044~membrane
organization,GO:0016050~vesicle organization,GO:0016192~vesicle-mediated transport,GO:0018988~molting cycle, protein-based cuticle,GO:0022404~molting cycle
process,GO:0035017~cuticle pattern formation,GO:0035293~chitin-based larval cuticle pattern formation,GO:0040003~chitin-based cuticle development,GO:0042303~molting
cycle,GO:0042335~cuticle development,GO:0042336~protein-based cuticle development during molting,GO:0042337~chitin-based cuticle development during molting,
IPR001680:WD40 repeat,IPR015943:WD40/YVTN repeat-like,IPR017986:WD40 repeat, region,IPR019781:WD40 repeat, subgroup,IPR019782:WD40 repeat 2,
SM00320:WD40, complete proteome,repeat,wd repeat,

1624888_at Dmel_CG7081 Drosophila melanogaster GO:0007031~peroxisome organization, GO:0005777~peroxisome,GO:0005778~peroxisomal
membrane,GO:0031090~organelle membrane,GO:0031903~microbody membrane,GO:0042579~microbody,GO:0044438~microbody part,GO:0044439~peroxisomal part,
GO:0008270~zinc ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,
IPR001841:Zinc finger, RING-type,IPR006845:Pex, N-terminal,IPR017907:Zinc finger, RING-type, conserved site,IPR018957:Zinc finger, C3HC4 RING-type,
SM00184:RING, complete proteome,metal-binding,zinc,zinc-finger,

1629476_at Dmel_CG7542 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type
endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on
L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin,IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site,
SM00020:Tryp_SPc, complete proteome,hydrolase,Protease,Serine protease,

1624984_at Dmel_CG8021 Drosophila melanogaster GO:0000166~nucleotide binding,GO:0003723~RNA binding,GO:0003729~mRNA binding, IPR000504:RNA recognition motif, RNP-1,IPR012677:Nucleotide-binding, alpha-beta plait, SM00360:RRM, complete proteome,

1637547_at Dmel_CG8199 Drosophila melanogaster Energy production and conversion, GO:0006637~acyl-CoA metabolic process,GO:0006732~coenzyme metabolic process,GO:0009108~coenzyme biosynthetic process,GO:0046949~acyl-CoA biosynthetic process,GO:0051186~cofactor metabolic process,GO:0051188~cofactor biosynthetic process,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0017086~3-methyl-2-oxobutanoate dehydrogenase (lipoamide) complex,GO:0031974~membrane-enclosed lumen,GO:0031980~mitochondrial lumen,GO:0043233~organelle lumen,GO:0044429~mitochondrial part,GO:0070013~intracellular organelle lumen, GO:0003863~3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity,GO:0016624~oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor, IPR001017:Dehydrogenase, E1 component, dme00280:Valine, leucine and isoleucine degradation, PIRSF000152:pyruvate dehydrogenase (lipoamide) alpha chain, complete proteome,oxidoreductase,

1623783_at Dmel_CG8489 Drosophila melanogaster GO:0003006~reproductive developmental process,GO:0007276~gamete generation,GO:0007281~germ cell development,GO:0007283~spermatogenesis,GO:0007286~spermatid development,GO:0007291~sperm individualization,GO:0007349~cellularization,GO:0019953~sexual reproduction,GO:0032504~multicellular organism reproduction,GO:0048232~male gamete generation,GO:0048515~spermatid differentiation,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process, complete proteome,developmental protein,differentiation,glycoprotein,spermatogenesis, chain:Male-specific protein scotti,glycosylation site:N-linked (GlcNAc...),

1633810_at Dmel_CG8793 Drosophila melanogaster complete proteome,

1625814_at Dymeclin Drosophila melanogaster IPR019142:Dymeclin, complete proteome,lipoprotein,myristate,phosphoprotein, chain:Dymeclin,lipid moiety-binding region:N-myristoyl glycine,modified residue,

1631877_a_at Histidyl-tRNA synthetase Drosophila melanogaster Translation, ribosomal structure and biogenesis, GO:0006399~tRNA metabolic process,GO:0006412~translation,GO:0006418~tRNA aminoacylation for protein translation,GO:0006427~histidyl-tRNA aminoacylation,GO:0034660~ncRNA metabolic process,GO:0043038~amino acid activation,GO:0043039~tRNA aminoacylation, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0004812~aminoacyl-tRNA ligase activity,GO:0004821~histidine-tRNA ligase activity,GO:0005524~ATP binding,GO:0016875~ligase activity, forming carbon-oxygen bonds,GO:0016876~ligase activity, forming aminoacyl-tRNA and related compounds,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding,

IPR000738:WHEP-TRS,IPR002314:Aminoacyl-tRNA synthetase, class II (G, H, P and S), conserved region,IPR004154:Anticodon-binding,IPR004516 :Histidyl-tRNA synthetase, class IIa,IPR006195:Aminoacyl-tRNA synthetase, class II, conserved region,IPR009068:S15/NS1, RNA-binding,IPR015807:Histidyl-tRNA synthetase, class IIa, subgroup,

dme00970:Aminoacyl-tRNA biosynthesis, PIRSF001549:His-tRNA_synth,PIRSF001549:histidyl-tRNA synthetase, Aminoacyl-tRNA synthetase,complete proteome,ligase,

1635821_at Mediator complex subunit 28 Drosophila melanogaster GO:0006350~transcription,GO:0006355~regulation of transcription, DNA-dependent,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0045449~regulation of transcription,GO:0051252~regulation of RNA metabolic process,

GO:0005654~nucleoplasm,GO:0016592~Srb-mediator complex,GO:0031974~membrane-enclosed lumen,GO:0031981~nuclear lumen,GO:0043233~organelle lumen,GO:0044451~nucleoplasm part,GO:0070013~intracellular organelle lumen, GO:0003702~RNA polymerase II transcription factor activity,GO:0016251~general RNA polymerase II transcription factor activity,GO:0016455~RNA polymerase II transcription mediator activity,GO:0030528~transcription regulator activity,

activator,coiled coil,complete proteome,nucleus,Transcription,transcription regulation,chain:Mediator of RNA polymerase II transcription subunit 28,compositionally biased region:Pro-rich,

1627459_at N(6)-adenine-specific DNA methyltransferase 2 homolog Drosophila melanogaster GO:0006730~one-carbon metabolic process,GO:0032259~methylation,

IPR002052:N-6 adenine-specific DNA methylase, conserved site,IPR019369:N-6 adenine-specific DNA methylase-related, eukaryotic,

complete proteome,methyltransferase,transferase, chain:N(6)-adenine-specific DNA methyltransferase 2 homolog,sequence conflict,

1627078_at Organic anion transporting polypeptide 58Dc Drosophila melanogaster GO:0006811~ion transport,GO:0006820~anion transport,GO:0015711~organic anion transport, GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane, GO:0008509~anion transmembrane transporter activity,GO:0008514~organic anion transmembrane transporter activity,GO:0015347~sodium-independent organic anion transmembrane transporter activity, IPR002350:Proteinase inhibitor I1, Kazal,IPR004156:Organic anion transporter polypeptide OATP,IPR011497:Protease inhibitor, Kazal-type, SM00280:KAZAL, 1638217_at Probable dolichol-phosphate mannosyltransferase Drosophila melanogaster GO:0006486~protein amino acid glycosylation,GO:0009100~glycoprotein metabolic process,GO:0009101~glycoprotein biosynthetic process,GO:0043413~biopolymer glycosylation,GO:0070085~glycosylation, GO:0005783~endoplasmic reticulum, GO:0000030~mannosyltransferase activity,GO:0004582~dolichyl-phosphate beta-D-mannosyltransferase activity, IPR001173:Glycosyl transferase, family 2, dme00510:N-Glycan biosynthesis, PIRSF005860:dolichyl-phosphate beta-D-mannosyltransferase, complete proteome,endoplasmic reticulum,glycosyltransferase,transferase, chain:Probable dolichol-phosphate mannosyltransferase,

1638350_at Probable ribosome production factor 1 Drosophila melanogaster GO:0006364~rRNA processing,GO:0006396~RNA processing,GO:0016072~rRNA metabolic process,GO:0022613~ribonucleoprotein complex biogenesis,GO:0034470~ncRNA processing,GO:0034660~ncRNA metabolic process,GO:0042254~ribosome biogenesis, GO:0005730~nucleolus,GO:0031974~membrane-enclosed lumen,GO:0031981~nuclear lumen,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0043233~organelle lumen,GO:0070013~intracellular organelle lumen, GO:0003723~RNA binding,GO:0019843~rRNA binding, IPR007109:Brix domain, PIRSF015949:U3 small nucleolar ribonucleoprotein (snoRNP) complex, Imp4p subunit, complete proteome,nucleus,ribosome biogenesis,rna-binding,rrna processing,rrna-binding, chain:Probable ribosome production factor 1,domain:Brix,region of interest:RNA-binding,

1639993_at Protein RFT1 homolog Drosophila melanogaster GO:0006869~lipid transport,GO:0010876~lipid localization, GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0005319~lipid transporter activity,IPR007594:RFT1, dme00510:N-Glycan biosynthesis, complete proteome,membrane,transmembrane, chain:Protein RFT1 homolog,transmembrane region,

