

Table S3 The gene ontology (GO) terms for the RBPs and Translational Factors that are required for dendrite morphogenesis in *Drosophila* da neurons were found by searching The Gene Ontology website (www.geneontology.org database release May 26, 2012). The GO terms are categorized as Biological Process, Cellular Component, and Molecular Function.

CG	Gene Name	Biological Process	Cellular Component	Molecular Function
CG1873	<i>Ef1a100E</i>	GO:0022008 : neurogenesis GO:0006412 : translation GO:0006414 : translational elongation	GO:0005737 : cytoplasm GO:0005853 : eukaryotic translation elongation factor 1 complex GO:0005811 : lipid particle	GO:0005525 : GTP binding GO:0003924 : GTPase activity GO:0003746 : translation elongation factor activity
CG3056	<i>ssx</i>			GO:0003729 : mRNA binding GO:0000166 : nucleotide binding GO:0003723 : RNA binding
CG3249	<i>spoon (yu)</i>	GO:0007298 : border follicle cell migration GO:0060269 : centripetally migrating follicle cell migration GO:0051276 : chromosome organization GO:0046843 : dorsal appendage formation GO:0008069 : dorsal/ventral axis specification, ovarian follicular epithelium GO:0008298 : intracellular mRNA localization GO:0007616 : long-term memory GO:0008070 : maternal determination of dorsal/ventral axis, ovarian follicular epithelium, germ-line encoded GO:0030837 : negative regulation of actin filament polymerization GO:0008104 : protein localization GO:0006403 : RNA localization GO:0006099 : tricarboxylic acid cycle	GO:0005794 : Golgi apparatus GO:0005739 : mitochondrion	GO:0051018 : protein kinase A binding GO:0003723 : RNA binding
CG3582	<i>U2af38</i>	GO:0007052 : mitotic spindle organization GO:0000398 : nuclear mRNA splicing, via spliceosome GO:0000381 : regulation of alternative nuclear mRNA splicing, via spliceosome GO:0008380 : RNA splicing	GO:0005634 : nucleus GO:0071011 : precatalytic spliceosome GO:0005681 : spliceosomal complex GO:0005686 : U2 snRNP	GO:0003729 : mRNA binding GO:0000166 : nucleotide binding GO:0008187 : poly-pyrimidine tract binding GO:0008270 : zinc ion binding
CG3806	<i>eIF2B-ε</i>	GO:0016070 : RNA metabolic process	GO:0005829 : cytosol	GO:0005085 : guanyl-nucleotide exchange factor activity

		GO:0006413 : translational initiation	GO:0005851 : eukaryotic translation initiation factor 2B complex	GO:0016779 : nucleotidyltransferase activity GO:0003743 : translation initiation factor activity
CG4119		GO:0000398 : nuclear mRNA splicing, via spliceosome GO:0000381 : regulation of alternative nuclear mRNA splicing, via spliceosome	GO:0005634 : nucleus GO:0071011 : precatalytic spliceosome	GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding
CG4152	<i>l(2)35Df</i>	GO:0022008 : neurogenesis GO:0000398 : nuclear mRNA splicing, via spliceosome	GO:0071013 : catalytic step 2 spliceosome	GO:0005524 : ATP binding GO:0004004 : ATP-dependent RNA helicase activity GO:0003676 : nucleic acid binding
CG4153	<i>eIF-2β</i>	GO:0016199 : axon midline choice point recognition GO:0001677 : formation of translation initiation ternary complex GO:0000022 : mitotic spindle elongation GO:0007052 : mitotic spindle organization GO:0006413 : translational initiation	GO:0005829 : cytosol GO:0005850 : eukaryotic translation initiation factor 2 complex GO:0005875 : microtubule associated complex	GO:0005525 : GTP binding GO:0003743 : translation initiation factor activity GO:0000049 : tRNA binding
CG4262	<i>elav</i>	GO:0007417 : central nervous system development GO:0031441 : negative regulation of mRNA 3'-end processing GO:0007399 : nervous system development GO:0016070 : RNA metabolic process	GO:0015030 : Cajal body GO:0005634 : nucleus	GO:0003729 : mRNA binding GO:0000166 : nucleotide binding GO:0008266 : poly(U) RNA binding GO:0003723 : RNA binding
CG4396	<i>fine</i>	GO:0051252 : regulation of RNA metabolic process	GO:0005737 : cytoplasm	GO:0003729 : mRNA binding GO:0000166 : nucleotide binding GO:0008266 : poly(U) RNA binding
CG4528	<i>snf</i>	GO:0019099 : female germ-line sex determination GO:0000398 : nuclear mRNA splicing, via spliceosome GO:0048477 : oogenesis GO:0007539 : primary sex determination, soma	GO:0071013 : catalytic step 2 spliceosome GO:0005634 : nucleus GO:0071011 : precatalytic spliceosome GO:0043234 : protein complex	GO:0003729 : mRNA binding GO:0000166 : nucleotide binding GO:0005515 : protein binding GO:0035614 : snRNA stem-loop binding

		GO:0000381 : regulation of alternative nuclear mRNA splicing, via spliceosome GO:0008380 : RNA splicing	GO:0030532 : small nuclear ribonucleoprotein complex GO:0005681 : spliceosomal complex GO:0005685 : U1 snRNP GO:0005692 : U11 snRNP GO:0005686 : U2 snRNP	GO:0030619 : U1 snRNA binding GO:0030620 : U2 snRNA binding
CG4602	<i>Srp54</i>	GO:0006376 : mRNA splice site selection GO:0022008 : neurogenesis GO:0000398 : nuclear mRNA splicing, via spliceosome GO:0000381 : regulation of alternative nuclear mRNA splicing, via spliceosome	GO:0071013 : catalytic step 2 spliceosome GO:0005634 : nucleus GO:0071011 : precatalytic spliceosome GO:0005681 : spliceosomal complex	GO:0003729 : mRNA binding GO:0000166 : nucleotide binding GO:0008187 : poly-pyrimidine tract binding
CG4792	<i>Dcr-1</i>	GO:0048813 : dendrite morphogenesis GO:0033227 : dsRNA transport GO:0035195 : gene silencing by miRNA GO:0042078 : germ-line stem cell division GO:0045448 : mitotic cell cycle, embryonic GO:0007279 : pole cell formation GO:0031054 : pre-miRNA processing GO:0035196 : production of miRNAs involved in gene silencing by miRNA GO:0030422 : production of siRNA involved in RNA interference GO:0016246 : RNA interference GO:0007367 : segment polarity determination GO:0035087 : siRNA loading onto RISC involved in RNA interference	GO:0005737 : cytoplasm GO:0005634 : nucleus GO:0016442 : RNA-induced silencing complex	GO:0005524 : ATP binding GO:0016443 : bidentate ribonuclease III activity GO:0003725 : double-stranded RNA binding GO:0004386 : helicase activity GO:0005515 : protein binding
CG4878	<i>eIF3-S9</i>	GO:0006413 : translational initiation	GO:0005829 : cytosol GO:0005852 : eukaryotic translation initiation factor 3 complex	GO:0003729 : mRNA binding GO:0000166 : nucleotide binding GO:0003743 : translation initiation factor activity
CG4886	<i>cyp33</i>	GO:0000398 : nuclear mRNA splicing, via spliceosome GO:0006911 : phagocytosis, engulfment GO:0006457 : protein folding	GO:0071013 : catalytic step 2 spliceosome GO:0005634 : nucleus GO:0071011 : precatalytic spliceosome	GO:0003729 : mRNA binding GO:0000166 : nucleotide binding GO:0003755 : peptidyl-prolyl cis-trans isomerase activity

				GO:0003723 : RNA binding
CG4887		GO:0000398 : nuclear mRNA splicing, via spliceosome	GO:0071011 : precatalytic spliceosome	GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding GO:0008270 : zinc ion binding
CG4912	<i>eEF1β</i>	GO:0006414 : translational elongation	GO:0005853 : eukaryotic translation elongation factor 1 complex GO:0005875 : microtubule associated complex	GO:0005085 : guanyl-nucleotide exchange factor activity GO:0003746 : translation elongation factor activity
CG4954	<i>eIF3-S8</i>	GO:0006413 : translational initiation	GO:0005829 : cytosol GO:0005852 : eukaryotic translation initiation factor 3 complex	GO:0003743 : translation initiation factor activity
CG5168				GO:0046872 : metal ion binding
CG5263	<i>smg</i>	GO:0051236 : establishment of RNA localization GO:0017148 : negative regulation of translation GO:0000289 : nuclear-transcribed mRNA poly(A) tail shortening GO:0043488 : regulation of mRNA stability	GO:0005737 : cytoplasm GO:0000932 : cytoplasmic mRNA processing body	GO:0003730 : mRNA 3'-UTR binding GO:0003729 : mRNA binding GO:0005515 : protein binding GO:0030371 : translation repressor activity GO:0000900 : translation repressor activity, nucleic acid binding
CG5439		GO:0007154 : cell communication		GO:0035091 : phosphatidylinositol binding
CG5589				GO:0005524 : ATP binding GO:0004004 : ATP-dependent RNA helicase activity GO:0003729 : mRNA binding
CG5605	<i>eRF1</i>	GO:0048102 : autophagic cell death GO:0006605 : protein targeting GO:0035071 : salivary gland cell autophagic cell death GO:0007224 : smoothed signaling pathway GO:0006415 : translational termination	GO:0005737 : cytoplasm GO:0005829 : cytosol GO:0018444 : translation release factor complex	GO:0003747 : translation release factor activity GO:0016149 : translation release factor activity, codon specific GO:0008079 : translation termination factor activity