1631648_at Signal recognition particle 9 kDa protein Drosophila melanogaster GO:0006417~regulation of translation,GO:0006448~regulation of translational elongation,GO:0006605~protein targeting,GO:0006612~protein targeting to membrane,GO:0006613~cotranslational protein targeting to membrane,GO:0006614~SRP-dependent cotranslational protein targeting to membrane,GO:0006886~intracellular protein transport,GO:0008104~protein localization,GO:0009890~negative regulation of biosynthetic process,GO:0010558~negative regulation of macromolecule biosynthetic process,GO:0010605~negative regulation of macromolecule metabolic process,GO:0010608~posttranscriptional regulation of gene expression,GO:0015031~protein transport,GO:0017148~negative regulation of translation,GO:0031327~negative regulation of cellular biosynthetic process,GO:0032268~regulation of cellular protein metabolic process,GO:0032269~negative regulation of cellular protein metabolic process,GO:0033365~protein localization in organelle,GO:0034613~cellular protein localization,GO:0045047~protein targeting to ER,GO:0045184~establishment of protein localization,GO:0045900~negative regulation of translational elongation,GO:0046907~intracellular transport,GO:0051248~negative regulation of protein metabolic process,GO:0070727~cellular macromolecule localization, GO:0005786~signal recognition particle, endoplasmic reticulum targeting,GO:0030529~ribonucleoprotein complex,GO:0048500~signal recognition particle, GO:0003723~RNA binding,GO:0003729~mRNA binding,GO:0008312~7S RNA binding, IPR008832:Signal recognition particle, SRP9 subunit,IPR009018:Signal recognition particle, SRP9/SRP14 subunit, dme03060:Protein export, PIRSF017029:signal recognition particle, 9 kDa protein,PIRSF017029:Signal_recog_particle_SRP9, complete proteome,cytoplasm,ribonucleoprotein,rna-binding,signal recognition particle, chain:Signal recognition particle 9 kDa protein,

1638272_at Signal recognition particle protein 19 Drosophila melanogaster GO:0006605~protein targeting,GO:0006612~protein targeting to membrane,GO:0006613~cotranslational protein targeting to membrane,GO:0006614~SRP-dependent cotranslational protein targeting to membrane,GO:0006886~intracellular protein transport,GO:0008104~protein localization,GO:0015031~protein transport,GO:0033365~protein localization in organelle,GO:0034613~cellular protein localization,GO:0045047~protein targeting to ER,GO:0045184~establishment of protein localization,GO:0046907~intracellular transport,GO:0070727~cellular macromolecule localization, GO:0005786~signal recognition particle, endoplasmic reticulum targeting,GO:0030529~ribonucleoprotein complex,GO:0048500~signal recognition particle, GO:0003723~RNA binding,GO:0008312~7S RNA binding, IPR002778:Signal recognition particle, SRP19 subunit, dme03060:Protein export, PIRSF006433:Signal recognition particle 19 kDa protein,PIRSF500827:Eukaryota signal recognition particle 19 kDa prot ein, complete proteome,cytoplasm,ribonucleoprotein,rna-binding,signal recognition particle, chain:Signal recognition particle 19 kDa protein,compositionally biased region:Poly-Gly,region of interest:Basic region, potentially involved in RNA-binding,sequence conflict,

1635305_s_at Trithorax-like Drosophila melanogaster GO:0000087~M phase of mitotic cell cycle,GO:0000278~mitotic cell cycle,GO:0000279~M phase,GO:0000280~nuclear division,GO:0002165~instar larval or pupal development,GO:0006323~DNA packaging,GO:0006325~chromatin organization,GO:0006333~chromatin assembly or disassembly,GO:0006350~transcription,GO:0006355~regulation of transcription, DNA-dependent,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0006461~protein complex assembly,GO:0007049~cell cycle,GO:0007067~mitosis,GO:0007276~gamete generation,GO:0007292~female gamete generation,GO:0007444~imaginal disc development,GO:0007472~wing disc morphogenesis,GO:0007476~imaginal disc-derived wing morphogenesis,GO:0007549~dosage compensation,GO:0007552~metamorphosis,GO:0007560~imaginal disc morphogenesis,GO:0009791~post-embryonic development,GO:0009886~post-embryonic morphogenesis,GO:0009891~positive regulation of biosynthetic process,GO:0010557~positive regulation of macromolecule biosyntheti c process,GO:0010604~positive regulation of macromolecule metabolic process,GO:0010628~positive regulation of gene expression,GO:0016568~chromatin modification,GO:0019953~sexual reproduction,GO:0022402~cell cycle process,GO:0022403~cell cycle phase,GO:0031328~positive regulation of cellular biosynthetic process,GO:0031497~chromatin assembly,GO:0032504~multicellular organism reproduction,GO:0033301~cell cycle comprising mitosis without cytokinesis,GO:0035107~appendage morphogenesis,GO:0035114~imaginal disc-derived appendage morphogenesis,GO:0035120~post-embryonic appendage morphogenesis,GO:0035186~syncytial blastoderm mitotic cell cycle,GO:0035220~wing disc development,GO:0040029~regulation of gene expression, epigenetic,GO:0043933~macromolecular complex subunit organization,GO:0045448~mitotic cell cycle, embryonic,GO:0045449~regulation of transcription,GO:0045893~positive regulation of transcription, DNA-dependent,GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,GO:0045941~positive regulation of transcription,GO:0048285~organelle fission,GO:0048477~oogenesis,GO:0048563~post-embryonic organ morphogenesis,GO:0048569~post-embryonic organ development,GO:0048609~reproductive process in a multicellular organism,GO:0048707~instar larval or pupal morphogenesis,GO:0048736~appendage development,GO:0048737~imaginal disc-derived appendage development,GO:0051173~positive regulation of nitrogen compound metabolic process,GO:0051252~regulation of RNA metabolic process,GO:0051254~positive regulation of RNA metabolic process,GO:0051259~protein oligomerization,GO:0051276~chromosome organization,GO:0051301~cell division,GO:0065003~macromolecular complex assembly,GO:0070271~protein complex biogenesis, GO:0000775~chromosome, centromeric region,GO:0000785~chromatin,GO:0000791~euchromatin,GO:0000792~heterochromatin,GO:0005694~chromosome,GO:0005700~polytene chromosome,GO:0005721~centromeric heterochromatin,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membr ane-bounded organelle,GO:0044427~chromosomal part,

GO:0003677~DNA binding,GO:0003702~RNA polymerase II transcription factor activity,GO:0003704~specific RNA polymerase II transcription factor activity,GO:0008270~zinc ion binding,GO:0016563~transcription activator activity,GO:0030528~transcription regulator activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,GO:0046982~protein heterodimerization activity,GO:0046983~protein dimerization activity,

IPR000210:BTB/POZ-like,IPR007087:Zinc finger, C2H2-type,IPR011333:BTB/POZ fold,IPR013069:BTB/POZ,IPR013087:Zinc finger, C2H2-type/integrase, DNA-binding,IPR015318:Zinc finger, GAGAG binding factor,IPR015880:Zinc finger, C2H2-like, SM00225:BTB,SM00355:ZnF_C2H2, 3d-structure,activator,alternative splicing,cell cycle,cell division,chromatin regulator,complete proteome,developmental protein,differentiation,direct protein sequencing,DNA binding,dna-binding,metal-binding,mitosis,nucleus,oogenesis,phosphoprotein,repressor,Transcription,transcription factor,transcription regulation,zinc,zinc-finger, chain:Transcription factor GAGA,compositionally biased region:Gln-rich,domain:BTB,helix,modified residue,region of interest:Interaction with E(bx),sequence conflict,splice variant,strand,turn,zinc finger region:C2H2-type; degenerate,

1631998_at Ubiquitin carrier protein Drosophila melanogaster GO:0006508~proteolysis,GO:0009057~macromolecule catabolic process,GO:0019941~modification-dependent protein catabolic process,GO:0030163~protein catabolic process,GO:0043632~modification-dependent macromolecule catabolic process,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051603~proteolysis involved in cellular protein catabolic process, GO:0004842~ubiquitin-protein ligase activity,GO:0016879~ligase activity, forming carbon-nitrogen bonds,GO:0016881~acid-amino acid ligase activity,GO:0019787~small conjugating protein ligase activity, IPR000608:Ubiquitin-conjugating enzyme, E2,IPR016135:Ubiquitin-conjugating enzyme/RWD-like, dme04120:Ubiquitin mediated proteolysis, PIRSF001567:ubiquitin-protein ligase E2, SM00212:UBCc, complete proteome,ligase,ubl conjugation pathway,

1631909_at baiser Drosophila melanogaster GO:0003002~regionalization,GO:0003006~reproductive developmental process,GO:0007276~gamete generation,GO:0007281~germ cell development,GO:0007292~female gamete generation,GO:0007308~oocyte construction,GO:0007309~oocyte axis specification,GO:0007310~oocyte dorsal/ventral axis specification,GO:0007311~maternal specification of dorsal/ventral axis, oocyte, germ-line encoded,GO:0007389~pattern specification process,GO:0009798~axis specification,GO:0009950~dorsal/ventral axis specification,GO:0009953~dorsal/ventral pattern formation,GO:0009994~oocyte differentiation,GO:0016192~vesicle-mediated transport,GO:0019953~sexual reproduction,GO:0021700~developmental maturation,GO:0032504~multicellular organism reproduction,GO:0048469~cell maturation,GO:0048477~oogenesis,GO:0048599~oocyte development,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process, GO:0005794~Golgi apparatus,GO:0005795~Golgi stack,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0044431~Golgi apparatus part, IPR000348:emp24/gp25L/p24,IPR009038:GOLD,IPR015720:TMP21 related, PIRSF005359:conserved hypothetical protein YHR110w, complete proteome,membrane,transmembrane,

1636921_at lethal (2) 06496 Drosophila melanogaster GO:0007017~microtubule-based process,GO:0007018~microtubule-based movement, GO:0005856~cytoskeleton,GO:0005869~dynactin complex,GO:0005875~microtubule associated complex,GO:0015629~actin cytoskeleton,GO:0015630~microtubule cytoskeleton,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0044430~cytoskeletal part,

complete proteome,

1635983_a_at no mechanoreceptor potential B Drosophila melanogaster GO:0000902~cell morphogenesis,GO:0007017~microtubule-based process,GO:0007018~microtubule-based movement,GO:0007600~sensory perception,GO:0007605~sensory perception of sound,GO:0009296~flagellum assembly,GO:0010970~microtubule-based transport,GO:0030030~cell projection organization,GO:0030031~cell projection assembly,GO:0030705~cytoskeleton-dependent intracellular transport,GO:0032989~cellular component morphogenesis,GO:0032990~cell part morphogenesis,GO:0035058~sensory cilium assembly,GO:0042073~intraflagellar transport,GO:0042384~cilium assembly,GO:0043064~flagellum organization,GO:0046907~intracellular transport,GO:0048858~cell projection morphogenesis,GO:0050877~neurological system process,GO:0050890~cognition,GO:0050954~sensory perception of mechanical stimulus,GO:0060271~cilium morphogenesis,