CG5637	<i>nos</i>	<p>GO:0008595 : anterior/posterior axis specification, embryo</p> <p>GO:0001709 : cell fate determination</p> <p>GO:0048813 : dendrite morphogenesis</p> <p>GO:0016321 : female meiosis chromosome segregation</p> <p>GO:0007281 : germ cell development</p> <p>GO:0008354 : germ cell migration</p> <p>GO:0048134 : germ-line cyst formation</p> <p>GO:0042078 : germ-line stem cell division</p> <p>GO:0030718 : germ-line stem cell maintenance</p> <p>GO:0006378 : mRNA polyadenylation</p> <p>GO:0043066 : negative regulation of apoptotic process</p> <p>GO:0045892 : negative regulation of transcription, DNA-dependent</p> <p>GO:0017148 : negative regulation of translation</p> <p>GO:0007314 : oocyte anterior/posterior axis specification</p> <p>GO:0048477 : oogenesis</p> <p>GO:0007280 : pole cell migration</p> <p>GO:0035282 : segmentation</p> <p>GO:0007283 : spermatogenesis</p>	GO:0045495 : pole plasm	<p>GO:0005515 : protein binding</p> <p>GO:0003723 : RNA binding</p> <p>GO:0008270 : zinc ion binding</p>
CG5705		GO:0006415 : translational termination	GO:0005739 : mitochondrion	GO:0016149 : translation release factor activity, codon specific
CG5800		<p>GO:0007526 : larval somatic muscle development</p> <p>GO:0022008 : neurogenesis</p>		<p>GO:0005524 : ATP binding</p> <p>GO:0008026 : ATP-dependent helicase activity</p> <p>GO:0003676 : nucleic acid binding</p> <p>GO:0003724 : RNA helicase activity</p>
CG6341	<i>Ef1β</i>	GO:0006414 : translational elongation	<p>GO:0005829 : cytosol</p> <p>GO:0005853 : eukaryotic translation elongation factor 1 complex</p> <p>GO:0005811 : lipid particle</p>	<p>GO:0005085 : guanyl-nucleotide exchange factor activity</p> <p>GO:0003746 : translation elongation factor activity</p> <p>GO:0003747 : translation release factor activity</p>
CG6375	<i>pit</i>		<p>GO:0005730 : nucleolus</p> <p>GO:0005634 : nucleus</p>	<p>GO:0005524 : ATP binding</p> <p>GO:0004004 : ATP-dependent RNA helicase activity</p>

				GO:0003724 : RNA helicase activity GO:0003676 : nucleic acid binding
CG6412	<i>mtEF-Ts</i>	GO:0006414 : translational elongation	GO:0005739 : mitochondrion	GO:0003746 : translation elongation factor activity
CG6418				GO:0005524 : ATP binding GO:0004004 : ATP-dependent RNA helicase activity GO:0004386 : helicase activity GO:0003676 : nucleic acid binding
CG6493	<i>Dcr-2</i>	GO:0006342 : chromatin silencing GO:0051607 : defense response to virus GO:0009597 : detection of virus GO:0033227 : dsRNA transport GO:0070868 : heterochromatin organization involved in chromatin silencing GO:0007626 : locomotory behavior GO:0006379 : mRNA cleavage GO:0031054 : pre-miRNA processing GO:0030422 : production of siRNA involved in RNA interference GO:0016246 : RNA interference GO:0035087 : siRNA loading onto RISC involved in RNA interference GO:0030423 : targeting of mRNA for destruction involved in RNA interference	GO:0005737 : cytoplasm GO:0005634 : nucleus GO:0016442 : RNA-induced silencing complex	GO:0005524 : ATP binding GO:0008026 : ATP-dependent helicase activity GO:0016887 : ATPase activity GO:0003725 : double-stranded RNA binding GO:0004386 : helicase activity GO:0004525 : ribonuclease III activity GO:0035197 : siRNA binding
CG6539	<i>Gem3</i>	GO:0007528 : neuromuscular junction development GO:0022618 : ribonucleoprotein complex assembly	GO:0015030 : Cajal body GO:0005737 : cytoplasm GO:0071254 : cytoplasmic U snRNP body	GO:0005524 : ATP binding GO:0004004 : ATP-dependent RNA helicase activity GO:0003676 : nucleic acid binding GO:0003724 : RNA helicase activity
CG6779	<i>RpS3</i>	GO:0006281 : DNA repair GO:0007067 : mitosis	GO:0005737 : cytoplasm GO:0022627 : cytosolic small ribosomal subunit	GO:0003906 : DNA-(apurinic or apyrimidinic site) lyase activity GO:0008534 : oxidized purine base lesion DNA N-glycosylase activity