IPR001440:Tetratricopeptide TPR-1,IPR011990:Tetratricopeptide-like helical,IPR013026:Tetratricopeptide region,IPR019734:Tetratricopeptide repeat,

SM00028:TPR, complete proteome,receptor,repeat,tpr repeat,

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C

+D

-D

Probe sets:

1623693_a_at
1624042_at
1624943_at
1625264_s_at
1625433_at
1625830_a_at
1626178_s_at
1626566_at
1627270_at
1627376_at
1627651_a_at
1629357_s_at
1629839_a_at
1629843_s_at
1630280_s_at
1630824_a_at
1630968_at
1631243_s_at

1631426_at
1632916_at
1633965_at
1634707_s_at
1634869_at
1634877_at
1635202_s_at
1635619_a_at
1635711_s_at
1636423_at
1636521_at
1636591_at
1636682_at
1638050_s_at
1638186_a_at
1638727_at
1638994_at
1639321_s_at
1640224_s_at
1640754_at
1641506_at

Functional annotation table:

ID Gene Name Species COG_ONTOLOGY GOTERM_BP_FAT GOTERM_CC_FAT GOTERM_MF_FAT INTERPRO KEGG_PATHWAY PIR_SUPERFAMILY SMART SP_PIR_KEYWORDS UP_SEQ_FEATURE

1635711_s_at Ankyrin Drosophila melanogaster GO:0007010~cytoskeleton organization,GO:0007016~cytoskeletal anchoring at plasma membrane,GO:0008104~protein localization,GO:0032507~maintenance of protein location in cell,GO:0045185~maintenance of protein location,GO:0051235~maintenance of location,GO:0051651~maintenance of location in cell, GO:0005886~plasma membrane,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0045169~fusome,GO:0045170~spectrosome, GO:0005198~structural molecule activity,GO:0005200~structural constituent of cytoskeleton,GO:0008092~cytoskeletal protein binding, IPR000488:Death,IPR000906:ZU5,IPR002110:Ankyrin, SM00005:DEATH,SM00218:ZU5,SM00248:ANK, ank repeat,complete proteome,repeat,

1625264_s_at Cysteine proteinase-1 Drosophila melanogaster GO:0002165~instar larval or pupal development,GO:0006508~proteolysis,GO:0007431~salivary gland development,GO:0007435~salivary gland morphogenesis,GO:0007552~metamorphosis,GO:0007559~histolysis,GO:0007586~digestion,GO:0008219~cell death,GO:0009057~macromolecule catabolic process,GO:0009791~post-embryonic development,GO:0009886~post-embryonic morphogenesis,GO:0012501~programmed cell death,GO:0016265~death,GO:0016271~tissue death,GO:0022612~gland morphogenesis,GO:0030163~protein catabolic process,GO:0035070~salivary gland histolysis,GO:0035071~salivary gland cell autophagic cell death,GO:0035272~exocrine system development,GO:0048102~autophagic cell death,GO:0048707~instar larval or pupal morphogenesis,GO:0048732~gland development, GO:0000323~lytic vacuole,GO:0005764~lysosome,GO:0005773~vacuole, GO:0004175~endopeptidase activity,GO:0004197~cysteine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008234~cysteine-type peptidase activity,GO: 0070011~peptidase activity, acting on L-amino acid peptides, IPR000169:Peptidase, cysteine peptidase active site,IPR000668:Peptidase C1A, papain C-terminal,IPR013128:Peptidase C1A, papain,IPR013201:Proteinase inhibitor I29, cathepsin propeptide, dme04142:Lysosome, PIRSF001182:papain, SM00645:Pept_C1, alternative splicing,complete proteome,developmental protein,digestion,disulfide bond,glycoprotein,hydrolase,lysosome,Protease,signal,thiol protease,zymogen, chain:Cathepsin L heavy chain,chain:Cathepsin L light chain,disulfide bond,glycosylation site:N-linked (GlcNAc...),propeptide:Activation peptide,sequence conflict,signal peptide,splice variant,

1638994_at Dmel_CG10627 Drosophila melanogaster GO:0000287~magnesium ion binding,GO:0004610~phosphoacetylglucosamine mutase activity,GO:0016866~intramolecular transferase activity,GO:0016868~intramolecular transferase activity, phosphotransferases,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding, IPR005843:Alpha-D-phosphohexomutase, C-terminal,IPR005844:Alpha-D-phosphohexomutase, alpha/beta/alpha domain I,IPR005845:Alpha-D-phosphohexomutase, alpha/beta/alpha domain II,IPR016055:Alpha-D-phosphohexomutase, alpha/beta/alpha I, II and III,IPR016066:Alpha-D-phosphohexomutase, conserved site,IPR016657:Phosphoacetylglucosamine mutase, dme00520:Amino sugar and nucleotide sugar metabolism, PIRSF016408:PAGM,PIRSF016408:phosphoacetylglucosamine mutase, complete proteome,Isomerase,magnesium,metal-binding,

1641506_at Dmel_CG12400 Drosophila melanogaster GO:0006091~generation of precursor metabolites and energy,GO:0006119~oxidative phosphorylation,GO:0006120~mitochondrial electron transport, NADH to ubiquinone,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0015980~energy derivation by oxidation of organic compounds,GO:0016310~phosphorylation,GO:0022900~electron transport chain,GO:0022904~respiratory electron transport chain,GO:0042773~ATP synthesis coupled electron transport,GO:0042775~mitochondrial ATP synthesis coupled electron transport,GO:0045333~cellular respiration,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005740~mitochondrial envelope,GO:0005743~mitochondrial inner membrane,GO:0005746~mitochondrial respiratory chain,GO:0005747~mitochondrial respiratory chain complex I,GO:0019866~organelle inner membrane,GO:0030964~NADH dehydrogenase complex,GO:0031090~organelle membrane,GO:0031966~mitochondrial membrane,GO:0031967~organelle envelope,GO:0031975~envelope,GO:0044429~mitochondrial part,GO:0044455~mitochondrial membrane part,GO:0045271~respiratory chain complex I,GO:0070469~respiratory chain, GO:0003954~NADH dehydrogenase activity,GO:0008137~NADH dehydrogenase (ubiquinone) activity,GO:0016651~oxidoreductase activity, acting on NADH or NADPH,GO:0016655~oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor,GO:0050136~NADH dehydrogenase (quinone) activity,

IPR009423:NADH:ubiquinone oxidoreductase, subunit b14.5b, dme00190:Oxidative phosphorylation, PIRSF017834:NADH-UbQ_OxRdtase_b14.5b,

complete proteome,oxidoreductase,

1640224_s_at Dmel_CG13796 Drosophila melanogaster GO:0006836~neurotransmitter transport, GO:0005886~plasma membrane,GO:0005887~integral to plasma membrane,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0031226~intrinsic to plasma membrane,GO:0044459~plasma membrane part,

GO:0005275~amine transmembrane transporter activity,GO:0005326~neurotransmitter transporter activity,GO:0005328~neurotransmitter:sodium symporter activity,GO:0015171~amino acid transmembrane transporter activity,GO:0015175~neutral amino acid transmembrane transporter activity,GO:0015187~glycine transmembrane transporter activity,GO:0015293~symporter activity,GO:0015294~solute:cation symporter activity,GO:0015370~solute:sodium symporter activity,

IPR000175:Sodium:neurotransmitter symporter,IPR000792:Transcription regulator LuxR, C-terminal, SM00421:HTH_LUXR,

Symport,transmembrane,transport,

1630968_at Dmel_CG13907 Drosophila melanogaster GO:0008028~monocarboxylic acid transmembrane transporter activity,GO:0015355~secondary active monocarboxylate transmembrane transporter activity, IPR011701:Major facilitator superfamily MFS-1,

complete proteome,

1634877_at Dmel_CG15546 Drosophila melanogaster complete proteome,

1624943_at Dmel_CG1636 Drosophila melanogaster complete proteome,

1636521_at Dmel_CG1981 Drosophila melanogaster GO:0006259~DNA metabolic process,GO:0006281~DNA repair,GO:0006289~nucleotide-excision repair,GO:0006298~mismatch repair,GO:0006974~response to DNA damage stimulus,GO:0033554~cellular response to stress,GO:0034984~cellular response to DNA damage stimulus, GO:0000700~mismatch base pair DNA N-glycosylase activity,GO:0003677~DNA binding,GO:0003690~double-stranded DNA binding,GO:0008263~pyrimidine-specific mismatch base pair DNA N-glycosylase activity,GO:0016799~hydrolase activity, hydrolyzing N-glycosyl compounds,GO:0019104~DNA N-glycosylase activity,GO:0043566~structure-specific DNA binding, IPR005122:Uracil-DNA glycosylase-like,IPR015637:DNA glycosylase, G/T mismatch,IPR017956:AT hook, DNA-binding, conserved site, dme03410:Base excision repair, SM00384:AT_hook, complete proteome,

1632916_at Dmel_CG31357 Drosophila melanogaster General function prediction only, IPR006594:LisH dimerisation motif,IPR006595:CTLH, C-terminal to LisH motif,IPR013144:Ran binding protein-like, CRA domain, SM00667:LisH,SM00668:CTLH,SM00757:CRA, complete proteome,

1636682_at Dmel_CG31778 Drosophila melanogaster GO:0004857~enzyme inhibitor activity,GO:0004866~endopeptidase inhibitor activity,GO:0004867~serine-type endopeptidase inhibitor activity,GO:0030414~peptidase inhibitor activity, IPR002223:Proteinase inhibitor I2, Kunitz metazoa, SM00131:KU, complete proteome,

1626178_s_at Dmel_CG32149 Drosophila melanogaster GO:0004427~inorganic diphosphatase activity, IPR000198:RhoGAP,IPR008162:Inorganic pyrophosphatase, SM00324:RhoGAP, complete proteome,hydrolase,