		GO:0043524 : negative regulation of neuron apoptotic process GO:0006974 : response to DNA damage stimulus GO:0006412 : translation	GO:0005811 : lipid particle GO:0005875 : microtubule associated complex GO:0016363 : nuclear matrix GO:0005634 : nucleus GO:0005840 : ribosome	GO:0003723 : RNA binding GO:0003735 : structural constituent of ribosome
CG6866	<i>loqs</i>	GO:0007417 : central nervous system development GO:0048132 : female germ-line stem cell division GO:0030718 : germ-line stem cell maintenance GO:0010586 : miRNA metabolic process GO:0031054 : pre-miRNA processing GO:0030422 : production of siRNA involved in RNA interference GO:0070918 : production of small RNA involved in gene silencing by RNA GO:0070920 : regulation of production of small RNA involved in gene silencing by RNA	GO:0005737 : cytoplasm	GO:0003725 : double-stranded RNA binding GO:0005515 : protein binding
CG6946	<i>glo</i>	GO:0051276 : chromosome organization GO:0060810 : intracellular mRNA localization involved in pattern specification process GO:0007311 : maternal specification of dorsal/ventral axis, oocyte, germ-line encoded GO:0048477 : oogenesis GO:0045451 : pole plasm oskar mRNA localization GO:0006417 : regulation of translation	GO:0043234 : protein complex	GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding GO:0005515 : protein binding
CG6961				GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding
CG6987	<i>SF2</i>	GO:0007095 : mitotic cell cycle G2/M transition DNA damage checkpoint GO:0006376 : mRNA splice site selection	GO:0071013 : catalytic step 2 spliceosome GO:0005634 : nucleus	GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding

		GO:0022008 : neurogenesis GO:0000398 : nuclear mRNA splicing, via spliceosome	GO:0071011 : precatalytic spliceosome GO:0005681 : spliceosomal complex	GO:0000166 : nucleotide binding GO:0005515 : protein binding
CG7082	<i>papi</i>			GO:0003723 : RNA binding
CG7269	<i>hel25E</i>	GO:0007052 : mitotic spindle organization GO:0006406 : mRNA export from nucleus GO:0000398 : nuclear mRNA splicing, via spliceosome GO:0000381 : regulation of alternative nuclear mRNA splicing, via spliceosome	GO:0005875 : microtubule associated complex GO:0005634 : nucleus GO:0005681 : spliceosomal complex	GO:0005524 : ATP binding GO:0004004 : ATP-dependent RNA helicase activity GO:0003676 : nucleic acid binding GO:0003724 : RNA helicase activity
CG7903				GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding
CG8053	<i>eIF-1a</i>	GO:0000022 : mitotic spindle elongation GO:0007052 : mitotic spindle organization GO:0006911 : phagocytosis, engulfment GO:0007224 : smoothed signaling pathway GO:0006412 : translation GO:0006413 : translational initiation	GO:0005829 : cytosol GO:0016282 : eukaryotic 43S preinitiation complex	GO:0003743 : translation initiation factor activity
CG8190	<i>eIF2B-gamma</i>	GO:0071456 : cellular response to hypoxia GO:0006413 : translational initiation	GO:0005829 : cytosol GO:0005851 : eukaryotic translation initiation factor 2B complex	GO:0016779 : nucleotidyltransferase activity GO:0003743 : translation initiation factor activity
CG8205	<i>fus</i>	GO:0007173 : epidermal growth factor receptor signaling pathway		GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding
CG8280	<i>Ef1a48D</i>	GO:0008340 : determination of adult lifespan GO:0006412 : translation GO:0006414 : translational elongation	GO:0005737 : cytoplasm GO:0005829 : cytosol GO:0005853 : eukaryotic translation elongation factor 1 complex GO:0005811 : lipid particle GO:0005875 : microtubule associated complex	GO:0005525 : GTP binding GO:0003924 : GTPase activity GO:0003746 : translation elongation factor activity

CG8636	<i>eIF3-S4</i>	GO:0007067 : mitosis GO:0000022 : mitotic spindle elongation GO:0007052 : mitotic spindle organization GO:0006413 : translational initiation	GO:0005852 : eukaryotic translation initiation factor 3 complex	GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding GO:0003743 : translation initiation factor activity GO:0008270 : zinc ion binding
CG8730	<i>droscha</i>	GO:0022008 : neurogenesis GO:0031053 : primary miRNA processing GO:0016075 : rRNA catabolic process	GO:0005634 : nucleus	GO:0003725 : double-stranded RNA binding GO:0004525 : ribonuclease III activity
CG8882	<i>eIF3-S2 (Trip1)</i>	GO:0006412 : translation GO:0006413 : translational initiation	GO:0005829 : cytosol GO:0005852 : eukaryotic translation initiation factor 3 complex GO:0005875 : microtubule associated complex	GO:0003743 : translation initiation factor activity
CG9054	<i>Ddx1</i>	GO:0001700 : embryonic development via the syncytial blastoderm GO:0006446 : regulation of translational initiation GO:0042254 : ribosome biogenesis GO:0000245 : spliceosomal complex assembly	GO:0005575 : cellular_component	GO:0005524 : ATP binding GO:0008026 : ATP-dependent helicase activity GO:0004386 : helicase activity GO:0003676 : nucleic acid binding
CG9075	<i>eIF-4a</i>	GO:0051297 : centrosome organization GO:0006268 : DNA unwinding involved in replication GO:0009950 : dorsal/ventral axis specification GO:0048132 : female germ-line stem cell division GO:0030718 : germ-line stem cell maintenance GO:0007446 : imaginal disc growth GO:0002168 : instar larval development GO:0007067 : mitosis GO:0000022 : mitotic spindle elongation GO:0007052 : mitotic spindle organization GO:0048477 : oogenesis	GO:0005813 : centrosome GO:0005829 : cytosol GO:0016281 : eukaryotic translation initiation factor 4F complex GO:0005875 : microtubule associated complex GO:0072686 : mitotic spindle GO:0005634 : nucleus	GO:0005524 : ATP binding GO:0008026 : ATP-dependent helicase activity GO:0003729 : mRNA binding GO:0000339 : RNA cap binding GO:0003724 : RNA helicase activity GO:0017116 : single-stranded DNA-dependent ATP-dependent DNA helicase activity GO:0003743 : translation initiation factor activity

		GO:000381 : regulation of alternative nuclear mRNA splicing, via spliceosome GO:0006974 : response to DNA damage stimulus GO:0006413 : translational initiation		
<i>CG9107</i>				GO:0000166 : nucleotide binding
<i>CG9124</i>	<i>elf-3p40</i>	GO:0022008 : neurogenesis GO:0006413 : translational initiation	GO:0005829 : cytosol GO:0005852 : eukaryotic translation initiation factor 3 complex	GO:0003743 : translation initiation factor activity
<i>CG9218</i>	<i>sm</i>	GO:0008343 : adult feeding behavior GO:0007411 : axon guidance	GO:0030529 : ribonucleoprotein complex	GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding
<i>CG9373</i>	<i>rump</i>	GO:0008595 : anterior/posterior axis specification, embryo GO:0009952 : anterior/posterior pattern specification GO:0008298 : intracellular mRNA localization GO:0007067 : mitosis GO:0007277 : pole cell development GO:0045451 : pole plasm <i>oskar</i> mRNA localization GO:0035282 : segmentation	GO:0005737 : cytoplasm GO:0005634 : nucleus GO:0030529 : ribonucleoprotein complex	GO:0003730 : mRNA 3'-UTR binding GO:0003729 : mRNA binding GO:0000166 : nucleotide binding
<i>CG9412</i>	<i>rin</i>	GO:0001752 : compound eye photoreceptor fate commitment GO:0000398 : nuclear mRNA splicing, via spliceosome GO:0016318 : ommatidial rotation GO:0007265 : Ras protein signal transduction GO:0006810 : transport	GO:0071013 : catalytic step 2 spliceosome GO:0005829 : cytosol GO:0005811 : lipid particle GO:0071011 : precatalytic spliceosome	GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding GO:0017124 : SH3 domain binding
<i>CG9680</i>	<i>Dbp73D</i>	GO:0022008 : neurogenesis		GO:0005524 : ATP binding GO:0008026 : ATP-dependent helicase activity GO:0004004 : ATP-dependent RNA helicase activity
<i>CG9755</i>	<i>pum</i>	GO:0008595 : anterior/posterior axis specification, embryo GO:0001709 : cell fate determination	GO:0005737 : cytoplasm	GO:0003730 : mRNA 3'-UTR binding GO:0003723 : RNA binding

		<p>GO:0016477 : cell migration</p> <p>GO:0048813 : dendrite morphogenesis GO:0007281 : germ cell development GO:0042078 : germ-line stem cell division GO:0008258 : head involution GO:0007616 : long-term memory GO:0007067 : mitosis GO:0045786 : negative regulation of cell cycle GO:0042059 : negative regulation of epidermal growth factor receptor signaling pathway GO:0045892 : negative regulation of transcription, DNA-dependent GO:0017148 : negative regulation of translation GO:0000288 : nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay GO:0048477 : oogenesis GO:0007280 : pole cell migration GO:0045727 : positive regulation of translation GO:0008582 : regulation of synaptic growth at neuromuscular junction GO:0050804 : regulation of synaptic transmission GO:0007268 : synaptic transmission</p>		<p>GO:0000900 : translation repressor activity, nucleic acid binding</p>
CG9769	<i>eIF3-S5</i>	<p>GO:0048102 : autophagic cell death</p> <p>GO:0035071 : salivary gland cell autophagic cell death GO:0006413 : translational initiation</p>	<p>GO:0005852 : eukaryotic translation initiation factor 3 complex</p>	<p>GO:0003743 : translation initiation factor activity</p>
CG9809	<i>Spargel</i>	<p>GO:0008286 : insulin receptor signaling pathway GO:0046627 : negative regulation of insulin receptor signaling pathway GO:0010821 : regulation of mitochondrion organization</p>		<p>GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding</p>