1631426_at Dmel_CG32412 Drosophila melanogaster GO:0006508~proteolysis, GO:0008233~peptidase activity,GO:0016603~glutaminyl-peptide cyclotransferase activity,GO:0016755~transferase activity, transferring amino-acyl groups, IPR007484:Peptidase M28, Acyltransferase,complete proteome,hydrolase,transferase,

1630824_a_at Dmel_CG33145 Drosophila melanogaster GO:0006486~protein amino acid glycosylation,GO:0009100~glycoprotein metabolic process,GO:0009101~glycoprotein biosynthetic process,GO:0043413~biopolymer glycosylation,GO:0070085~glycosylation, GO:0005794~Golgi apparatus,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0008378~galactosyltransferase activity,GO:0008499~UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity,GO:0035250~UDP-galactosyltransferase activity,GO:0048531~beta-1,3-galactosyltransferase activity, IPR002659:Glycosyl transferase, family 31, complete proteome,glycosyltransferase,golgi apparatus,membrane,transferase,transmembrane,

1623693_a_at Dmel_CG3365 Drosophila melanogaster GO:0032012~regulation of ARF protein signal transduction,GO:0032312~regulation of ARF GTPase activity,GO:0032318~regulation of Ras GTPase activity,GO:0043087~regulation of GTPase activity,GO:0046578~regulation of Ras protein signal transduction,GO:0051056~regulation of small GTPase mediated signal transduction,GO:0051336~regulation of hydrolase activity, GO:0005083~small GTPase regulator activity,GO:0005096~GTPase activator activity,GO:0008047~enzyme activator activity,GO:0008060~ARF GTPase activator activity,GO:0008270~zinc ion binding,GO:0030695~GTPase regulator activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,GO:0060589~nucleoside-triphosphatase regulator activity, IPR001164:Arf GTPase activating protein, SM00105:ArfGap, complete proteome,

1627270_at Dmel_CG42240 Drosophila melanogaster complete proteome,

1630280_s_at Dmel_CG42353; Dmel_CG42354 Drosophila melanogaster complete proteome,

1634869_at Dmel_CG4581 Drosophila melanogaster GO:0006631~fatty acid metabolic process,GO:0006635~fatty acid beta-oxidation,GO:0009062~fatty acid catabolic process,GO:0016042~lipid catabolic process,GO:0016054~organic acid catabolic process,GO:0019395~fatty acid oxidation,GO:0030258~lipid modification,GO:0034440~lipid oxidation,GO:0044242~cellular lipid catabolic process,GO:0046395~carboxylic acid catabolic process,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0005811~lipid particle,GO:0016507~fatty acid beta-oxidation multienzyme complex,GO:0031974~membrane-enclosed lumen,GO:0031980~mitochondrial lumen,GO:0043233~organelle lumen,GO:0044429~mitochondrial part,GO:0070013~intracellular organelle lumen, GO:0003988~acetyl-CoA C-acyltransferase activity,GO:0016408~C-acyltransferase activity,GO:0016509~long-chain-3-hydroxyacyl-CoA dehydrogenase activity, IPR002155:Thiolase,IPR016038:Thiolase-like, subgroup, dme00062:Fatty acid elongation in mitochondria,dme00071:Fatty acid metabolism,dme00280:Valine, leucine and isoleucine degradation, PIRSF000429:Ac-CoA_Ac_transf, Acyltransferase,complete proteome,oxidoreductase,transferase,

1635202_s_at Dmel_CG5640 Drosophila melanogaster IPR001440:Tetratricopeptide TPR-1,IPR003347:Transcription factor jumonji/aspartyl beta-hydroxylase,IPR011990:Tetratricopeptide-like helical,IPR013026:Tetratricopeptide region,IPR013129:Transcription factor jumonji,IPR019734:Tetratricopeptide repeat, SM00028:TPR,SM00558:JmjC, complete proteome,repeat,tpr repeat,

1633965_at Dmel_CG6020 Drosophila melanogaster GO:0006091~generation of precursor metabolites and energy,GO:0006119~oxidative phosphorylation,GO:0006120~mitochondrial electron transport, NADH to ubiquinone,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0015980~energy derivation by oxidation of organic compounds,GO:0016310~phosphorylation,GO:0022900~electron transport chain,GO:0022904~respiratory electron transport chain,GO:0042773~ATP synthesis coupled electron transport,GO:0042775~mitochondrial ATP synthesis coupled electron transport,GO:0045333~cellular respiration,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005740~mitochondrial envelope,GO:0005743~mitochondrial inner membrane,GO:0005746~mitochondrial respiratory chain,GO:0005747~mitochondrial respiratory chain complex I,GO:0019866~organelle inner membrane,GO:0030964~NADH

dehydrogenase complex,GO:0031090~organelle membrane,GO:0031966~mitochondrial membrane,GO:0031967~organelle envelope,GO:0031975~envelope
,GO:0044429~mitochondrial part,GO:0044455~mitochondrial membrane part,GO:0045271~respiratory chain complex I,GO:0070469~respiratory chain,
GO:0003954~NADH dehydrogenase activity,GO:0008137~NADH dehydrogenase (ubiquinone) activity,GO:0016651~oxidoreductase activity, acting on NADH or
NADPH,GO:0016655~oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor,GO:0048037~cofactor binding,GO:0050136~NADH
dehydrogenase (quinone) activity,GO:0050662~coenzyme binding, IPR001509:NAD-dependent epimerase/dehydratase,IPR016040:NAD(P)-binding domain,
dme00190:Oxidative phosphorylation, complete proteome,oxidoreductase,
1636423_at Dmel_CG8012 Drosophila melanogaster complete proteome,
1636591_at Dmel_CG8881 Drosophila melanogaster Posttranslational modification, protein turnover, chaperones,
GO:0006508~proteolysis,GO:0006511~ubiquitin-dependent protein catabolic process,GO:0009057~macromolecule catabolic process,GO:0019941~modification-
dependent protein catabolic process,GO:0030163~protein catabolic process,GO:0043632~modification-dependent macromolecule catabolic process,GO:0044257~cellular protein
catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051603~proteolysis involved in cellular protein catabolic process, IPR001232:SKP1
component,IPR011333:BTB/POZ fold,IPR016072:SKP1 component, dimerisation,IPR016073:SKP1 component, POZ,IPR016897:E3 ubiquitin ligase, SCF complex, Skp subunit,
dme04120:Ubiquitin mediated proteolysis,dme04310:Wnt signaling pathway,dme04350:TGF-beta signaling pathway, PIRSF028729:E3_ubiquit_lig_SCF_Skp,
SM00512:Skp1, complete proteome,
1638727_at Dmel_CG9821 Drosophila melanogaster complete proteome,
1629839_a_at G protein gamma 1Drosophila melanogaster GO:0007010~cytoskeleton organization,GO:0007015~actin filament organization,GO:0007155~cell
adhesion,GO:0007166~cell surface receptor linked signal transduction,GO:0007186~G-protein coupled receptor protein signaling pathway,GO:0007405~neuroblast
proliferation,GO:0007507~heart development,GO:0007584~response to nutrient,GO:0007610~behavior,GO:0007635~chemosensory behavior,GO:0007637~proboscis extension
reflex,GO:0008104~protein localization,GO:0008105~asymmetric protein localization,GO:0008283~cell proliferation,GO:0008360~regulation of cell shape,GO:0009991~response to
extracellular stimulus,GO:0017145~stem cell division,GO:0022604~regulation of cell morphogenesis,GO:0022610~biological adhesion,GO:0030029~actin filament-based
process,GO:0030036~actin cytoskeleton organization,GO:0031667~response to nutrient levels,GO:0035050~embryonic heart tube development,GO:0035295~tube

development,GO:0045165~cell fate commitment,GO:0045176~apical protein localization,GO:0048103~somatic stem cell division,GO:0051301~cell division,GO:0051780~behavioral response to nutrient,GO:0055057~neuroblast division,GO:0055059~asymmetric neuroblast division,GO:0060004~reflex, GO:0005834~heterotrimeric G-protein complex,GO:0005886~plasma membrane,GO:0009898~internal side of plasma membrane,GO:0019897~extrinsic to plasma membrane,GO:0019898~extrinsic to membrane,GO:0044459~plasma membrane part, GO:0003924~GTPase activity, IPR001770:G-protein, gamma subunit,IPR015898:G-protein, gamma-like subunit, PIRSF002398:GTP-binding regulatory protein gamma chain, SM00224:GGL, cell membrane,complete proteome,GTP binding,lipoprotein,membrane,methylated carboxyl end,methylation,prenylated cysteine,prenylation,transducer, chain:Guanine nucleotide-binding protein subunit gamma-1,lipid moiety-binding region:S-geranylgeranyl cysteine,modified residue,propeptide:Removed in mature form,