		GO:0006355 : regulation of transcription, DNA-dependent		
CG9841	<i>Efsec</i>	GO:0006414 : translational elongation GO:0006451 : translational readthrough		GO:0005525 : GTP binding GO:0003924 : GTPase activity GO:0003746 : translation elongation factor activity
CG9946	<i>eIF-2α</i>	GO:0001677 : formation of translation initiation ternary complex GO:0000022 : mitotic spindle elongation GO:0007052 : mitotic spindle organization GO:0006413 : translational initiation	GO:0005829 : cytosol GO:0005850 : eukaryotic translation initiation factor 2 complex GO:0005851 : eukaryotic translation initiation factor 2B complex GO:0005875 : microtubule associated complex	GO:0005525 : GTP binding GO:0003743 : translation initiation factor activity GO:0000049 : tRNA binding
CG10084	<i>swm</i>	GO:0006397 : mRNA processing GO:0045879 : negative regulation of smoothed signaling pathway GO:0007346 : regulation of mitotic cell cycle	GO:0005634 : nucleus	GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding GO:0008270 : zinc ion binding
CG10124	<i>eIF4E-4</i>	GO:0006413 : translational initiation	GO:0016281 : eukaryotic translation initiation factor 4F complex	GO:0031370 : eukaryotic initiation factor 4G binding GO:0005515 : protein binding GO:0000340 : RNA 7-methylguanosine cap binding GO:0000339 : RNA cap binding GO:0003743 : translation initiation factor activity
CG10203	<i>x16</i>	GO:0006376 : mRNA splice site selection GO:0007399 : nervous system development GO:0000398 : nuclear mRNA splicing, via spliceosome GO:0008380 : RNA splicing	GO:0071013 : catalytic step 2 spliceosome GO:0005634 : nucleus GO:0071011 : precatalytic spliceosome GO:0005681 : spliceosomal complex	GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding GO:0005515 : protein binding GO:0003723 : RNA binding GO:0008270 : zinc ion binding
CG10315	<i>eIF2B-β</i>	GO:0022008 : neurogenesis GO:0006413 : translational initiation	GO:0005829 : cytosol GO:0005851 : eukaryotic translation initiation factor 2B complex	GO:0003743 : translation initiation factor activity
CG10466		GO:0000398 : nuclear mRNA splicing, via spliceosome	GO:0071013 : catalytic step 2 spliceosome	GO:0003729 : mRNA binding

			GO:0071011 : precatalytic spliceosome	GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding
CG10719	<i>brat</i>	GO:0008356 : asymmetric cell division GO:0055060 : asymmetric neuroblast division resulting in ganglion mother cell formation GO:0007411 : axon guidance GO:0007420 : brain development GO:0007402 : ganglion mother cell fate determination GO:0008285 : negative regulation of cell proliferation GO:0007406 : negative regulation of neuroblast proliferation GO:0007405 : neuroblast proliferation GO:0022008 : neurogenesis GO:0030182 : neuron differentiation GO:0048477 : oogenesis GO:0006911 : phagocytosis, engulfment GO:0051726 : regulation of cell cycle GO:0006417 : regulation of translation GO:0016072 : rRNA metabolic process GO:0009303 : rRNA transcription GO:0035282 : segmentation	GO:0035282 : segmentation GO:0045180 : basal cortex GO:0005737 : cytoplasm	GO:0005515 : protein binding GO:0045182 : translation regulator activity GO:0030371 : translation repressor activity GO:0008270 : zinc ion binding
CG10777				GO:0005524 : ATP binding GO:0008026 : ATP-dependent helicase activity GO:0003676 : nucleic acid binding GO:0003724 : RNA helicase activity
CG10868	<i>orb</i>	GO:0000578 : embryonic axis specification GO:0007281 : germ cell development GO:0048134 : germ-line cyst formation GO:0007294 : germarium-derived oocyte fate determination GO:0008298 : intracellular mRNA localization GO:0006378 : mRNA polyadenylation GO:0007314 : oocyte anterior/posterior axis specification	GO:0005737 : cytoplasm	GO:0003729 : mRNA binding GO:0000166 : nucleotide binding GO:0005515 : protein binding GO:0017131 : uridine-rich cytoplasmic polyadenylation element binding