1624042_at G protein-coupled receptor kinase 2 Drosophila melanogaster GO:0006468~protein amino acid phosphorylation,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0007166~cell surface receptor linked signal transduction,GO:0007186~G-protein coupled receptor protein signaling pathway,GO:0007224~smoothened signaling pathway,GO:0007276~gamete generation,GO:0007292~female gamete generation,GO:0008277~regulation of G-protein coupled receptor protein signaling pathway,GO:0016310~phosphorylation,GO:0019953~sexual reproduction,GO:0032504~multicellular organism reproduction,GO:0048477~oogenesis,GO:0048609~reproductive process in a multicellular organism, GO:0005886~plasma membrane, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0004672~protein kinase activity,GO:0004674~protein serine/threonine kinase activity,GO:0004703~G-protein coupled receptor kinase activity,GO:0005524~ATP binding,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding, IPR000239:GPCR kinase,IPR000342:Regulator of G protein signalling,IPR000719:Protein kinase, core,IPR000961:AGC-kinase, C-terminal,IPR002290:Serine/threonine protein kinase,IPR008271:Serine/threonine protein kinase, active site,IPR017441:Protein kinase, ATP binding site,IPR017442:Serine/threonine protein kinase-related, dme04144:Endocytosis, SM00133:S_TK_X,SM00220:S_TKc,SM00315:RGS, ATP,atp-binding,complete proteome,developmental protein,differentiation,kinase,membrane,nucleotide-binding,oogenesis,phosphoprotein,phosphotransferase,repeat,serine/threonine-protein kinase,serine/threonine-specific protein kinase,transferase, active site:Proton acceptor,binding site:ATP,chain:G protein-coupled receptor kinase 2,compositionally biased region:Asn-rich,domain:AGC-kinase C-terminal,domain:Protein kinase,domain:RGS 1,domain:RGS 2,modified residue,nucleotide phosphate-binding region:ATP,region of interest:N-terminal,sequence conflict, 1634707_s_at Glutamine:fructose-6-phosphate aminotransferase 1 Drosophila melanogaster Cell envelope biogenesis, outer membrane, GO:0016051~carbohydrate biosynthetic process, GO:0004360~glutamine-fructose-6-phosphate transaminase (isomerizing) activity,GO:0005529~sugar binding,GO:0008483~transaminase activity,GO:0016769~transferase activity, transferring nitrogenous groups,GO:0030246~carbohydrate binding, IPR000583:Glutamine amidotransferase, class-II,IPR001347:Sugar isomerase (SIS),IPR005855:Glucosamine-fructose-6-phosphate aminotransferase, isomerising,IPR017932:Glutamine amidotransferase, type II, dme00250:Alanine, aspartate and glutamate metabolism,dme00520:Amino sugar and nucleotide sugar metabolism, Aminotransferase,complete proteome,transferase,

1626566_at Probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial Drosophila melanogaster Lipid metabolism, GO:0006631~fatty acid metabolic process,GO:0006635~fatty acid beta-oxidation,GO:0009062~fatty acid catabolic process,GO:0016042~lipid catabolic process,GO:0016054~organic acid catabolic process,GO:0019395~fatty acid oxidation,GO:0030258~lipid modification,GO:0034440~lipid oxidation,GO:0044242~cellular lipid catabolic process,GO:0046395~carboxylic acid catabolic process,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0005811~lipid particle,GO:0031974~membrane-enclosed lumen,GO:0031980~mitochondrial lumen,GO:0043233~organelle lumen,GO:0044429~mitochondrial part,GO:0070013~intracellular organelle lumen, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0003995~acyl-CoA dehydrogenase activity,GO:0009055~electron carrier activity,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding ,GO:0048037~cofactor binding,GO:0050660~FAD binding,GO:0050662~coenzyme binding, IPR006089:Acyl-CoA dehydrogenase, conserved site,IPR006090:Acyl-CoA oxidase/dehydrogenase, type 1,IPR006091:Acyl-CoA oxidase/dehydrogenase, central region,IPR006092:Acyl-CoA dehydrogenase, N-terminal,IPR013764:Acyl-CoA oxidase/dehydrogenase, type1/2, C-terminal,IPR013786:Acyl-CoA dehydrogenase/oxidase, N-terminal, dme00071:Fatty acid metabolism,dme00280:Valine, leucine and isoleucine degradation,dme00410:beta-Alanine metabolism,dme00640:Propanoate metabolism, PIRSF000182:acyl-CoA dehydrogenase, complete proteome,FAD,fatty acid metabolism,Flavoprotein,lipid metabolism,mitochondrion,oxidoreductase,transit peptide, active site:Proton acceptor,binding site:Substrate; via amide nitrogen,binding site:Substrate; via carbonyl oxygen,chain:Probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial,nucleotide phosphate-binding region:FAD,region of interest:Substrate binding,transit peptide:Mitochondrion, 1638186_a_at Protein fem-1 homolog B Drosophila melanogaster GO:0006508~proteolysis,GO:0009057~macromolecule catabolic process,GO:0019941~modification-dependent protein catabolic process,GO:0030163~protein catabolic process,GO:0031396~regulation of protein ubiquitination,GO:0031399~regulation of protein modification process,GO:0032268~regulation of cellular protein metabolic process,GO:0043632~modification-dependent macromolecule catabolic process,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051340~regulation of ligase activity,GO:0051438~regulation of ubiquitin-protein ligase activity,GO:0051603~proteolysis involved in cellular protein catabolic process, GO:0004842~ubiquitin-protein ligase activity,GO:0016879~ligase activity, forming carbon-nitrogen bonds,GO:0016881~acid-amino acid ligase activity,GO:0019787~small conjugating protein ligase activity, IPR002110:Ankyrin, SM00248:ANK, alternative splicing,ank repeat,complete proteome,repeat,ubl conjug ation pathway, chain:Protein fem-1 homolog B,repeat:ANK 1,repeat:ANK 2,repeat:ANK 3,repeat:ANK 4,repeat:ANK 5,repeat:ANK 6,repeat:ANK 7,splice variant,

1627376_at Relish Drosophila melanogaster GO:0002684~positive regulation of immune system process,GO:0002697~regulation of immune effector process,GO:0002700~regulation of production of molecular mediator of immune response,GO:0002759~regulation of antimicrobial humoral response,GO:0002784~regulation of antimicrobial peptide production,GO:0002786~regulation of antibacterial peptide production,GO:0002788~regulation of antifungal peptide production,GO:0002805~regulation of antimicrobial peptide biosynthetic process,GO:0002807~positive regulation of antimicrobial peptide biosynthetic process,GO:0002808~regulation of antibacterial peptide biosynthetic process,GO:0002810~regulation of antifungal peptide biosynthetic process,GO:0002813~regulation of biosynthetic process of antibacterial peptides active against Gram-negative bacteria,GO:0002831~regulation of response to biotic stimulus,GO:0002920~regulation of humoral immune response,GO:0006350~transcription,GO:0006355~regulation of transcription, DNA-dependent,GO: 0006357~regulation of transcription from RNA polymerase II promoter,GO:0006952~defense response,GO:0006955~immune response,GO:0006959~humoral immune response,GO:0006963~positive regulation of antibacterial peptide biosynthetic process,GO:0006964~positive regulation of biosynthetic process of antibacterial peptides active against Gram-negative bacteria,GO:0006967~positive regulation of antifungal peptide biosynthetic process,GO:0007166~cell surface receptor linked signal transduction,GO:0008063~Toll signaling pathway,GO:0009267~cellular response to starvation,GO:0009617~response to bacterium,GO:0009891~positive regulation of biosynthetic process,GO:0009991~response to extracellular stimulus,GO:0010551~regulation of specific transcription from RNA polymerase II promoter,GO:0010552~positive regulation of specific transcription from RNA polymerase II promoter,GO:0010557~positive regulation of macromolecule biosynthetic process,GO:0010604~positive regulation of macromolecule metabolic process,GO:0010628~positive regulation of gene

			expression,GO:0019730~antimicrobial humoral response,GO:0031328~positive regulation of cellular biosynthetic process,GO:0031349~positive regulation of defense response,GO:0031667~response to nutrient levels,GO:0031668~cellular response to extracellular stimulus,GO:0031669~cellular response to nutrient levels,GO:0032583~regulation of gene-specific transcription,GO:0033554~cellular response to stress,GO:0034198~cellular response to amino acid starvation,GO:0042594~response to starvation,GO:0042742~defense response to bacterium,GO:0043193~positive regulation of gene-specific transcription,GO:0043900~regulation of multi-organism process,GO:0045087~innate immune response,GO:0045088~regulation of innate immune response,GO:0045089~positive regulation of innate immune response,GO:0045428~regulation of nitric oxide biosynthetic process,GO:0045429~positive regulation of nitric oxide biosynthetic process,GO:0045449~regulation of transcription,GO:0045893~positive regulation of transcription, DNA-dependent,GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,GO:0045941~positive regulation of transcription,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0048584~positive regulation of response to stimulus,GO:0050778~positive regulation of immune response,GO:0050829~defense response to Gram-negative bacterium,GO:0051173~positive regulation of nitrogen compound metabolic process,GO:0051252~regulation of RNA metabolic process,GO:0051254~positive regulation of RNA metabolic process,	GO:0003677~DNA binding,GO:0003700~transcription factor activity,GO:0030528~transcription regulator activity,	IPR000451:NF-kappa-B/Rel/dorsal,IPR002110:Ankyrin,IPR002909:Cell surface receptor IPT/TIG,IPR011539:Rel homology,IPR013783:Immunoglobulin-like fold,	SM00248:ANK,SM00429:IPT,	activator,alternative splicing,ank repeat,complete proteome,cytoplasm,direct protein sequencing,immune response,innate immunity,nucleus,phosphoprotein,repeat,Transcription,transcription regulation,	chain:Nuclear factor NF-kappa-B p110 subunit,chain:Nuclear factor NF-kappa-B p49 subunit,chain:Nuclear factor NF-kappa-B p68 subunit,domain:RHD,modified residue,mutagenesis site,repeat:ANK 1,repeat:ANK 2,repeat:ANK 3,repeat:ANK 4,repeat:ANK 5,sequence conflict,sequence variant,short sequence motif:Nuclear localization signal,site:Cleavage (when cotranslationally processed),splice variant,
1629357_s_at	SNF1A/AMP-activated protein kinase	Drosophila melanogaster	GO:0000278~mitotic cell cycle,GO:0000902~cell morphogenesis,GO:0006468~protein amino acid phosphorylation,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0007049~cell cycle,GO:0007163~establishment or maintenance of cell polarity,GO:0010324~membrane invagination,GO:0016044~membrane organization,GO:0016192~vesicle-mediated transport,GO:0016310~phosphorylation,GO:0032989~cellular component morphogenesis,GO:0035088~establishment or maintenance of apical/basal cell polarity,GO:0045197~establishment or maintenance of epithelial cell apical/basal					

polarity, GO:0031588~AMP-activated protein kinase complex, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0004672~protein kinase activity,GO:0004674~protein serine/threonine kinase activity,GO:0004679~AMP-activated protein kinase activity,GO:0004703~G-protein coupled receptor kinase activity,GO:0005524~ATP binding,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding, IPR000719:Protein kinase, core,IPR002290:Serine/threonine protein kinase,IPR008271:Serine/threonine protein kinase, active site,IPR015741:Snf1-like protein AMPK,IPR017441:Protein kinase, ATP binding site,IPR017442:Serine/threonine protein kinase-related, dme04140:Regulation of autophagy,dme04150:mTOR signaling pathway, PIRSF000590:Snf1/AMPK-type protein kinases, catalytic subunits, SM00220:S_TKc, atp-binding,complete proteome,kinase,nucleotide-binding,serine/threonine-protein kinase,transferase,

1625433_at Sarcoplasmic calcium-binding protein 1 Drosophila melanogaster GO:0005783~endoplasmic reticulum,GO:0016528~sarcoplasm,GO:0016529~sarcoplasmic reticulum, GO:0005509~calcium ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding, IPR002048:Calcium-binding EF-hand,IPR011992:EF-Hand type,IPR018247:EF-HAND 1,IPR018248:EF hand,IPR018249:EF-HAND 2, SM00054:EFh, calcium,

1638050_s_at Sox box protein 14 Drosophila melanogaster GO:0006350~transcription,GO:0045449~regulation of transcription, GO:0003677~DNA binding,GO:0003700~transcription factor activity,GO:0030528~transcription regulator activity, IPR000910:High mobility group, HMG1/HMG2, SM00398:HMG, complete proteome,DNA binding,dna-binding,nucleus,Transcription,transcription regulation, chain:Putative transcription factor SOX-14,compositionally biased region:Poly-Ala,compositionally biased region:Poly-Asn,DNA-binding region:HMG box,sequence conflict,

1639321_s_at Toll Drosophila melanogaster Function unknown,GO:0000578~embryonic axis specification,GO:0000910~cytokinesis,GO:0002520~immune system development,GO:0002697~regulation of immune effector process,GO:0002700~regulation of production of molecular mediator of immune response,GO:0002759~regulation of antimicrobial humoral response,GO:0002784~regulation of antimicrobial peptide production,GO:0002786~regulation of antibacterial peptide production,GO:0002788~regulation of antifungal peptide production,GO:0002805~regulation of antimicrobial peptide biosynthetic process,GO:0002807~positive regulation of antimicrobial peptide biosynthetic process,GO:0002808~regulation of antibacterial peptide biosynthetic process,GO:0002810~regulation of antifungal peptide biosynthetic process,GO:0002831~regulation of response to biotic stimulus,GO:0002920~regulation of humoral immune response,GO:0003002~regionalization,GO:0006952~defense response,GO:0006955~immune

			response,GO:0006959~humoral immune response,GO:0006963~positive regulation of antibacterial peptide biosynthetic process,GO:0006967~positive regulation of antifungal peptide biosynthetic process,GO:0007155~cell adhesion,GO:0007166~cell surface receptor linked signal transduction,GO:0007352~zygotic determination of dorsal/ventral axis,GO:0007389~pattern specification process,GO:0007416~synaptogenesis,GO:0008063~Toll signaling pathway,GO:0008283~cell proliferation,GO:0009617~response to bacterium,GO:0009620~response to fungus,GO:0009798~axis specification,GO:0009880~embryonic pattern specification,GO:0009891~positive regulation of biosynthetic process,GO:0009950~dorsal/ventral axis specification,GO:0009953~dorsal/ventral pattern formation,GO:0019730~antimicrobial humoral response,GO:0019732~antifungal humoral response,GO:0022610~biological adhesion,GO:0030097~hemopoiesis,GO:0031328~positive regulation of cellular biosynthetic process,GO:0035007~regulation of melanization defense response,GO:0035172~hemocyte proliferation,GO:0042742~defense response to bacterium,GO:0043062~extracellular structure organization,GO:0043455~regulation of secondary metabolic process,GO:0043900~regulation of multi-organism process,GO:0045087~innate immune response,GO:0045088~regulation of innate immune response,GO:0045610~regulation of hemocyte differentiation,GO:0048534~hemopoietic or lymphoid organ development,GO:0050808~synapse organization,GO:0050830~defense response to Gram-positive bacterium,GO:0050832~defense response to fungus,GO:0051301~cell division, GO:0005886~plasma membrane,GO:0005887~integral to plasma membrane,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0031226~intrinsic to plasma membrane,GO:0044459~plasma membrane part, GO:0019955~cytokine binding,GO:0042802~identical protein binding, IPR000157:Toll-Interleukin receptor,IPR000372:Leucine-rich repeat, cysteine-rich flanking region, N-terminal,IPR000483:Cysteine-rich flanking region, C-terminal,IPR001611:Leucine-rich repeat,IPR003591:Leucine-rich repeat, typical subtype,IPR004075:Interleukin-1 receptor, type I/Toll precursor, SM00013:LRRNT,SM00082:LRRCT,SM00255:TIR,SM00369:LRR_TYP, cell adhesion,cell membrane,complete proteome,developmental protein,disulfide bond,glycoprotein,leucine-rich repeat,membrane,polymorphism,repeat,signal,transmembrane,transmembrane protein, chain:Protein toll,domain:TIR,glycosylation site:N-linked (GlcNAc...),repeat:LRR 1,repeat:LRR 10,repeat:LRR 11,repeat:LRR 12,repeat:LRR 13,repeat:LRR 14,repeat:LRR 15,repeat:LRR 16,repeat:LRR 17,repeat:LRR 18,repeat:LRR 19,repeat:LRR 2,repeat:LRR 20,repeat:LRR 21,repeat:LRR 3,repeat:LRR 4,repeat:LRR 5,repeat:LRR 6,repeat:LRR 7,repeat:LRR 8,repeat:LRR 9,sequence conflict,sequence variant,signal peptide,topological domain:Cytoplasmic,topological domain:Extracellular,transmembrane region,
1629843_s_at	Ubiquitin carrier protein	Drosophila melanogaster	GO:0006508~proteolysis,GO:0009057~macromolecule catabolic process,GO:0016567~protein ubiquitination,GO:0019941~modification-dependent protein catabolic process,GO:0030163~protein catabolic process,GO:0032446~protein modification by small protein

conjugation,GO:0043632~modification-dependent macromolecule catabolic process,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051603~proteolysis involved in cellular protein catabolic process,GO:0070647~protein modification by small protein conjugation or removal,

GO:0004842~ubiquitin-protein ligase activity,GO:0016879~ligase activity, forming carbon-nitrogen bonds,GO:0016881~acid-amino acid ligase activity,GO:0019787~small conjugating protein ligase activity, IPR000608:Ubiquitin-conjugating enzyme, E2,IPR015581:Ubiquitin-conjugating enzyme,IPR016135:Ubiquitin-conjugating enzyme/RWD-like,

dme04120:Ubiquitin mediated proteolysis, SM00212:UBCc, complete proteome,ligase,ubl conjugation pathway,

1640754_at brummer Drosophila melanogaster GO:0006638~neutral lipid metabolic process,GO:0006639~acylglycerol metabolic process,GO:0006641~triglyceride metabolic process,GO:0006642~triglyceride mobilization,GO:0006662~glycerol ether metabolic process,GO:0007568~aging,GO:0008340~determination of adult life span,GO:0010259~multicellular organismal aging,GO:0016042~lipid catabolic process,GO:0018904~organic ether metabolic process,GO:0019433~triglyceride catabolic process,GO:0044242~cellular lipid catabolic process,GO:0044269~glycerol ether catabolic process,GO:0046461~neutral lipid catabolic process,GO:0046464~acylglycerol catabolic process,GO:0046486~glycerolipid metabolic process,GO:0046503~glycerolipid catabolic process, GO:0005811~lipid particle, GO:0004091~carboxylesterase activity,GO:0004806~triacylglycerol lipase activity,GO:0016298~lipase activity, IPR002641:Patatin, complete proteome,hydrolase,lipid degradation,

1635619_a_at centrosomin Drosophila melanogaster GO:0000087~M phase of mitotic cell cycle,GO:0000226~microtubule cytoskeleton organization,GO:0000278~mitotic cell cycle,GO:0000279~M phase,GO:0000280~nuclear division,GO:0007010~cytoskeleton organization,GO:0007017~microtubule-based process,GO:0007049~cell cycle,GO:0007051~spindle organization,GO:0007052~mitotic spindle organization,GO:0007059~chromosome segregation,GO:0007067~mitosis,GO:0007098~centrosome cycle,GO:0007126~meiosis,GO:0007143~female meiosis,GO:0007422~peripheral nervous system development,GO:0007494~midgut development,GO:0016321~female meiosis chromosome segregation,GO:0022402~cell cycle process,GO:0022403~cell cycle phase,GO:0031023~microtubule organizing center organization,GO:0045132~meiotic chromosome segregation,GO:0048285~organelle fission,GO:0048565~gut development,GO:0051297~centrosome organization,GO:0051301~cell division,GO:0051321~meiotic cell cycle,GO:0051327~M phase of meiotic cell cycle,

GO:0000242~pericentriolar material,GO:0005813~centrosome,GO:0005815~microtubule organizing center,GO:0005856~cytoskeleton,GO:0005875~microtubule associated complex,GO:0005929~cilium,GO:0005932~microtubule basal body,GO:0015629~actin cytoskeleton,GO:0015630~microtubule cytoskeleton,GO:0016459~myosin complex,GO:0019861~flagellum,GO:0042995~cell projection,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0044430~cytoskeletal part,GO:0044450~microtubule organizing center part,GO:0044463~cell projection part, GO:0008017~microtubule binding,GO:0008092~cytoskeletal protein binding,GO:0015631~tubulin binding,GO:0016887~ATPase activity,GO:0042624~ATPase activity, uncoupled, IPR012943:Spindle associated, alternative splicing,cell cycle,cell division,cell projection,cilium,coiled coil,complete proteome,cytoplasm,cytoskeleton,developmental protein,flagellum,hydrolase,leucine zipper,meiosis,mitosis,phosphoprotein, chain:Centrosomin,modified residue,sequence conflict,short sequence motif:Nuclear localization signal,splice variant,