		<p>GO:0007309 : oocyte axis specification GO:0007310 : oocyte dorsal/ventral axis specification GO:0048477 : oogenesis GO:0007315 : pole plasm assembly GO:0045451 : pole plasm oskar mRNA localization GO:0046012 : positive regulation of oskar mRNA translation GO:0045727 : positive regulation of translation GO:0046011 : regulation of oskar mRNA translation</p>		
CG10881	<i>eIF3-S4</i>	<p>GO:0006413 : translational initiation</p>	<p>GO:0005852 : eukaryotic translation initiation factor 3 complex</p>	<p>GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding GO:0003743 : translation initiation factor activity GO:0008270 : zinc ion binding</p>
CG10901	<i>osk</i>	<p>GO:0008595 : anterior/posterior axis specification, embryo GO:0007281 : germ cell development GO:0007616 : long-term memory GO:0046594 : maintenance of pole plasm mRNA location GO:0007314 : oocyte anterior/posterior axis specification GO:0008103 : oocyte microtubule cytoskeleton polarization GO:0048477 : oogenesis GO:0030719 : P granule organization GO:0007277 : pole cell development GO:0007278 : pole cell fate determination GO:0007279 : pole cell formation GO:0007315 : pole plasm assembly GO:0019094 : pole plasm mRNA localization GO:0007318 : pole plasm protein localization GO:0045727 : positive regulation of translation</p>	<p>GO:0043186 : P granule GO:0045495 : pole plasm</p>	<p>GO:0016787 : hydrolase activity</p>

		GO:0007359 : posterior abdomen determination GO:0043488 : regulation of mRNA stability GO:0046011 : regulation of oskar mRNA translation GO:0007632 : visual behavior GO:0008542 : visual learning		
CG11266		GO:0000398 : nuclear mRNA splicing, via spliceosome GO:0000381 : regulation of alternative nuclear mRNA splicing, via spliceosome GO:0008380 : RNA splicing	GO:0071013 : catalytic step 2 spliceosome GO:0005634 : nucleus GO:0071011 : precatalytic spliceosome GO:0005681 : spliceosomal complex	GO:0003729 : mRNA binding GO:0000166 : nucleotide binding GO:0003723 : RNA binding
CG11334		GO:0006412 : translation GO:0035220 : wing disc development	GO:0005851 : eukaryotic translation initiation factor 2B complex	GO:0045182 : translation regulator activity
CG11454				GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding
CG11505		GO:0008150 : biological_process	GO:0005575 : cellular_component	GO:0003676 : nucleic acid binding
CG11726				GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding
CG12493			GO:0005634 : nucleus	GO:0003725 : double-stranded RNA binding GO:0035197 : siRNA binding
CG13425	<i>bl</i>	GO:0035107 : appendage morphogenesis GO:0045165 : cell fate commitment GO:0008283 : cell proliferation GO:0007446 : imaginal disc growth GO:0000381 : regulation of alternative nuclear mRNA splicing, via spliceosome	GO:0000785 : chromatin GO:0005737 : cytoplasm GO:0005634 : nucleus GO:0035062 : omega speckle GO:0030529 : ribonucleoprotein complex	GO:0003729 : mRNA binding GO:0003723 : RNA binding GO:0008134 : transcription factor binding
CG14718			GO:0005622 : intracellular	GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding GO:0008270 : zinc ion binding
CG14891				GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding

CG16901	<i>sqd</i>	<p>GO:0008069 : dorsal/ventral axis specification, ovarian follicular epithelium</p> <p>GO:0009953 : dorsal/ventral pattern formation</p> <p>GO:0007293 : germarium-derived egg chamber formation</p> <p>GO:0008298 : intracellular mRNA localization</p> <p>GO:0006406 : mRNA export from nucleus</p> <p>GO:0033119 : negative regulation of RNA splicing</p> <p>GO:0017148 : negative regulation of translation</p> <p>GO:0000398 : nuclear mRNA splicing, via spliceosome</p> <p>GO:0000184 : nuclear-transcribed mRNA catabolic process, nonsense-mediated decay</p> <p>GO:0007314 : oocyte anterior/posterior axis specification</p> <p>GO:0030720 : oocyte localization involved in germarium-derived egg chamber formation</p> <p>GO:0016325 : oocyte microtubule cytoskeleton organization</p> <p>GO:0048477 : oogenesis</p> <p>GO:0007297 : ovarian follicle cell migration</p> <p>GO:0019094 : pole plasm mRNA localization</p> <p>GO:0045451 : pole plasm oskar mRNA localization</p> <p>GO:0000381 : regulation of alternative nuclear mRNA splicing, via spliceosome</p> <p>GO:0006405 : RNA export from nucleus</p>	<p>GO:0071013 : catalytic step 2 spliceosome</p> <p>GO:0000785 : chromatin</p> <p>GO:0005737 : cytoplasm</p> <p>GO:0005730 : nucleolus</p> <p>GO:0005634 : nucleus</p> <p>GO:0035062 : omega speckle</p> <p>GO:0005703 : polytene chromosome puff</p> <p>GO:0071011 : precatalytic spliceosome</p> <p>GO:0030529 : ribonucleoprotein complex</p>	<p>GO:0003730 : mRNA 3'-UTR binding</p> <p>GO:0003729 : mRNA binding</p> <p>GO:0003676 : nucleic acid binding</p> <p>GO:0000166 : nucleotide binding</p>
CG17492	<i>mib2</i>	<p>GO:0046716 : muscle cell homeostasis</p> <p>GO:0007520 : myoblast fusion</p> <p>GO:0016567 : protein ubiquitination</p>	<p>GO:0005737 : cytoplasm</p> <p>GO:0031430 : M band</p> <p>GO:0030018 : Z disc</p>	<p>GO:0032038 : myosin II heavy chain binding</p> <p>GO:0032033 : myosin II light chain binding</p> <p>GO:0004842 : ubiquitin-protein ligase activity</p> <p>GO:0008270 : zinc ion binding</p>
CG17686	<i>DIP1</i>		GO:0000785 : chromatin	GO:0003682 : chromatin binding