1631243_s_at lethal (3) 05822 Drosophila melanogaster IPR000108:Neutrophil cytosol factor 2,IPR001452:Src homology-3 domain, SM00326:SH3, complete proteome,sh3 domain,

1627651_a_at locomotion defectsDrosophila melanogaster GO:0000902~cell morphogenesis,GO:0001885~endothelial cell development,GO:0002009~morphogenesis of an epithelium,GO:0002064~epithelial cell development,GO:0003002~regionalization,GO:0003006~reproductive developmental process,GO:0007010~cytoskeleton organization,GO:0007043~cell-cell junction assembly,GO:0007163~establishment or maintenance of cell polarity,GO:0007276~gamete generation,GO:0007292~female gamete generation,GO:0007300~ovarian nurse cell to oocyte transport,GO:0007303~cytoplasmic transport, nurse cell to oocyte,GO:0007389~pattern specification process,GO:0007405~neuroblast proliferation,GO:0007419~ventral cord development,GO:0008069~dorsal/ventral axis specification, ovarian follicular epithelium,GO:0008104~protein localization,GO:0008105~asymmetric protein localization,GO:0008277~regulation of G-protein coupled receptor protein signaling pathway,GO:0008283~cell proliferation,GO:0009798~axis specification,GO:0009950~dorsal/ventral axis specification,GO:0009953~dorsal/ventral pattern formation,GO:0010001~glial cell differentiation,GO:0014045~establishment of endothelial blood-brain barrier,GO:0016333~morphogenesis of follicular epithelium,GO:0016334~establishment or maintenance of polarity of follicular epithelium,GO:0016482~cytoplasmic transport,GO:0017145~stem cell division,GO:0019953~sexual reproduction,GO:0019991~septate junction assembly,GO:0021782~glial cell development,GO:0030029~actin filament-based process,GO:0030036~actin cytoskeleton organization,GO:0030707~ovarian follicle cell development,GO:0030855~epithelial cell differentiation,GO:0030865~cortical cytoskeleton organization,GO:0030866~cortical actin cytoskeleton organization,GO:0032504~multicellular organism reproduction,GO:0032989~cellular component morphogenesis,GO:0034329~cell junction assembly,GO:0034330~cell junction organization,GO:0042063~gliogenesis,GO:0043297~apical junction assembly,GO:0045165~cell fate commitment,GO:0045216~cell-cell junction organization,GO:0045446~endot helial cell differentiation,GO:0046907~intracellular transport,GO:0048103~somatic stem cell division,GO:0048477~oogenesis,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process,GO:0048729~tissue morphogenesis,GO:0051301~cell division,GO:0055057~neuroblast division,GO:0055059~asymmetric neuroblast division,GO:0060429~epithelium development,

GO:0005886~plasma membrane,GO:0005938~cell cortex,GO:0044448~cell cortex part,GO:0045177~apical part of cell,GO:0045179~apical cortex, GO:0001965~G-protein alpha-subunit binding,GO:0005096~GTPase activator activity,GO:0008047~enzyme activator activity,GO:0030695~GTPase regulator activity,GO:0060589~nucleoside-triphosphatase regulator activity, IPR000342:Regulator of G protein signalling,IPR001478:PDZ/DHR/GLGF,IPR003109:GoLoco motif,IPR003116:Raf-like Ras-binding,IPR006020:Phosphotyrosine interaction region, SM00228:PDZ,SM00315:RGS,SM00390:GoLoco,SM00455:RBD,SM00462:PTB, complete proteome,

1625830_a_at scruin like at the midline Drosophila melanogaster IPR006652:Kelch repeat type 1,IPR015915:Kelch-type beta propeller, SM00612:Kelch, complete proteome,

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+D

C

-D

Probe sets:

1625199_s_at 1633654_s_at 1634814_at 1638325_at 1638875_at

Functional annotation table:

-D C +D

ID	Gene Name	Species	GOTERM_BP_FAT	GOTERM_CC_FAT	GOTERM_MF_FAT	INTERPRO	KEGG_PATHWAY	PIR_SUPERFAMILY	SP_PIR_KEYWORDS	UP_SEQ_FEATURE
1638875_at	Egg-derived tyrosine phosphatase	Drosophila melanogaster	GO:0006470~protein amino acid dephosphorylation,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0016311~dephosphorylation,		GO:0004721~phosphoprotein phosphatase activity,GO:0004725~protein tyrosine phosphatase activity,GO:0016791~phosphatase activity,	IPR016130:Protein-tyrosine phosphatase, active site,			complete proteome,hydrolase,	
1638325_at	Henna	Drosophila melanogaster	GO:0006558~L-phenylalanine metabolic process,GO:0006559~L-phenylalanine catabolic process,GO:0006575~cellular amino acid derivative metabolic process,GO:0006576~biogenic amine metabolic process,GO:0006586~indolalkylamine metabolic process,GO:0006726~eye pigment biosynthetic process,GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0009063~cellular amino acid catabolic process,GO:0009072~aromatic amino acid family metabolic process,GO:0009074~aromatic amino acid family catabolic process,GO:0009309~amine biosynthetic process,GO:0009310~amine catabolic process,GO:0010324~membrane invagination,GO:0016044~membrane organization,GO:0016054~organic acid catabolic process,GO:0016192~vesicle-mediated transport,GO:0018130~heterocycle biosynthetic process,GO:0019439~aromatic compound catabolic process,GO:0042398~cellular amino acid derivative biosynthetic process,GO:0042401~biogenic amine biosynthetic process,GO:0042427~serotonin biosynthetic process,GO:0042428~serotonin metabolic process,GO:0042430~indole and derivative metabolic process,GO:0042434~indole derivative metabolic process,GO:0042435~indole derivative biosynthetic process,GO:0042440~pigment metabolic process,GO:0042441~eye pigment metabolic process,GO:0043473~pigmentation,GO:0044271~nitrogen compound biosynthetic process,GO:0046148~pigment biosynthetic process,GO:0046219~indolalkylamine biosynthetic process,GO:0046395~carboxylic acid catabolic process,GO:0048066~pigmentation during development,GO:0048069~eye pigmentation,GO:0055114~oxidation reduction,	GO:0005811~lipid particle,	GO:0004505~phenylalanine 4-monooxygenase activity,GO:0004510~tryptophan 5-monooxygenase activity,GO:0005506~iron ion binding,GO:0016597~amino acid binding,GO:0016714~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced pteridine as one donor, and incorporation of one atom of oxygen,GO:0031406~carboxylic acid binding,GO:0043167~ion binding,GO:0043169~cation					

binding,GO:0043176~amine binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR001273:Aromatic amino acid hydroxylase,IPR002912:Amino acid-binding ACT,IPR005961:Phenylalanine-4-hydroxylase, tetrameric form,IPR018301:Aromatic amino acid hydroxylase, iron/copper binding site,IPR019773:Tyrosine 3-monooxygenase-like,IPR019774:Aromatic amino acid hydroxylase, C-terminal, dme00360:Phenylalanine metabolism,dme00400:Phenylalanine, tyrosine and tryptophan biosynthesis, PIRSF000336:TH,PIRSF000336:tyrosine 3-monooxygenase, allosteric enzyme,biopterin,complete proteome,iron,metal-binding,metalloprotein,Monooxygenase,oxidoreductase,phenylalanine catabolism,phenylketonuria,phosphoprotein,serotonin biosynthesis, chain:Protein henna,domain:ACT,metal ion-binding site:Iron,modified residue,sequence conflict,

1633654_s_at Inositol 1,4,5-triphosphate kinase 2 Drosophila melanogaster GO:0006020~inositol metabolic process,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0016310~phosphorylation,GO:0019751~polyol metabolic process,GO:0046835~carbohydrate phosphorylation,GO:0046853~inositol and derivative phosphorylation, GO:0004428~inositol or phosphatidylinositol kinase activity,GO:0005516~calmodulin binding,GO:0008440~inositol trisphosphate 3-kinase activity,GO:0048306~calcium-dependent protein binding,GO:0051766~inositol trisphosphate kinase activity, IPR005522:Inositol polyphosphate kinase, dme00562:Inositol phosphate metabolism,dme04070:Phosphatidylinositol signaling system, complete proteome,kinase,transferase,

1634814_at UPF0183 protein CG7083 Drosophila melanogaster IPR005373:Uncharacterised protein family UPF0183, PIRSF015809:hypothetical protein, Caenorhabditis elegans T01G9.2b type, complete proteome, chain:UPF0183 protein CG7083,