			GO:0005737 : cytoplasm GO:0005634 : nucleus	GO:0003725 : double-stranded RNA binding GO:0070883 : pre-miRNA binding GO:0005515 : protein binding
CG18259				GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding
CG31061	<i>Gr98d</i>	GO:0050909 : sensory perception of taste	GO:0016021 : integral to membrane	GO:0008527 : taste receptor activity
CG31762	<i>aret (bruno)</i>	GO:0007281 : germ cell development GO:0042078 : germ-line stem cell division GO:0030727 : germlarium-derived female germ-line cyst formation GO:0002121 : inter-male aggressive behavior GO:0006378 : mRNA polyadenylation GO:0007319 : negative regulation of oskar mRNA translation GO:0017148 : negative regulation of translation GO:0048477 : oogenesis GO:0031536 : positive regulation of exit from mitosis GO:0000381 : regulation of alternative nuclear mRNA splicing, via spliceosome GO:0046011 : regulation of oskar mRNA translation GO:0007286 : spermatid development	GO:0005634 : nucleus GO:0043186 : P granule	GO:0003730 : mRNA 3'-UTR binding GO:0003729 : mRNA binding GO:0000166 : nucleotide binding GO:0005515 : protein binding GO:0003723 : RNA binding
CG32423	<i>shep</i>	GO:0042332 : gravitaxis	GO:0005575 : cellular_component	GO:0003729 : mRNA binding GO:0000166 : nucleotide binding GO:0003723 : RNA binding
CG32706		GO:0008150 : biological_process	GO:0005575 : cellular_component	GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding
CG33100	<i>4EHP</i>	GO:0002121 : inter-male aggressive behavior GO:0017148 : negative regulation of translation GO:0022008 : neurogenesis GO:0006413 : translational initiation	GO:0016281 : eukaryotic translation initiation factor 4F complex	GO:0031370 : eukaryotic initiation factor 4G binding GO:0005515 : protein binding GO:0000340 : RNA 7-methylguanosine cap binding GO:0003743 : translation initiation factor activity GO:0030371 : translation repressor activity

CG33106	<i>mask</i>	<p>GO:0019730 : antimicrobial humoral response GO:0008283 : cell proliferation</p> <p>GO:0009987 : cellular process GO:0051298 : centrosome duplication GO:0001751 : compound eye photoreceptor cell differentiation GO:0007016 : cytoskeletal anchoring at plasma membrane GO:0007169 : transmembrane receptor protein tyrosine kinase signaling pathway</p>	GO:0005811 : lipid particle	<p>GO:0003723 : RNA binding</p> <p>GO:0005200 : structural constituent of cytoskeleton</p>
CG33197	<i>mbl</i>	<p>GO:0006915 : apoptotic process GO:0001751 : compound eye photoreceptor cell differentiation GO:0009790 : embryo development</p> <p>GO:0007517 : muscle organ development GO:0007422 : peripheral nervous system development GO:0045924 : regulation of female receptivity GO:0007525 : somatic muscle development</p>	<p>GO:0005737 : cytoplasm GO:0005634 : nucleus</p> <p>GO:0048471 : perinuclear region of cytoplasm</p>	<p>GO:0003677 : DNA binding GO:0003676 : nucleic acid binding</p> <p>GO:0008270 : zinc ion binding</p>
CG34354				<p>GO:0003729 : mRNA binding GO:0003676 : nucleic acid binding GO:0000166 : nucleotide binding</p>
CG40351	<i>Set1</i>	<p>GO:0006338 : chromatin remodeling</p> <p>GO:0051568 : histone H3-K4 methylation</p> <p>GO:0080182 : histone H3-K4 trimethylation</p>	<p>GO:0005634 : nucleus</p> <p>GO:0048188 : Set1C/COMPASS complex</p>	<p>GO:0042800 : histone methyltransferase activity (H3-K4 specific) GO:0018024 : histone-lysine N-methyltransferase activity GO:0003676 : nucleic acid binding</p> <p>GO:0000166 : nucleotide binding</p>