1625199_s_at dacapo Drosophila melanogaster GO:0000079~regulation of cyclin-dependent protein kinase activity,GO:0000082~G1/S transition of mitotic cell cycle,GO:0000278~mitotic cell cycle,GO:0001709~cell fate determination,GO:0002165~instar larval or pupal development,GO:0003006~reproductive developmental process,GO:0007049~cell cycle,GO:0007050~cell cycle arrest,GO:0007090~regulation of S phase of mitotic cell cycle,GO:0007276~gamete generation,GO:0007292~female gamete generation,GO:0007293~germarium-derived egg chamber formation,GO:0007294~germarium-derived oocyte fate determination,GO:0007346~regulation of mitotic cell cycle,GO:0007423~sensory organ development,GO:0007424~open tracheal system development,GO:0007444~imaginal disc development,GO:0007488~histoblast morphogenesis,GO:0007552~metamorphosis,GO:0007560~imaginal disc morphogenesis,GO:0008356~asymmetric cell division,GO:0009791~post-embryonic development,GO:0009886~post-embryonic morphogenesis,GO:0009994~oocyte differentiation,GO:0010563~negative regulation of phosphorus metabolic process,GO:0010564~regulation of cell cycle process,GO:0010605~negative regulation of macromolecule metabolic process,GO:0010948~negative regulation of cell cycle process,GO:0019220~regulation of phosphate metabolic process,GO:0019953~sexual reproduction,GO:0022402~cell cycle process,GO:0022403~cell cycle phase,GO:0030706~germarium-derived oocyte differentiation,GO:0030716~oocyte fate determination,GO:0031399~regulation of protein modification process,GO:0031400~negative regulation of protein modification process,GO:0032268~regulation of cellular protein metabolic process,GO:0032269~negative regulation of cellular protein metabolic process,GO:0032504~multicellular organism reproduction,GO:0033261~regulation of S phase,GO:0035303~regulation of dephosphorylation,GO:0035304~regulation of protein amino acid dephosphorylation,GO:0035305~negative regulation of dephosphorylation,GO:0035308~negative regulation of protein amino acid dephosphorylation,GO:0042325~regulation of phosphorylation,GO:0043549~regulation of kinase activity,GO:0045035~sensory organ precursor cell division,GO:0045165~cell fate commitment,GO:0045749~negative regulation of S phase of mitotic cell cycle,GO:0045786~negative regulation of cell cycle,GO:0045859~regulation of protein kinase activity,GO:0045930~negative regulation of mitotic cell cycle,GO:0045936~negative regulation of phosphate metabolic process,GO:0048477~oogenesis,GO:0048563~post-embryonic organ morphogenesis,GO:0048569~post-embryonic organ development,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process,GO:0048707~instar larval or pupal morphogenesis,GO:0051174~regulation of phosphorus metabolic process,GO:0051248~negative regulation of protein metabolic process,GO:0051301~cell division,GO:0051318~G1 phase,GO:0051325~interphase,GO:0051329~interphase of mitotic cell cycle,GO:0051338~regulation of transferase activity,GO:0051726~regulation of cell cycle,GO:0060541~respiratory system development, GO:0004857~enzyme inhibitor activity,GO:0004860~protein kinase inhibitor activity,GO:0004861~cyclin-dependent protein kinase inhibitor activity,GO:0016538~cyclin-dependent protein kinase regulator activity,GO:0019207~kinase regulator activity,GO:0019210~kinase inhibitor activity,GO:0019887~protein kinase regulator activity,GO:0030291~protein serine/threonine kinase inhibitor activity, IPR003175:Cyclin-dependent kinase inhibitor,

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-D

C

+D

Probe sets:

1625519_at
1628429_at
1632834_a_at
1639762_at
1628194_at
1635065_at
1635491_s_at
1636639_at

Functional annotation table:

ID	Gene Name	Species	GOTERM_BP_FAT	GOTERM_CC_FAT	GOTERM_MF_FAT	INTERPRO	KEGG_PATHWAY	PIR_SUPERFAMILY	SMART	SP_PIR_KEYWORDS	UP_SEQ_FEATURE
1635491_s_at	Dmel_CG11642	Drosophila melanogaster	GO:0006605~protein targeting,GO:0006612~protein targeting to membrane,GO:0006613~cotranslational protein targeting to membrane,GO:0006614~SRP-dependent cotranslational protein targeting to membrane,GO:0006886~intracellular protein transport,GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0008104~protein localization,GO:0010324~membrane invagination,GO:0015031~protein transport,GO:0016044~membrane organization,GO:0016192~vesicle-mediated transport,GO:0033365~protein localization in organelle,GO:0034613~cellular protein localization,GO:0045047~protein targeting to ER,GO:0045184~establishment of protein localization,GO:0046907~intracellular transport,GO:0070727~cellular macromolecule localization,	GO:0005783~endoplasmic reticulum,GO:0005811~lipid particle,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,		IPR006634:TRAM, LAG1 and CLN8 homology,IPR013599:TRAM1-like protein,IPR016447:Translocation associated membrane protein,		PIRSF005449:translocation associated membrane protein,PIRSF005449:Translocation_assoc_membrane,	SM00724:TLC,	membrane,transmembrane,	

1628194_at	Dmel_CG2918	Drosophila melanogaster	GO:0006457~protein folding,	GO:0005811~lipid particle,	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0005524~ATP binding,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding,	IPR001023:Heat shock protein Hsp70,IPR013126:Heat shock protein 70,IPR018181:Heat shock protein 70, conserved site,				atp-binding,complete proteome,nucleotide-binding,
1639762_at	Dmel_CG3734	Drosophila melanogaster	GO:0006508~proteolysis,		GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides,	IPR008758:Peptidase S28,		PIRSF016539:Lysosomal Pro-X carboxypeptidase / Dipeptidyl-peptidase 2,		complete proteome,
1632834_a_at	Dmel_CG5946	Drosophila melanogaster	GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0010324~membrane invagination,GO:0016044~membrane organization,GO:0016192~vesicle-mediated transport,GO:0055114~oxidation reduction,		GO:0004128~cytochrome-b5 reductase activity,GO:0009055~electron carrier activity,GO:0016651~oxidoreductase activity, acting on NADH or NADPH,GO:0016653~oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor,	IPR001433:Oxidoreductase FAD/NAD(P)-binding,IPR001709:Flavoprotein pyridine nucleotide cytochrome reductase,IPR001834:NADH:cytochrome b5 reductase (CBR),IPR008333:Oxidoreductase FAD-binding region,IPR017927:Ferredoxin reductase-type FAD-binding domain,	dme00520:Amino sugar and nucleotide sugar metabolism,	PIRSF000206:cytochrome-b5 reductase,		complete proteome,FAD,Flavoprotein,nad,oxidoreductase,
1625519_at	Dmel_CG6453	Drosophila melanogaster		GO:0005783~endoplasmic reticulum,GO:0017177~alpha-glucosidase II complex,GO:0044432~endoplasmic reticulum part,	GO:0004558~alpha-glucosidase activity,GO:0015926~glucosidase activity,	IPR002172:Low density lipoprotein-receptor, class A, cysteine-rich,IPR012913:Glucosidase II beta subunit-like,IPR018247:EF-HAND 1,		PIRSF017177:uncharacterized conserved protein,	SM00192:LDLa,	complete proteome,glycosidase,hydrolase,
1635065_at	Dmel_CG7025	Drosophila melanogaster	GO:0006508~proteolysis,		GO:0004180~carboxypeptidase activity,GO:0004181~metallocarboxypeptidase activity,GO:0008233~peptidase activity,GO:0008235~metalloexopeptidase activity,GO:0008237~metallopeptidase activity,GO:0008238~exopeptidase activity,GO:0008270~zinc ion					

binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR000834:Peptidase M14, carboxypeptidase A, SM00631:Zn_pept, carboxypeptidase,complete proteome,hydrolase,

1628429_at Protein transport protein Sec61 gamma-2 subunit Drosophila melanogaster GO:0006605~protein targeting,GO:0006612~protein targeting to membrane,GO:0006613~cotranslational protein targeting to membrane,GO:0006614~SRP-dependent cotranslational protein targeting to membrane,GO:0006616~SRP-dependent cotranslational protein targeting to membrane, translocation,GO:0006886~intracellular protein transport,GO:0007033~vacuole organization,GO:0007040~lysosome organization,GO:0008104~protein localization,GO:0009894~regulation of catabolic process,GO:0009895~negative regulation of catabolic process,GO:0010506~regulation of autophagy,GO:0010507~negative regulation of autophagy,GO:0015031~protein transport,GO:0031329~regulation of cellular catabolic process,GO:0031330~negative regulation of cellular catabolic process,GO:0033365~protein localization in organelle,GO:0034613~cellular protein localization,GO:0045047~protein targeting to ER,GO:0045184~establishment of protein localization,GO:0046907~intracellular transport,GO:0055085~transmembrane transport,GO:0065002~intracellular protein transmembrane transport,GO:0070727~cellular macromolecule localization, GO:0005783~endoplasmic reticulum,GO:0005784~translocon complex,GO:0005789~endoplasmic reticulum membrane,GO:0005791~rough endoplasmic reticulum,GO:0012505~endomembrane system,GO:0016021~integral to membrane,GO:0030176~integral to endoplasmic reticulum membrane,GO:0030867~rough endoplasmic reticulum membrane,GO:0031090~organelle membrane,GO:0031224~intrinsic to membrane,GO:0031227~intrinsic to endoplasmic reticulum membrane,GO:0031300~intrinsic to organelle membrane,GO:0031301~integral to organelle membrane,GO:0042175~nuclear envelope-endoplasmic reticulum network,GO:0044432~endoplasmic reticulum part, GO:0008320~protein transmembrane transporter activity,GO:0008565~protein transporter activity,GO:0015399~primary active transmembrane transporter activity,GO:0015405~P-P-bond-hydrolysis-driven transmembrane transporter activity,GO:0015450~P-P-bond-hydrolysis-driven protein transmembrane transporter activity,GO:0022884~macromolecule transmembrane transporter activity, IPR001901:Protein secE/sec61-gamma protein,IPR008158:Protein translocase SEC61 complex gamma subunit, PIRSF005525:preprotein translocase Sec, SecE/Sec61-gamma subunit,PIRSF500209:preprotein translocase Sec, Sec61-gamma subunit, complete proteome,endoplasmic reticulum,membrane,protein transport,translocation,transmembrane,transport, chain:Protein transport protein Sec61 gamma-2 subunit,topological domain:Cytoplasmic,topological domain:Extracellular,transmembrane region,

1636639_at	Signal peptide protease	Drosophila melanogaster	GO:0006508~proteolysis,GO:0007424~open tracheal system development,GO:0009057~macromolecule catabolic process,GO:0030163~protein catabolic process,GO:0033619~membrane protein proteolysis,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051603~proteolysis involved in cellular protein catabolic process,GO:0060541~respiratory system development,	GO:0005783~endoplasmic reticulum,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,	GO:0004175~endopeptidase activity,GO:0004190~aspartic-type endopeptidase activity,GO:0008233~peptidase activity,GO:0042500~aspartic endopeptidase activity, intramembrane cleaving,GO:0070001~aspartic-type peptidase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides,	IPR006639:Peptidase A22, presenilin signal peptide,IPR007369:Peptidase A22B, signal peptide peptidase,	SM00730:PSN,	complete proteome,hydrolase,Protease,